5'-most EST	LIB3156-010-Q1-K1-E6
Seq. No.	271352
Contig ID	32541_1.R1011
5'-most EST	LIB3156-010-Q1-K1-F1
Seq. No.	271353
Contig ID	32543_1.R1011
5'-most EST	xmt700260942.h1
Seq. No.	271354
Contig ID	32550_1.R1011
5'-most EST	bdu700383064.h1
Seq. No.	271355
Contig ID	32553_1.R1011
5'-most EST	vux700158310.h1
Seq. No.	271356
Contig ID	32553_2.R1011
5'-most EST	ntr700071665.h1
Method	BLASTX
NCBI GI	g4191788
BLAST score	303
E value	2.0e-27
Match length	133
% identity	44
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]
Seq. No.	271357
Contig ID	32553_3.R1011
5'-most EST	uC-zmf1b73359h06a2
Seq. No.	271358
Contig ID	32567_2.R1011
5'-most EST	xjt700092723.h1
Method	BLASTX
NCBI GI	g4185139
BLAST score	884
E value	4.0e-95
Match length	250
% identity	61
NCBI Description	(AC005724) putative diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.	271359
Contig ID	32576_1.R1011
5'-most EST	uC-zmroteosinte012g10b1
Method	BLASTX
NCBI GI	g3292832
BLAST score	167
E value	2.0e-11
Match length	77
% identity	53
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	271360
Contig ID	32578_1.R1011
5'-most EST	uC-zmflb73161e07b2
Method	BLASTX
NCBI GI	g4580513
BLAST score	1011
E value	1.0e-110
Match length	290
% identity	66
NCBI Description	(AF036300) scarecrow-like 1 [Arabidopsis thaliana]

Seq. No.	271361
Contig ID	32582_1.R1011
5'-most EST	LIB3067-045-Q1-K1-F1
Method	BLASTX
NCBI GI	g2352492
BLAST score	885
E value	3.0e-95
Match length	358
% identity	52
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	271362
Contig ID	32583_1.R1011
5'-most EST	ceu700429049.h1

Seq. No.	271363
Contig ID	32589_1.R1011
5'-most EST	LIB3062-039-Q1-K1-H12
Method	BLASTX
NCBI GI	g3395427
BLAST score	148
E value	7.0e-09
Match length	48
% identity	52
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	271364
Contig ID	32589_2.R1011
5'-most EST	uer700576710.h1
Method	BLASTX
NCBI GI	g3395427
BLAST score	158
E value	2.0e-10
Match length	54
% identity	56
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	271365
Contig ID	32604_1.R1011
5'-most EST	xsy700213061.h1

Seq. No.	271366
Contig ID	32606_1.R1011
5'-most EST	LIB3137-030-Q1-K1-D4

Seq. No.	271367
Contig ID	32606_2.R1011
5'-most EST	LIB3156-011-Q1-K1-F12

Seq. No.	271368
Contig ID	32609_1.R1011
5'-most EST	pmx700091661.h1
Method	BLASTX
NCBI GI	g1845195
BLAST score	217
E value	5.0e-17
Match length	78
% identity	50
NCBI Description	(Y08297) HMGc1 [Zea mays]

Seq. No.	271369
Contig ID	32609_2.R1011
5'-most EST	LIB3156-011-Q1-K1-F4

Seq. No.	271370
Contig ID	32616_1.R1011
5'-most EST	LIB3156-011-Q1-K1-H10

Seq. No.	271371
Contig ID	32628_1.R1011
5'-most EST	xyt700344434.h1
Method	BLASTX
NCBI GI	g3885340
BLAST score	473
E value	6.0e-70
Match length	249
% identity	59
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	271372
Contig ID	32629_1.R1011
5'-most EST	nbm700471001.h1
Method	BLASTX
NCBI GI	g1353239
BLAST score	863
E value	8.0e-93
Match length	264
% identity	61
NCBI Description	(U10245) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	271373
Contig ID	32630_1.R1011
5'-most EST	cyk700050676.f1
Method	BLASTX
NCBI GI	g4164408
BLAST score	277
E value	1.0e-24
Match length	96
% identity	49
NCBI Description	(AJ132228) amino acid carrier [Ricinus communis]

Seq. No.	271374
Contig ID	32637_1.R1011
5'-most EST	fC-zmst1700336546f1
Method	BLASTX
NCBI GI	g478809
BLAST score	308
E value	7.0e-28
Match length	152
% identity	44
NCBI Description	protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449) protein kinase [Glycine max] >gi_444789_prf__1908223A protein kinase [Glycine max]

Seq. No.	271375
Contig ID	32639_1.R1011
5'-most EST	LIB3156-012-Q1-K1-B7

Seq. No.	271376
Contig ID	32646_1.R1011
5'-most EST	vux700160107.h1

Seq. No.	271377
Contig ID	32657_1.R1011
5'-most EST	uC-zmflb73122h09b2
Method	BLASTX
NCBI GI	g3695059
BLAST score	454
E value	9.0e-45
Match length	157
% identity	59
NCBI Description	(AF064787) rac GTPase activating protein 1 [Lotus japonicus]

Seq. No.	271378
Contig ID	32660_1.R1011
5'-most EST	wen700336295.h1
Method	BLASTX
NCBI GI	g3461820
BLAST score	583
E value	8.0e-60
Match length	218
% identity	56
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	271379
Contig ID	32660_2.R1011
5'-most EST	uC-zmflb73028a02b1

Seq. No.	271380
Contig ID	32660_3.R1011
5'-most EST	uC-zmflb73028a07a1
Method	BLASTX
NCBI GI	g3461820
BLAST score	184
E value	1.0e-13
Match length	86
% identity	52

NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	271381
Contig ID	32661_2.R1011
5'-most EST	uC-zmroteosinte031c04b1
Method	BLASTX
NCBI GI	g2109293
BLAST score	824
E value	1.0e-101
Match length	265
% identity	71
NCBI Description	(U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	271382
Contig ID	32666_1.R1011
5'-most EST	qmh700028758.f1
Method	BLASTX
NCBI GI	g2735841
BLAST score	198
E value	2.0e-14
Match length	212
% identity	27
NCBI Description	(AF010283) No definition line found [Sorghum bicolor]

Seq. No.	271383
Contig ID	32666_2.R1011
5'-most EST	LIB3059-048-Q1-K1-A10

Seq. No.	271384
Contig ID	32667_2.R1011
5'-most EST	LIB3156-012-Q1-K1-E2

Seq. No.	271385
Contig ID	32679_1.R1011
5'-most EST	LIB3069-030-Q1-K1-C2
Method	BLASTX
NCBI GI	g1848225
BLAST score	281
E value	1.0e-24
Match length	62
% identity	76
NCBI Description	(U88090) nonspecific lipid transfer protein [Hordeum vulgare]

Seq. No.	271386
Contig ID	32680_1.R1011
5'-most EST	uC-zmflmo17335e03a1

Seq. No.	271387
Contig ID	32685_1.R1011
5'-most EST	pmx700087726.h1
Method	BLASTX
NCBI GI	g3445208
BLAST score	445
E value	5.0e-44
Match length	113

% identity	76
NCBI Description	(AC004786) putative amino-acid acetyltransferase [Arabidopsis thaliana]

Seq. No.	271388
Contig ID	32689_1.R1011
5'-most EST	wyr700241392.h1

Seq. No.	271389
Contig ID	32691_1.R1011
5'-most EST	nbm700476066.h1

Seq. No.	271390
Contig ID	32692_1.R1011
5'-most EST	LIB3156-012-Q1-K1-G6

Seq. No.	271391
Contig ID	32698_1.R1011
5'-most EST	cyk700051738.f1
Method	BLASTX
NCBI GI	g4325339
BLAST score	823
E value	5.0e-88
Match length	255
% identity	59
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	271392
Contig ID	32707_1.R1011
5'-most EST	uC-zmflb73166b07b2
Method	BLASTX
NCBI GI	g4503511
BLAST score	159
E value	2.0e-10
Match length	111
% identity	34
NCBI Description	UNKNOWN >gi_3264861 (U97670) eukaryotic translation initiation factor eIF3, p35 subunit [Homo sapiens]

Seq. No.	271393
Contig ID	32708_1.R1011
5'-most EST	zuv700354350.h1
Method	BLASTX
NCBI GI	g1174870
BLAST score	243
E value	2.0e-20
Match length	62
% identity	73
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN >gi_633685_emb_CAA55861_ (X79274) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	271394
Contig ID	32708_2.R1011
5'-most EST	hvj700620311.h1

Seq. No.	271395

Contig ID	32711_1.R1011
5'-most EST	LIB3156-013-Q1-K1-A4

Seq. No.	271396
Contig ID	32712_1.R1011
5'-most EST	uC-zmrob73077a03b1
Method	BLASTX
NCBI GI	g1762945
BLAST score	401
E value	1.0e-38
Match length	143
% identity	52
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	271397
Contig ID	32721_1.R1011
5'-most EST	uC-zmflb73040h06b1

Seq. No.	271398
Contig ID	32721_3.R1011
5'-most EST	uC-zmflmo17061g11b1

Seq. No.	271399
Contig ID	32721_5.R1011
5'-most EST	pmx700090703.h1

Seq. No.	271400
Contig ID	32728_1.R1011
5'-most EST	xyt700345438.h1
Method	BLASTX
NCBI GI	g2129552
BLAST score	1070
E value	1.0e-117
Match length	267
% identity	75
NCBI Description	calcium-dependent protein kinase 19 - Arabidopsis thaliana (fragment)

Seq. No.	271401
Contig ID	32739_1.R1011
5'-most EST	uC-zmflb73038f12b1

Seq. No.	271402
Contig ID	32739_2.R1011
5'-most EST	uC-zmroteosinte016a09b1

Seq. No.	271403
Contig ID	32743_1.R1011
5'-most EST	LIB3062-044-Q1-K1-C11
Method	BLASTX
NCBI GI	g3953478
BLAST score	440
E value	2.0e-43
Match length	203
% identity	48
NCBI Description	(AC002328) F22O2.23 [Arabidopsis thaliana]

Seq. No.	271404
Contig ID	32747_1.R1011
5'-most EST	LIB3156-013-Q1-K1-E3
Method	BLASTX
NCBI GI	g2982434
BLAST score	291
E value	7.0e-26
Match length	145
% identity	47
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	271405
Contig ID	32751_1.R1011
5'-most EST	uC-zmromo17080b04a1

Seq. No.	271406
Contig ID	32756_1.R1011
5'-most EST	uC-zmflmo17189g05a1

Seq. No.	271407
Contig ID	32764_1.R1011
5'-most EST	LIB3156-013-Q1-K1-G9
Method	BLASTN
NCBI GI	g5091496
BLAST score	99
E value	4.0e-48
Match length	202
% identity	92
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	271408
Contig ID	32770_1.R1011
5'-most EST	LIB83-011-Q1-E1-D5
Method	BLASTX
NCBI GI	g2832642
BLAST score	638
E value	1.0e-66
Match length	170
% identity	70
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	271409
Contig ID	32776_1.R1011
5'-most EST	ymt700223604.h1
Method	BLASTX
NCBI GI	g2499851
BLAST score	143
E value	8.0e-09
Match length	59
% identity	46
NCBI Description	PROTEASE II (OLIGOPEPTIDASE B) >gi_1084058_pir__JC4185 proteinase II (EC 3.4.21.-) - Moraxella lacunata >gi_551625_dbj_BAA07460_ (D38405) protease II [Moraxella lacunata]

Seq. No.	271410
Contig ID	32777_1.R1011
5'-most EST	LIB3156-014-Q1-K1-A2
Method	BLASTX
NCBI GI	g3643610
BLAST score	417
E value	9.0e-41
Match length	93
% identity	84
NCBI Description	(AC005395) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	271411
Contig ID	32778_1.R1011
5'-most EST	mwy700441404.h1

Seq. No.	271412
Contig ID	32779_1.R1011
5'-most EST	LIB3156-014-Q1-K1-A4

Seq. No.	271413
Contig ID	32780_1.R1011
5'-most EST	gct701167240.h1
Method	BLASTX
NCBI GI	g2921304
BLAST score	318
E value	4.0e-29
Match length	106
% identity	60
NCBI Description	(AF033496) herbicide safener binding protein [Zea mays]

Seq. No.	271414
Contig ID	32780_3.R1011
5'-most EST	wyr700244301.h1

Seq. No.	271415
Contig ID	32782_1.R1011
5'-most EST	LIB3156-014-Q1-K1-A7
Method	BLASTX
NCBI GI	g3935168
BLAST score	367
E value	4.0e-35
Match length	124
% identity	61
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	271416
Contig ID	32784_1.R1011
5'-most EST	LIB3156-014-Q1-K1-E10
Method	BLASTX
NCBI GI	g2462749
BLAST score	225
E value	2.0e-18
Match length	88
% identity	60
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	271417
Contig ID	32784_2.R1011
5'-most EST	dyk700105324.h1

Seq. No.	271418
Contig ID	32790_1.R1011
5'-most EST	LIB3156-014-Q1-K1-B6

Seq. No.	271419
Contig ID	32795_1.R1011
5'-most EST	LIB3137-018-Q1-K1-F11
Method	BLASTX
NCBI GI	g1172754
BLAST score	996
E value	1.0e-108
Match length	252
% identity	79
NCBI Description	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) >gi_541885_pir__JQ2256 phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) precursor - Arabidopsis thaliana >gi_289188 (L12457) 5'-phosphoribosyl-5-aminoimidazole synthetase [Arabidopsis thaliana]

Seq. No.	271420
Contig ID	32795_2.R1011
5'-most EST	uC-zmflmo17301c09b1
Method	BLASTX
NCBI GI	g1709925
BLAST score	466
E value	2.0e-52
Match length	156
% identity	69
NCBI Description	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) >gi_945060 (U30895) aminoimidazole ribonucleotide (AIRS) synthetase [Vigna unguiculata]

Seq. No.	271421
Contig ID	32798_1.R1011
5'-most EST	ntr700073365.h1
Method	BLASTX
NCBI GI	g2959767
BLAST score	816
E value	2.0e-87
Match length	222
% identity	68
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	271422
Contig ID	32804_1.R1011
5'-most EST	LIB3156-014-Q1-K1-D3

Seq. No.	271423
Contig ID	32813_1.R1011
5'-most EST	xyt700343929.h1
Method	BLASTX
NCBI GI	g4220527
BLAST score	896
E value	2.0e-96
Match length	295
% identity	57
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	271424
Contig ID	32813_3.R1011
5'-most EST	uC-zmflb73078b09b2
Method	BLASTX
NCBI GI	g4220527
BLAST score	199
E value	3.0e-15
Match length	82
% identity	51
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	271425
Contig ID	32815_1.R1011
5'-most EST	LIB3156-014-Q1-K1-F1

Seq. No.	271426
Contig ID	32815_2.R1011
5'-most EST	uC-zmflb73045f07a2

Seq. No.	271427
Contig ID	32820_1.R1011
5'-most EST	uC-zmflmo17036h04a1
Method	BLASTX
NCBI GI	g2827659
BLAST score	169
E value	6.0e-12
Match length	57
% identity	63
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	271428
Contig ID	32824_1.R1011
5'-most EST	uC-zmflb73244b06a1

Seq. No.	271429
Contig ID	32838_1.R1011
5'-most EST	LIB3156-015-Q1-K1-A12

Seq. No.	271430
Contig ID	32844_1.R1011
5'-most EST	LIB3156-015-Q1-K1-B1
Method	BLASTX
NCBI GI	g1652591
BLAST score	167
E value	2.0e-11
Match length	109

% identity	43
NCBI Description	(D90906) chloroplast import-associated channel IAP75 [Synechocystis sp.]

Seq. No.	271431
Contig ID	32851_1.R1011
5'-most EST	fC-zmle700433779a1

Seq. No.	271432
Contig ID	32859_1.R1011
5'-most EST	uC-zmflmo17047b06a1
Method	BLASTX
NCBI GI	g4559358
BLAST score	266
E value	7.0e-23
Match length	97
% identity	52
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	271433
Contig ID	32859_2.R1011
5'-most EST	wyr700238048.h1
Method	BLASTX
NCBI GI	g4559358
BLAST score	154
E value	7.0e-10
Match length	54
% identity	54
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	271434
Contig ID	32859_3.R1011
5'-most EST	LIB3067-005-Q1-K1-H10

Seq. No.	271435
Contig ID	32859_4.R1011
5'-most EST	xmt700264449.h1

Seq. No.	271436
Contig ID	32869_1.R1011
5'-most EST	nbm700473318.h1
Method	BLASTX
NCBI GI	g2829883
BLAST score	167
E value	9.0e-11
Match length	325
% identity	26
NCBI Description	(AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No.	271437
Contig ID	32869_2.R1011
5'-most EST	LIB3059-001-Q1-K2-F4

Seq. No.	271438
Contig ID	32869_3.R1011

5'-most EST	uC-zmflb73177e09a1
Seq. No.	271439
Contig ID	32875_1.R1011
5'-most EST	uC-zmflmo17332h10a1
Method	BLASTX
NCBI GI	g4006872
BLAST score	239
E value	4.0e-20
Match length	72
% identity	60
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]
Seq. No.	271440
Contig ID	32884_1.R1011
5'-most EST	uC-zmflb73038d08b1
Seq. No.	271441
Contig ID	32886_1.R1011
5'-most EST	LIB3156-015-Q1-K1-F4
Seq. No.	271442
Contig ID	32889_1.R1011
5'-most EST	LIB3156-015-Q1-K1-F7
Seq. No.	271443
Contig ID	32897_1.R1011
5'-most EST	LIB3156-015-Q1-K1-G5
Seq. No.	271444
Contig ID	32908_1.R1011
5'-most EST	xsy700209286.h1
Seq. No.	271445
Contig ID	32908_2.R1011
5'-most EST	LIB3279-011-P1-K1-E10
Seq. No.	271446
Contig ID	32913_1.R1011
5'-most EST	uC-zmflm017084g09b1
Method	BLASTX
NCBI GI	g3157949
BLAST score	208
E value	8.0e-16
Match length	79
% identity	44
NCBI Description	(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb_Z28697 from Nicotiana tabacum. ESTs gb_Z18185 and gb_AA605362 come from this gene. [Arabidopsis thaliana]
Seq. No.	271447
Contig ID	32932_1.R1011
5'-most EST	LIB3066-052-Q1-K1-E3
Method	BLASTX
NCBI GI	g4455309
BLAST score	403

E value	4.0e-39
Match length	142
% identity	57
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271448
Contig ID	32937_1.R1011
5'-most EST	uC-zmf1b73149f05b1
Method	BLASTX
NCBI GI	g3426042
BLAST score	460
E value	1.0e-45
Match length	184
% identity	52
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	271449
Contig ID	32949_1.R1011
5'-most EST	LIB3156-016-Q1-K1-D9
Method	BLASTX
NCBI GI	g2598461
BLAST score	227
E value	1.0e-18
Match length	131
% identity	35
NCBI Description	(Z98048) HIP (HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) [Homo sapiens] >gi_4049268 (U17714) putative tumor suppressor ST13 [Homo sapiens]

Seq. No.	271450
Contig ID	32956_1.R1011
5'-most EST	LIB3156-016-Q1-K1-D8

Seq. No.	271451
Contig ID	32958_1.R1011
5'-most EST	LIB3062-020-Q1-K1-E6
Method	BLASTX
NCBI GI	g98837
BLAST score	181
E value	8.0e-13
Match length	310
% identity	25
NCBI Description	enantiomer-selective amidase - Rhodococcus sp >gi_152052 (M74531) enantiomerase-selective amidase [Rhodococcus sp.]

Seq. No.	271452
Contig ID	32958_2.R1011
5'-most EST	ymt700224195.h1

Seq. No.	271453
Contig ID	32962_1.R1011
5'-most EST	wty700171365.h1
Method	BLASTX
NCBI GI	g1076315
BLAST score	466
E value	2.0e-46
Match length	138

% identity	62
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]
Seq. No.	271454
Contig ID	32962_2.R1011
5'-most EST	wty700172305.h1
Method	BLASTX
NCBI GI	g1076315
BLAST score	148
E value	6.0e-10
Match length	37
% identity	62
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]
Seq. No.	271455
Contig ID	32964_1.R1011
5'-most EST	LIB3279-057-P1-K1-G2
Seq. No.	271456
Contig ID	32964_2.R1011
5'-most EST	LIB3156-016-Q1-K1-E5
Seq. No.	271457
Contig ID	32970_1.R1011
5'-most EST	LIB3156-016-Q1-K1-F10
Method	BLASTX
NCBI GI	g4510375
BLAST score	369
E value	5.0e-35
Match length	105
% identity	69
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]
Seq. No.	271458
Contig ID	32974_1.R1011
5'-most EST	clt700044871.f1
Seq. No.	271459
Contig ID	32980_1.R1011
5'-most EST	cat700017155.r1
Seq. No.	271460
Contig ID	32989_1.R1011
5'-most EST	uC-zmflb73146h06a2
Seq. No.	271461
Contig ID	32996_1.R1011
5'-most EST	xdb700339490.h1
Seq. No.	271462

Contig ID	32999_1.R1011
5'-most EST	LIB3067-030-Q1-K1-A12

Seq. No.	271463
Contig ID	33005_1.R1011
5'-most EST	LIB143-050-Q1-E1-C4
Method	BLASTX
NCBI GI	g3955073
BLAST score	889
E value	0.0e+00
Match length	387
% identity	89
NCBI Description	(AJ223471) phytase [Zea mays]

Seq. No.	271464
Contig ID	33005_2.R1011
5'-most EST	LIB143-001-Q1-E1-B6
Method	BLASTX
NCBI GI	g3955073
BLAST score	292
E value	2.0e-26
Match length	61
% identity	100
NCBI Description	(AJ223471) phytase [Zea mays]

Seq. No.	271465
Contig ID	33014_1.R1011
5'-most EST	LIB3156-017-Q1-K1-B7
Method	BLASTX
NCBI GI	g4585907
BLAST score	186
E value	7.0e-14
Match length	39
% identity	85
NCBI Description	(AC006298) unknown protein [Arabidopsis thaliana]

Seq. No.	271466
Contig ID	33017_1.R1011
5'-most EST	LIB3067-010-Q1-K1-G3
Method	BLASTX
NCBI GI	g1870203
BLAST score	741
E value	1.0e-78
Match length	191
% identity	77
NCBI Description	(Y11403) cytochrome p450 [Zea mays]

Seq. No.	271467
Contig ID	33028_1.R1011
5'-most EST	LIB3069-053-Q1-K1-G3

Seq. No.	271468
Contig ID	33031_1.R1011
5'-most EST	rvt700550692.h1

Seq. No.	271469
Contig ID	33036_1.R1011

5'-most EST	wyr700237408.h1
Method	BLASTX
NCBI GI	g1060971
BLAST score	228
E value	3.0e-18
Match length	166
% identity	29
NCBI Description	(D26076) chloride channel [Oryctolagus cuniculus]

Seq. No.	271470
Contig ID	33037_1.R1011
5'-most EST	LIB3069-033-Q1-K1-H8

Seq. No.	271471
Contig ID	33041_1.R1011
5'-most EST	LIB3156-017-Q1-K1-F2

Seq. No.	271472
Contig ID	33052_1.R1011
5'-most EST	LIB3156-017-Q1-K1-G1

Seq. No.	271473
Contig ID	33058_1.R1011
5'-most EST	pmx700082995.h1

Seq. No.	271474
Contig ID	33058_2.R1011
5'-most EST	nwy700446876.h1

Seq. No.	271475
Contig ID	33060_1.R1011
5'-most EST	LIB3156-017-Q1-K1-G6
Method	BLASTX
NCBI GI	g2832625
BLAST score	300
E value	5.0e-27
Match length	74
% identity	66
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	271476
Contig ID	33061_1.R1011
5'-most EST	nbm700468116.h1
Method	BLASTX
NCBI GI	g2494736
BLAST score	148
E value	1.0e-09
Match length	49
% identity	55
NCBI Description	GLUCOSE INHIBITED DIVISION PROTEIN A >gi_1001595_dbj_BAA10223_ (D64000) glucose inhibited division protein A [Synechocystis sp.]

Seq. No.	271477
Contig ID	33062_1.R1011
5'-most EST	LIB3136-021-Q1-K1-A8
Method	BLASTX

NCBI GI g2832643
BLAST score 862
E value 2.0e-92
Match length 350
% identity 56
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No. 271478
Contig ID 33073_1.R1011
5'-most EST uC-zmflb73210e04a1

Seq. No. 271479
Contig ID 33081_1.R1011
5'-most EST xmt700261935.h1
Method BLASTX
NCBI GI g3461814
BLAST score 939
E value 1.0e-101
Match length 286
% identity 62
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 271480
Contig ID 33081_2.R1011
5'-most EST uC-zmrob73023h09a1
Method BLASTN
NCBI GI g497241
BLAST score 67
E value 5.0e-29
Match length 102
% identity 91
NCBI Description Zea mays W22 plasma-membrane H+ ATPase (Zmpma1) gene, exons 4-11, partial cds

Seq. No. 271481
Contig ID 33081_3.R1011
5'-most EST uC-zmflb73049d09b1

Seq. No. 271482
Contig ID 33081_4.R1011
5'-most EST uC-zmrob73054c11a1
Method BLASTX
NCBI GI g3461814
BLAST score 217
E value 2.0e-17
Match length 61
% identity 67
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 271483
Contig ID 33096_1.R1011
5'-most EST tzu700201408.h1

Seq. No. 271484
Contig ID 33104_2.R1011
5'-most EST uC-zmflmo17289a05b1
Method BLASTX

NCBI GI	g3152613
BLAST score	396
E value	7.0e-38
Match length	299
% identity	32
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271485
Contig ID	33114_1.R1011
5'-most EST	LIB3156-020-Q1-K1-B7

Seq. No.	271486
Contig ID	33116_1.R1011
5'-most EST	LIB3156-020-Q1-K1-C10

Seq. No.	271487
Contig ID	33121_1.R1011
5'-most EST	uC-zmflb73130a03b2
Method	BLASTX
NCBI GI	g2832658
BLAST score	281
E value	1.0e-24
Match length	120
% identity	48
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	271488
Contig ID	33123_1.R1011
5'-most EST	LIB3156-020-Q1-K1-D10
Method	BLASTX
NCBI GI	g1707898
BLAST score	559
E value	3.0e-57
Match length	223
% identity	52
NCBI Description	GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) >gi_2117767_pir__JC6012 glutamine--fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - yeast (Candida albicans) >gi_1429267_emb_CAA64380_ (X94753) glucosamine--fructose-6-phosphate aminotransferase (isomerizing) [Candida albicans]

Seq. No.	271489
Contig ID	33125_1.R1011
5'-most EST	uC-zmflmo17219b10b1
Method	BLASTX
NCBI GI	g4507125
BLAST score	248
E value	4.0e-21
Match length	137
% identity	42
NCBI Description	small nuclear ribonucleoprotein polypeptides B and B1 >gi_88613_pir__S10594 snRNP protein B - human >gi_29410_emb_CAA33902_ (X15893) B/B' protein (AA 1-231) [Homo sapiens]

Seq. No.	271490
Contig ID	33129_1.R1011
5'-most EST	wyr700244127.h1

Seq. No.	271491
Contig ID	33139_1.R1011
5'-most EST	tzu700203936.h1
Method	BLASTX
NCBI GI	g2589162
BLAST score	2153
E value	0.0e+00
Match length	496
% identity	84
NCBI Description	(D88451) aldehyde oxidase [Zea mays]

Seq. No.	271492
Contig ID	33149_1.R1011
5'-most EST	LIB3061-053-Q1-K1-B1

Seq. No.	271493
Contig ID	33150_1.R1011
5'-most EST	LIB3156-020-Q1-K1-G9

Seq. No.	271494
Contig ID	33154_1.R1011
5'-most EST	LIB3156-021-Q1-K1-A1
Method	BLASTX
NCBI GI	g1170949
BLAST score	249
E value	5.0e-21
Match length	159
% identity	37
NCBI Description	SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir__S38327 protein kinase - Arabidopsis thaliana >gi_166811 (L07249) protein kinase [Arabidopsis thaliana]

Seq. No.	271495
Contig ID	33161_1.R1011
5'-most EST	uC-zmroteosinte064f12b1

Seq. No.	271496
Contig ID	33166_1.R1011
5'-most EST	LIB3156-021-Q1-K1-B11

Seq. No.	271497
Contig ID	33184_1.R1011
5'-most EST	LIB3156-021-Q1-K1-D10

Seq. No.	271498
Contig ID	33188_1.R1011
5'-most EST	uC-zmflmo17310a09b1
Method	BLASTX
NCBI GI	g118484
BLAST score	337
E value	4.0e-31
Match length	168

% identity	43
NCBI Description	DEHYDRIN DHN1 (M3) (RAB-17 PROTEIN) >gi_100919_pir__S08633 RAB-17 protein - maize >gi_295856_emb_CAA34123_ (X15994) RAB-17 [Zea mays]

Seq. No.	271499
Contig ID	33188_2.R1011
5'-most EST	uC-zmroteosinte059f05b1
Method	BLASTX
NCBI GI	g82684
BLAST score	295
E value	3.0e-26
Match length	124
% identity	51
NCBI Description	dehydrin 3 - maize >gi_18964_emb_CAA33364_ (X15290) dehydrin (AA 1-167) [Zea mays]

Seq. No.	271500
Contig ID	33188_3.R1011
5'-most EST	LIB143-024-Q1-E1-E11
Method	BLASTX
NCBI GI	g82684
BLAST score	193
E value	1.0e-14
Match length	48
% identity	75
NCBI Description	dehydrin 3 - maize >gi_18964_emb_CAA33364_ (X15290) dehydrin (AA 1-167) [Zea mays]

Seq. No.	271501
Contig ID	33191_1.R1011
5'-most EST	uC-zmflmo17054b12b1
Method	BLASTX
NCBI GI	g3914801
BLAST score	455
E value	5.0e-45
Match length	180
% identity	52
NCBI Description	DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT) >gi_2739048 (AF025424) RNA polymerase I 127 kDa subunit [Rattus norvegicus]

Seq. No.	271502
Contig ID	33197_1.R1011
5'-most EST	LIB3060-016-Q1-K1-H6
Method	BLASTX
NCBI GI	g4115379
BLAST score	271
E value	8.0e-24
Match length	95
% identity	57
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	271503
Contig ID	33201_1.R1011

5'-most EST	LIB3153-005-Q1-K1-C12
Seq. No.	271504
Contig ID	33203_1.R1011
5'-most EST	LIB3156-021-Q1-K1-F11
Method	BLASTX
NCBI GI	g3935165
BLAST score	150
E value	3.0e-09
Match length	82
% identity	41
NCBI Description	(AC004557) F17L21.8 [Arabidopsis thaliana]
Seq. No.	271505
Contig ID	33204_1.R1011
5'-most EST	wen700334040.h1
Method	BLASTX
NCBI GI	g4091080
BLAST score	659
E value	6.0e-69
Match length	219
% identity	57
NCBI Description	(AF045571) nucleic acid binding protein [Oryza sativa]
Seq. No.	271506
Contig ID	33204_2.R1011
5'-most EST	LIB3137-027-Q1-K1-D2
Method	BLASTX
NCBI GI	g4091117
BLAST score	302
E value	6.0e-31
Match length	89
% identity	72
NCBI Description	(AF047428) nucleic acid binding protein [Oryza sativa]
Seq. No.	271507
Contig ID	33204_4.R1011
5'-most EST	LIB3069-034-Q1-K1-G9
Method	BLASTX
NCBI GI	g3319341
BLAST score	201
E value	1.0e-15
Match length	38
% identity	82
NCBI Description	(AF077407) similar to Medicago sativa nucleic acid binding protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]
Seq. No.	271508
Contig ID	33205_1.R1011
5'-most EST	LIB3156-021-Q1-K1-F2
Method	BLASTX
NCBI GI	g1016270
BLAST score	316
E value	5.0e-29
Match length	92
% identity	72
NCBI Description	(U35123) p-glycoprotein [Urechis caupo]

Seq. No.	271509
Contig ID	33206_1.R1011
5'-most EST	LIB3156-021-Q1-K1-F3
Method	BLASTX
NCBI GI	g3080400
BLAST score	323
E value	2.0e-30
Match length	111
% identity	65
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	271510
Contig ID	33208_1.R1011
5'-most EST	nbm700468560.h1
Method	BLASTX
NCBI GI	g3549670
BLAST score	920
E value	1.0e-139
Match length	305
% identity	79
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	271511
Contig ID	33212_1.R1011
5'-most EST	wyr700237430.h1
Method	BLASTX
NCBI GI	g4584255
BLAST score	838
E value	7.0e-90
Match length	152
% identity	95
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	271512
Contig ID	33212_2.R1011
5'-most EST	uC-zmflb73003d04b1
Method	BLASTX
NCBI GI	g4584255
BLAST score	1065
E value	1.0e-118
Match length	226
% identity	88
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	271513
Contig ID	33212_3.R1011
5'-most EST	uC-zmflb73239a02a1
Method	BLASTX
NCBI GI	g3264611
BLAST score	216
E value	2.0e-17
Match length	44
% identity	95
NCBI Description	(AF061511) seven in absentia homolog [Zea mays]

Seq. No.	271514
Contig ID	33213_1.R1011
5'-most EST	pmx700083637.h1

Seq. No.	271515
Contig ID	33219_1.R1011
5'-most EST	LIB3156-021-Q1-K1-G6
Method	BLASTX
NCBI GI	g2245020
BLAST score	251
E value	5.0e-21
Match length	156
% identity	37
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	271516
Contig ID	33235_1.R1011
5'-most EST	nbm700466091.h1
Method	BLASTX
NCBI GI	g2708744
BLAST score	543
E value	2.0e-55
Match length	207
% identity	50
NCBI Description	(AC003952) putative Bop-like zinc finger protein [Arabidopsis thaliana]

Seq. No.	271517
Contig ID	33236_1.R1011
5'-most EST	nwy700445756.h1

Seq. No.	271518
Contig ID	33239_1.R1011
5'-most EST	uC-zmflB73111c03b2

Seq. No.	271519
Contig ID	33242_1.R1011
5'-most EST	tzu700204661.h1
Method	BLASTX
NCBI GI	g1848225
BLAST score	253
E value	1.0e-21
Match length	62
% identity	71
NCBI Description	(U88090) nonspecific lipid transfer protein [Hordeum vulgare]

Seq. No.	271520
Contig ID	33248_1.R1011
5'-most EST	LIB3157-002-Q1-K1-D9

Seq. No.	271521
Contig ID	33250_1.R1011
5'-most EST	pmx700085701.h1
Method	BLASTX
NCBI GI	g417587

BLAST score	362
E value	4.0e-34
Match length	163
% identity	47
NCBI Description	DNA REPAIR PROTEIN RAD5 >gi_2131233_pir__S64859 DNA repair protein RAD5 - yeast (Saccharomyces cerevisiae) >gi_172347 (M96644) RAD5 protein [Saccharomyces cerevisiae] >gi_1360348_emb_CAA97556_ (Z73204) ORF YLR032w [Saccharomyces cerevisiae]

Seq. No.	271522
Contig ID	33254_1.R1011
5'-most EST	uC-zmflb73182a10a1
Method	BLASTN
NCBI GI	g22204
BLAST score	146
E value	2.0e-76
Match length	206
% identity	93
NCBI Description	Maize Bz-McC gene for UDPglucose flavonoid glycosyl-transferase

Seq. No.	271523
Contig ID	33254_2.R1011
5'-most EST	nbm700473265.h1
Method	BLASTX
NCBI GI	g1362152
BLAST score	603
E value	2.0e-62
Match length	151
% identity	74
NCBI Description	ribosomal protein S6 kinase homolog (clone Aspk11) - oat >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]

Seq. No.	271524
Contig ID	33254_4.R1011
5'-most EST	xyt700344238.h1
Method	BLASTN
NCBI GI	g22204
BLAST score	100
E value	4.0e-49
Match length	164
% identity	90
NCBI Description	Maize Bz-McC gene for UDPglucose flavonoid glycosyl-transferase

Seq. No.	271525
Contig ID	33257_1.R1011
5'-most EST	vux700161573.h1

Seq. No.	271526
Contig ID	33259_1.R1011
5'-most EST	LIB3157-002-Q1-K1-A7

Seq. No.	271527
Contig ID	33261_1.R1011

5'-most EST	xyt700346760.h1
Method	BLASTX
NCBI GI	g542200
BLAST score	550
E value	4.0e-56
Match length	206
% identity	50
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	271528
Contig ID	33261_2.R1011
5'-most EST	uwc700150621.h1
Method	BLASTX
NCBI GI	g542200
BLAST score	330
E value	1.0e-30
Match length	108
% identity	54
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	271529
Contig ID	33264_1.R1011
5'-most EST	LIB3157-001-Q1-K1-F12
Method	BLASTX
NCBI GI	g2341045
BLAST score	152
E value	7.0e-10
Match length	70
% identity	44
NCBI Description	(AC000104) F19P19.16 [Arabidopsis thaliana]

Seq. No.	271530
Contig ID	33270_1.R1011
5'-most EST	LIB3059-005-Q1-K1-H9

Seq. No.	271531
Contig ID	33275_1.R1011
5'-most EST	LIB3067-029-Q1-K1-D9
Method	BLASTN
NCBI GI	g312178
BLAST score	60
E value	8.0e-25
Match length	111
% identity	53
NCBI Description	Z.mays GapC2 gene

Seq. No.	271532
Contig ID	33277_1.R1011
5'-most EST	uer700583213.h1

Seq. No.	271533
Contig ID	33278_1.R1011
5'-most EST	cyk700048191.f1

Seq. No.	271534
Contig ID	33278_2.R1011
5'-most EST	LIB3066-024-Q1-K1-F1

Seq. No.	271535
Contig ID	33292_1.R1011
5'-most EST	LIB3157-003-Q1-K1-B6

Seq. No.	271536
Contig ID	33298_1.R1011
5'-most EST	uer700581210.h1
Method	BLASTX
NCBI GI	g2286123
BLAST score	185
E value	1.0e-13
Match length	60
% identity	58
NCBI Description	(U95607) testis specific DNAj-homolog [Mus musculus]

Seq. No.	271537
Contig ID	33306_1.R1011
5'-most EST	tzu700202835.h1
Method	BLASTX
NCBI GI	g2281085
BLAST score	494
E value	1.0e-49
Match length	166
% identity	56
NCBI Description	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	271538
Contig ID	33314_1.R1011
5'-most EST	LIB3157-003-Q1-K1-F7

Seq. No.	271539
Contig ID	33316_1.R1011
5'-most EST	hvj700620693.h1
Method	BLASTX
NCBI GI	g4510428
BLAST score	284
E value	3.0e-25
Match length	88
% identity	64
NCBI Description	(AC006929) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	271540
Contig ID	33318_1.R1011
5'-most EST	LIB3157-003-Q1-K1-G8

Seq. No.	271541
Contig ID	33319_1.R1011
5'-most EST	LIB143-022-Q1-E1-C7
Method	BLASTX
NCBI GI	g3367596

BLAST score 943
E value 1.0e-102
Match length 421
% identity 49
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 271542
Contig ID 33319_3.R1011
5'-most EST uC-zmf1b73062h12b1
Method BLASTX
NCBI GI g3367596
BLAST score 397
E value 1.0e-61
Match length 188
% identity 60
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 271543
Contig ID 33321_1.R1011
5'-most EST hbs701180880.h1
Method BLASTX
NCBI GI g4580525
BLAST score 222
E value 4.0e-18
Match length 78
% identity 50
NCBI Description (AF036306) scarecrow-like 9 [Arabidopsis thaliana]

Seq. No. 271544
Contig ID 33336_1.R1011
5'-most EST yne700379575.h1

Seq. No. 271545
Contig ID 33350_1.R1011
5'-most EST uC-zmflmo17023e05b1

Seq. No. 271546
Contig ID 33354_1.R1011
5'-most EST LIB3157-004-Q1-K1-E10
Method BLASTX
NCBI GI g2809246
BLAST score 570
E value 8.0e-59
Match length 158
% identity 65
NCBI Description (AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No. 271547
Contig ID 33357_2.R1011
5'-most EST LIB3180-022-P2-M1-C10
Method BLASTX
NCBI GI g2500543
BLAST score 279
E value 1.0e-27
Match length 154
% identity 43
NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

	HELICASE EEED8.5 >gi_733602 (U23484) similar to S. cerevisiae pre-mRNA splicing factor RNA helicase PRP22 (SP:PR22_YEAST, P24384) and other DEAH subfamily members of the DEAD box family helicases [Caenorhabditis elegans]
Seq. No.	271548
Contig ID	33368_1.R1011
5'-most EST	uC-zmflmo17334h08a1
Seq. No.	271549
Contig ID	33376_1.R1011
5'-most EST	LIB3157-004-Q1-K1-H4
Seq. No.	271550
Contig ID	33400_1.R1011
5'-most EST	wty700169578.h1
Method	BLASTX
NCBI GI	g3128212
BLAST score	176
E value	2.0e-12
Match length	48
% identity	69
NCBI Description	(AC004077) putative HMG protein [Arabidopsis thaliana] >gi_3337373 (AC004481) putative HMG protein [Arabidopsis thaliana]
Seq. No.	271551
Contig ID	33400_2.R1011
5'-most EST	uC-zmflmo17067f08b1
Method	BLASTX
NCBI GI	g729737
BLAST score	214
E value	7.0e-17
Match length	74
% identity	51
NCBI Description	HMG1/2-LIKE PROTEIN >gi_541981_pir__S39556 HMG protein - fava bean
Seq. No.	271552
Contig ID	33412_1.R1011
5'-most EST	mwy700440647.h1
Method	BLASTX
NCBI GI	g2435519
BLAST score	1886
E value	0.0e+00
Match length	549
% identity	68
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]
Seq. No.	271553
Contig ID	33412_2.R1011
5'-most EST	LIB3067-060-Q1-K1-E12
Seq. No.	271554
Contig ID	33417_1.R1011

5'-most EST	LIB3157-005-Q1-K1-E3
Seq. No.	271555
Contig ID	33426_2.R1011
5'-most EST	LIB3157-005-Q1-K1-F3
Seq. No.	271556
Contig ID	33427_1.R1011
5'-most EST	wty700172527.h1
Seq. No.	271557
Contig ID	33431_1.R1011
5'-most EST	uC-zmroteosinte070g05b1
Method	BLASTX
NCBI GI	g2213602
BLAST score	262
E value	4.0e-22
Match length	185
% identity	43
NCBI Description	(AC000348) T7N9.22 [Arabidopsis thaliana]
Seq. No.	271558
Contig ID	33432_1.R1011
5'-most EST	uC-zmflb73014e03b1
Method	BLASTX
NCBI GI	g4336747
BLAST score	286
E value	2.0e-25
Match length	95
% identity	60
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]
Seq. No.	271559
Contig ID	33446_1.R1011
5'-most EST	uC-zmflmo17306g10b1
Method	BLASTX
NCBI GI	g2160166
BLAST score	524
E value	3.0e-79
Match length	352
% identity	50
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.	271560
Contig ID	33449_1.R1011
5'-most EST	LIB3157-006-Q1-K1-A5
Seq. No.	271561
Contig ID	33454_1.R1011
5'-most EST	hbs701185340.h1
Method	BLASTX
NCBI GI	g100903
BLAST score	393
E value	5.0e-38
Match length	77
% identity	51
NCBI Description	nucleic acid-binding protein - maize >gi_168526 (M74566)

nucleic acid-binding protein [Zea mays]

Seq. No.	271562
Contig ID	33454_2.R1011
5'-most EST	uC-zmrob73062a11a1
Method	BLASTN
NCBI GI	g22378
BLAST score	258
E value	1.0e-143
Match length	274
% identity	99
NCBI Description	Z.mays gene for nucleic acid binding protein

Seq. No.	271563
Contig ID	33470_1.R1011
5'-most EST	nbm700476108.h1
Method	BLASTX
NCBI GI	g2443886
BLAST score	159
E value	3.0e-10
Match length	122
% identity	34
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	271564
Contig ID	33470_2.R1011
5'-most EST	kem700611717.h1

Seq. No.	271565
Contig ID	33483_1.R1011
5'-most EST	xmt700265419.h1

Seq. No.	271566
Contig ID	33494_1.R1011
5'-most EST	ceu700431150.h1
Method	BLASTX
NCBI GI	g1778095
BLAST score	190
E value	4.0e-14
Match length	58
% identity	66
NCBI Description	(U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	271567
Contig ID	33494_2.R1011
5'-most EST	hbs701185884.h2

Seq. No.	271568
Contig ID	33495_1.R1011
5'-most EST	LIB3157-007-Q1-K1-F12

Seq. No.	271569
Contig ID	33499_1.R1011
5'-most EST	LIB3067-045-Q1-K1-F3
Method	BLASTN

NCBI GI	g4140643
BLAST score	55
E value	5.0e-22
Match length	75
% identity	95
NCBI Description	Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	271570
Contig ID	33501_1.R1011
5'-most EST	uC-zmflb73276f12a1

Seq. No.	271571
Contig ID	33504_1.R1011
5'-most EST	ceu700424426.h1
Method	BLASTX
NCBI GI	g2388580
BLAST score	332
E value	9.0e-31
Match length	69
% identity	80
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	271572
Contig ID	33515_1.R1011
5'-most EST	uC-zmflb73216d04b2

Seq. No.	271573
Contig ID	33515_2.R1011
5'-most EST	tfd700575766.h1

Seq. No.	271574
Contig ID	33526_1.R1011
5'-most EST	LIB3157-007-Q1-K1-B8
Method	BLASTX
NCBI GI	g2459442
BLAST score	406
E value	2.0e-39
Match length	142
% identity	63
NCBI Description	(AC002332) putative DNA-binding protein PD1 [Arabidopsis thaliana]

Seq. No.	271575
Contig ID	33535_1.R1011
5'-most EST	uC-zmflb73125e07b2

Seq. No.	271576
Contig ID	33536_1.R1011
5'-most EST	cjh700193818.h1

Seq. No.	271577
Contig ID	33543_1.R1011
5'-most EST	LIB3117-003-Q1-K1-B6
Method	BLASTX
NCBI GI	g3687224

BLAST score	261
E value	2.0e-22
Match length	66
% identity	77
NCBI Description	(AC005169) putative N-acetyl-gamma-glutamyl-phosphate reductase [Arabidopsis thaliana]

Seq. No.	271578
Contig ID	33554_1.R1011
5'-most EST	LIB3068-009-Q1-K1-H1
Method	BLASTX
NCBI GI	g3702317
BLAST score	160
E value	1.0e-10
Match length	38
% identity	84
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana] >gi_4559376_gb_AAD23036.1_AC006526_1 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	271579
Contig ID	33556_1.R1011
5'-most EST	LIB3062-002-Q1-K2-D11

Seq. No.	271580
Contig ID	33556_3.R1011
5'-most EST	uC-zmflmo17139g11b1

Seq. No.	271581
Contig ID	33569_1.R1011
5'-most EST	LIB3157-007-Q1-K1-H9

Seq. No.	271582
Contig ID	33573_1.R1011
5'-most EST	rvt700548931.h1

Seq. No.	271583
Contig ID	33573_2.R1011
5'-most EST	LIB3062-031-Q1-K1-B10

Seq. No.	271584
Contig ID	33573_3.R1011
5'-most EST	LIB3066-035-Q1-K1-B8

Seq. No.	271585
Contig ID	33573_4.R1011
5'-most EST	uC-zmflb73339f07a1

Seq. No.	271586
Contig ID	33573_5.R1011
5'-most EST	wty700172820.h1

Seq. No.	271587
Contig ID	33576_1.R1011
5'-most EST	LIB3117-005-Q1-K1-E8
Method	BLASTX
NCBI GI	g3668091

BLAST score	269
E value	5.0e-23
Match length	255
% identity	7
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271588
Contig ID	33576_2.R1011
5'-most EST	LIB84-005-Q1-E1-C6

Seq. No.	271589
Contig ID	33587_1.R1011
5'-most EST	mwy700439332.h1
Method	BLASTX
NCBI GI	g3402705
BLAST score	254
E value	9.0e-22
Match length	133
% identity	47
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271590
Contig ID	33595_1.R1011
5'-most EST	uC-zmflmo17340a02b1
Method	BLASTX
NCBI GI	g2911076
BLAST score	212
E value	2.0e-28
Match length	173
% identity	42
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	271591
Contig ID	33597_1.R1011
5'-most EST	LIB3062-049-Q1-K1-E4

Seq. No.	271592
Contig ID	33601_1.R1011
5'-most EST	kem700612070.h1
Method	BLASTX
NCBI GI	g3023453
BLAST score	169
E value	1.0e-11
Match length	76
% identity	47
NCBI Description	CBBY PROTEIN >gi_1825471 (U67781) CbbY [Rhodobacter sphaeroides]

Seq. No.	271593
Contig ID	33606_1.R1011
5'-most EST	LIB143-015-Q1-E1-E11
Method	BLASTX
NCBI GI	g400094
BLAST score	263
E value	2.0e-22
Match length	161
% identity	37

NCBI Description	23 KD JASMONATE-INDUCED PROTEIN >gi_282989_pir__S22514 jasmonate-induced protein 1 - barley
Seq. No.	271594
Contig ID	33606_2.R1011
5'-most EST	dyk700103122.h1
Method	BLASTX
NCBI GI	g1561618
BLAST score	256
E value	7.0e-22
Match length	144
% identity	40
NCBI Description	(X98124) jasmonate-induced protein [Hordeum vulgare]
Seq. No.	271595
Contig ID	33606_3.R1011
5'-most EST	hvj700618859.h1
Seq. No.	271596
Contig ID	33608_1.R1011
5'-most EST	LIB3068-017-Q1-K1-G10
Seq. No.	271597
Contig ID	33613_1.R1011
5'-most EST	ceu700421855.h1
Seq. No.	271598
Contig ID	33618_1.R1011
5'-most EST	LIB3059-027-Q1-K1-A10
Method	BLASTX
NCBI GI	g2961357
BLAST score	258
E value	3.0e-22
Match length	88
% identity	65
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]
Seq. No.	271599
Contig ID	33625_1.R1011
5'-most EST	LIB3157-009-Q1-K1-A7
Method	BLASTX
NCBI GI	g729905
BLAST score	261
E value	4.0e-37
Match length	144
% identity	62
NCBI Description	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PK7 >gi_320562_pir__JC1385 protein kinase (EC 2.7.1.37) - Arabidopsis thaliana >gi_303500_dbj_BAA01716_ (D10910) serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	271600
Contig ID	33626_1.R1011
5'-most EST	uC-zmrob73054d03a1
Seq. No.	271601
Contig ID	33634_1.R1011

5'-most EST	uC-zmflb73049d12b1
Seq. No.	271602
Contig ID	33634_2.R1011
5'-most EST	LIB3062-021-Q1-K1-A3
Seq. No.	271603
Contig ID	33634_3.R1011
5'-most EST	uC-zmflb73082f05a2
Method	BLASTX
NCBI GI	g4558462
BLAST score	930
E value	1.0e-100
Match length	209
% identity	47
NCBI Description	(AF079404) cell cycle switch protein [Medicago sativa subsp. X varia]
Seq. No.	271604
Contig ID	33634_4.R1011
5'-most EST	rvt700551883.h1
Seq. No.	271605
Contig ID	33639_1.R1011
5'-most EST	LIB3157-009-Q1-K1-C12
Seq. No.	271606
Contig ID	33641_1.R1011
5'-most EST	uC-zmflb73140f04b1
Seq. No.	271607
Contig ID	33641_2.R1011
5'-most EST	LIB3157-009-Q1-K1-D12
Seq. No.	271608
Contig ID	33648_1.R1011
5'-most EST	uC-zmflmo17023f08b1
Method	BLASTX
NCBI GI	g4507229
BLAST score	401
E value	1.0e-38
Match length	124
% identity	60
NCBI Description	Succinic semialdehyde dehydrogenase >gi_3766467_emb_CAA72076_ (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens] >gi_4164365_emb_CAA20248_ (AL031230) dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24)) [Homo sapiens]
Seq. No.	271609
Contig ID	33648_2.R1011
5'-most EST	uC-zmflmo17375g02a1
Method	BLASTX
NCBI GI	g1711534
BLAST score	252
E value	1.0e-21

Match length	67
% identity	69
NCBI Description	SUCCINATE SEMIALDEHYDE DEHYDROGENASE (NAD(+)-DEPENDENT SUCCINIC SEMIALDEHYDE DEHYDROGENASE) >gi_2136207_pir__A55773 succinate-semialdehyde dehydrogenase (EC 1.2.1.24) - human (fragment) >gi_556221 (L34820) succinate semialdehyde dehydrogenase [Homo sapiens]

Seq. No.	271610
Contig ID	33651_1.R1011
5'-most EST	xjt700094083.h1
Method	BLASTX
NCBI GI	g3004558
BLAST score	204
E value	2.0e-21
Match length	131
% identity	45
NCBI Description	(AC003673) peroxidase ATP22a [Arabidopsis thaliana]

Seq. No.	271611
Contig ID	33663_1.R1011
5'-most EST	fC-zmle700580159a2
Method	BLASTX
NCBI GI	g2648032
BLAST score	1178
E value	1.0e-129
Match length	337
% identity	65
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	271612
Contig ID	33663_2.R1011
5'-most EST	fdz701163331.h1

Seq. No.	271613
Contig ID	33698_1.R1011
5'-most EST	uC-zmroB73070c07b1

Seq. No.	271614
Contig ID	33702_1.R1011
5'-most EST	uC-zmflmo17217c08a1

Seq. No.	271615
Contig ID	33703_1.R1011
5'-most EST	LIB3059-040-Q1-K1-H5

Seq. No.	271616
Contig ID	33705_1.R1011
5'-most EST	LIB3157-011-Q1-K1-F12
Method	BLASTX
NCBI GI	g3157949
BLAST score	223
E value	6.0e-18
Match length	67
% identity	58
NCBI Description	(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase

precursor gb_Z28697 from Nicotiana tabacum. ESTs gb_Z18185 and gb_AA605362 come from this gene. [Arabidopsis thaliana]

Seq. No.	271617
Contig ID	33708_1.R1011
5'-most EST	uC-zmroteosinte027e11b1
Method	BLASTX
NCBI GI	g2511533
BLAST score	1195
E value	1.0e-131
Match length	307
% identity	80
NCBI Description	(AF008121) alpha-tubulin 2 [Eleusine indica]

Seq. No.	271618
Contig ID	33711_1.R1011
5'-most EST	gct701172482.h1
Method	BLASTX
NCBI GI	g2252631
BLAST score	282
E value	6.0e-25
Match length	68
% identity	75
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271619
Contig ID	33713_1.R1011
5'-most EST	tfd700573344.h1
Method	BLASTX
NCBI GI	g4544412
BLAST score	162
E value	9.0e-11
Match length	66
% identity	41
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271620
Contig ID	33720_1.R1011
5'-most EST	uC-zmrob73019a06b1

Seq. No.	271621
Contig ID	33728_1.R1011
5'-most EST	uC-zmflmo17290c10a1
Method	BLASTX
NCBI GI	g3135258
BLAST score	159
E value	7.0e-11
Match length	76
% identity	42
NCBI Description	(AC003058) salt inducible protein-like [Arabidopsis thaliana]

Seq. No.	271622
Contig ID	33730_1.R1011
5'-most EST	uC-zmflmo17153e11a1

Seq. No.	271623

Contig ID	33731_1.R1011
5'-most EST	LIB3157-012-Q1-K1-B10
Seq. No.	271624
Contig ID	33732_1.R1011
5'-most EST	ymt700222945.h1
Seq. No.	271625
Contig ID	33732_3.R1011
5'-most EST	xjt700092361.h1
Seq. No.	271626
Contig ID	33733_1.R1011
5'-most EST	rvt700552644.h1
Method	BLASTX
NCBI GI	g461532
BLAST score	633
E value	9.0e-66
Match length	177
% identity	64
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1362500_pir__D49993 ADP-ribosylation factor - Ajellomyces capsulata >gi_407693 (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
Seq. No.	271627
Contig ID	33741_1.R1011
5'-most EST	uC-zmflmo17374h12a1
Seq. No.	271628
Contig ID	33741_2.R1011
5'-most EST	uC-zmflb73151b08b1
Method	BLASTX
NCBI GI	g2444180
BLAST score	159
E value	3.0e-10
Match length	42
% identity	64
NCBI Description	(U94785) unconventional myosin [Helianthus annuus]
Seq. No.	271629
Contig ID	33741_3.R1011
5'-most EST	uer700577110.h1
Seq. No.	271630
Contig ID	33743_1.R1011
5'-most EST	uC-zmflMo17018g01b1
Method	BLASTX
NCBI GI	g3367522
BLAST score	460
E value	4.0e-74
Match length	290
% identity	51
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]
Seq. No.	271631
Contig ID	33743_2.R1011

5'-most EST	uC-zmflmo17331f12a1
Method	BLASTX
NCBI GI	g3367522
BLAST score	1279
E value	1.0e-141
Match length	426
% identity	58
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	271632
Contig ID	33743_3.R1011
5'-most EST	uC-zmflmo17307h04b1
Method	BLASTX
NCBI GI	g3367522
BLAST score	265
E value	5.0e-23
Match length	96
% identity	54
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	271633
Contig ID	33743_4.R1011
5'-most EST	LIB3279-050-P1-K1-E3
Method	BLASTX
NCBI GI	g2894569
BLAST score	221
E value	6.0e-18
Match length	130
% identity	43
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	271634
Contig ID	33743_5.R1011
5'-most EST	uC-zmroB73001f07b1
Method	BLASTX
NCBI GI	g3367522
BLAST score	388
E value	2.0e-37
Match length	123
% identity	62
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	271635
Contig ID	33747_1.R1011
5'-most EST	nwy700444426.h1

Seq. No.	271636
Contig ID	33748_1.R1011
5'-most EST	LIB3157-012-Q1-K1-D1

Seq. No.	271637
Contig ID	33749_1.R1011
5'-most EST	LIB3136-012-Q1-K1-B2
Method	BLASTX

NCBI GI	g2316016
BLAST score	265
E value	1.0e-22
Match length	85
% identity	61
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	271638
Contig ID	33750_1.R1011
5'-most EST	uC-zmflb73193g03a1

Seq. No.	271639
Contig ID	33750_2.R1011
5'-most EST	uC-zmflmo17277g02a1

Seq. No.	271640
Contig ID	33753_1.R1011
5'-most EST	gct701173895.h1
Method	BLASTX
NCBI GI	g1084461
BLAST score	365
E value	1.0e-34
Match length	82
% identity	79
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	271641
Contig ID	33755_1.R1011
5'-most EST	ceu700421969.h1

Seq. No.	271642
Contig ID	33757_1.R1011
5'-most EST	zuv700355680.h1
Method	BLASTX
NCBI GI	g861366
BLAST score	455
E value	3.0e-45
Match length	160
% identity	56
NCBI Description	(U28991) coded for by C. elegans cDNA cm21c7 [Caenorhabditis elegans]

Seq. No.	271643
Contig ID	33757_2.R1011
5'-most EST	fC-zmst700164377a1
Method	BLASTX
NCBI GI	g2388956
BLAST score	178
E value	2.0e-18
Match length	90
% identity	61
NCBI Description	(Z98979) ribulose-phosphate 3-epimerase [Schizosaccharomyces pombe]

Seq. No.	271644
Contig ID	33763_1.R1011
5'-most EST	LIB3061-030-Q1-K1-B11

Seq. No.	271645
Contig ID	33767_1.R1011
5'-most EST	LIB3157-012-Q1-K1-G1

Seq. No.	271646
Contig ID	33777_1.R1011
5'-most EST	LIB3062-036-Q1-K1-C2

Seq. No.	271647
Contig ID	33782_1.R1011
5'-most EST	ntr700075078.h1
Method	BLASTX
NCBI GI	g4454464
BLAST score	911
E value	3.0e-98
Match length	269
% identity	64
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	271648
Contig ID	33782_3.R1011
5'-most EST	uC-zmflb73018b11b1

Seq. No.	271649
Contig ID	33782_4.R1011
5'-most EST	wty700166273.h1
Method	BLASTX
NCBI GI	g4454464
BLAST score	500
E value	2.0e-50
Match length	128
% identity	77
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	271650
Contig ID	33782_5.R1011
5'-most EST	xsy700214218.h1
Method	BLASTX
NCBI GI	g4454464
BLAST score	254
E value	9.0e-22
Match length	63
% identity	78
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	271651
Contig ID	33782_6.R1011
5'-most EST	rvt700552815.h1
Method	BLASTX
NCBI GI	g4454464
BLAST score	185
E value	7.0e-22
Match length	87
% identity	72
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	271652
Contig ID	33800_1.R1011
5'-most EST	uC-zmflmo17035e09a1

Seq. No.	271653
Contig ID	33805_1.R1011
5'-most EST	uC-zmflmo17364h04a1

Seq. No.	271654
Contig ID	33817_1.R1011
5'-most EST	tfd700572908.h1
Method	BLASTN
NCBI GI	g22118
BLAST score	52
E value	1.0e-20
Match length	68
% identity	94
NCBI Description	Z.mays DNA for Adh1-Cm allele

Seq. No.	271655
Contig ID	33818_1.R1011
5'-most EST	uer700578476.h1
Method	BLASTX
NCBI GI	g4314370
BLAST score	943
E value	1.0e-102
Match length	317
% identity	58
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271656
Contig ID	33818_3.R1011
5'-most EST	LIB3136-026-Q1-K1-D11
Method	BLASTX
NCBI GI	g4314370
BLAST score	304
E value	1.0e-27
Match length	71
% identity	77
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271657
Contig ID	33818_4.R1011
5'-most EST	yne700378522.h1

Seq. No.	271658
Contig ID	33826_1.R1011
5'-most EST	qmh700027264.f1

Seq. No.	271659
Contig ID	33826_2.R1011
5'-most EST	gct701177147.h1

Seq. No.	271660
Contig ID	33828_1.R1011
5'-most EST	wyr700235266.h1

Seq. No.	271661
Contig ID	33830_1.R1011
5'-most EST	LIB3157-014-Q1-K1-B4

Seq. No.	271662
Contig ID	33838_1.R1011
5'-most EST	uC-zmf1b73355d03a1

Seq. No.	271663
Contig ID	33846_1.R1011
5'-most EST	gct701179934.h1
Method	BLASTX
NCBI GI	g2285885
BLAST score	500
E value	2.0e-50
Match length	152
% identity	58
NCBI Description	(D89631) sulfate transporter [Arabidopsis thaliana]

Seq. No.	271664
Contig ID	33849_1.R1011
5'-most EST	ntr700076492.h1
Method	BLASTX
NCBI GI	g1705585
BLAST score	2428
E value	0.0e+00
Match length	662
% identity	95
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) >gi_82710_pir__JH0667 phosphoenolpyruvate carboxylase (EC 4.1.1.31) C3-form - maize >gi_429149_emb_CAA43709_ (X61489) phosphoenolpyruvate carboxylase [Zea mays]

Seq. No.	271665
Contig ID	33850_1.R1011
5'-most EST	LIB3157-014-Q1-K1-E3
Method	BLASTX
NCBI GI	g3334112
BLAST score	356
E value	8.0e-34
Match length	83
% identity	78
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1938236_emb_CAA70200_ (Y08996) acyl-CoA-binding protein [Ricinus communis]

Seq. No.	271666
Contig ID	33853_1.R1011
5'-most EST	fdz701164342.h1

Seq. No.	271667
Contig ID	33856_1.R1011
5'-most EST	uwc700155618.h1
Method	BLASTX
NCBI GI	g4314378
BLAST score	374
E value	2.0e-35
Match length	168

% identity	44
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.	271668
Contig ID	33856_2.R1011
5'-most EST	LIB3157-014-Q1-K1-E9
Seq. No.	271669
Contig ID	33856_3.R1011
5'-most EST	uC-zmflmo17022d02b1
Method	BLASTX
NCBI GI	g2129636
BLAST score	308
E value	5.0e-28
Match length	173
% identity	38
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]
Seq. No.	271670
Contig ID	33856_5.R1011
5'-most EST	uwc700153821.h1
Seq. No.	271671
Contig ID	33866_1.R1011
5'-most EST	fwa700101367.h1
Method	BLASTX
NCBI GI	g2498864
BLAST score	505
E value	1.0e-58
Match length	268
% identity	47
NCBI Description	RRP5 PROTEIN HOMOLOG (KIAA0185) >gi_1136430_dbj_BAA11502_ (D80007) similar to hypothetical protein YM9959.11C of S.cerevisiae. [Homo sapiens]
Seq. No.	271672
Contig ID	33870_1.R1011
5'-most EST	nbm700464837.h1
Method	BLASTX
NCBI GI	g1399038
BLAST score	267
E value	1.0e-22
Match length	274
% identity	30
NCBI Description	(U40762) glycerophosphodiester phosphodiesterase [Borrelia hermsii] >gi_1513213 (U65980) 38 kDa lipoprotein Gpd [Borrelia hermsii]
Seq. No.	271673
Contig ID	33870_3.R1011
5'-most EST	uC-zmflb73366e07a1
Seq. No.	271674
Contig ID	33871_1.R1011
5'-most EST	uC-zmroteosinte075g09b1
Method	BLASTX

NCBI GI	g1931645
BLAST score	519
E value	2.0e-52
Match length	164
% identity	63
NCBI Description	(U95973) Fe(II) transporter isolog [Arabidopsis thaliana]

Seq. No.	271675
Contig ID	33874_1.R1011
5'-most EST	tfd700573356.h1

Seq. No.	271676
Contig ID	33879_1.R1011
5'-most EST	uC-zmroteosinte102g04b2

Seq. No.	271677
Contig ID	33895_1.R1011
5'-most EST	wty700167006.h1
Method	BLASTX
NCBI GI	g3859944
BLAST score	420
E value	5.0e-41
Match length	123
% identity	69
NCBI Description	(AF084570) FKBP12 interacting protein [Arabidopsis thaliana]

Seq. No.	271678
Contig ID	33899_1.R1011
5'-most EST	LIB84-003-Q1-E1-H6

Seq. No.	271679
Contig ID	33904_1.R1011
5'-most EST	uC-zmroteosinte027c11b1

Seq. No.	271680
Contig ID	33910_1.R1011
5'-most EST	uC-zmflmo17317h12a1

Seq. No.	271681
Contig ID	33915_2.R1011
5'-most EST	tfd700572554.h1
Method	BLASTX
NCBI GI	g2589162
BLAST score	460
E value	8.0e-46
Match length	94
% identity	99
NCBI Description	(D88451) aldehyde oxidase [Zea mays]

Seq. No.	271682
Contig ID	33920_1.R1011
5'-most EST	uer700581662.h1

Seq. No.	271683
Contig ID	33921_1.R1011
5'-most EST	tfd700569210.h2

Method	BLASTX
NCBI GI	g2505877
BLAST score	241
E value	5.0e-20
Match length	97
% identity	49
NCBI Description	(Y12776) dehydrogenase [Arabidopsis thaliana]

Seq. No.	271684
Contig ID	33925_1.R1011
5'-most EST	uC-zmflmo17166e12b1
Method	BLASTX
NCBI GI	g4314388
BLAST score	470
E value	7.0e-47
Match length	122
% identity	70
NCBI Description	(AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271685
Contig ID	33925_2.R1011
5'-most EST	uC-zmflmo17166f12b1
Method	BLASTX
NCBI GI	g4314388
BLAST score	243
E value	3.0e-20
Match length	111
% identity	46
NCBI Description	(AC006232) hypothetical protein [Arabidop thaliana]

Seq. No.	271686
Contig ID	33932_1.R1011
5'-most EST	uC-zmflb73166b07a1

Seq. No.	271687
Contig ID	33935_1.R1011
5'-most EST	fdz70l165161.h1

Seq. No.	271688
Contig ID	33936_1.R1011
5'-most EST	uC-zmflmo17267g05a1

Seq. No.	271689
Contig ID	33942_2.R1011
5'-most EST	pmx700083248.h1

Seq. No.	271690
Contig ID	33943_1.R1011
5'-most EST	ntr700077411.h1

Seq. No.	271691
Contig ID	33947_1.R1011
5'-most EST	uC-zmflmo17292b07b1

Seq. No.	271692
Contig ID	33952_1.R1011
5'-most EST	xjt700095396.h1

Method	BLASTX
NCBI GI	g3880440
BLAST score	146
E value	6.0e-09
Match length	106
% identity	33
NCBI Description	(Z82062) cDNA EST yk415c12.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	271693
Contig ID	33954_1.R1011
5'-most EST	uC-zmflb73028c01a1
Method	BLASTX
NCBI GI	g4584429
BLAST score	298
E value	5.0e-27
Match length	109
% identity	51
NCBI Description	(AJ237751) aquaglyceroporin [Nicotiana tabacum]

Seq. No.	271694
Contig ID	33958_1.R1011
5'-most EST	uC-zmflm017089b01b1

Seq. No.	271695
Contig ID	33958_2.R1011
5'-most EST	nbm700469055.h1

Seq. No.	271696
Contig ID	33961_1.R1011
5'-most EST	LIB3157-016-Q1-K1-E8

Seq. No.	271697
Contig ID	33966_1.R1011
5'-most EST	uC-zmroteosinte040d05b1
Method	BLASTX
NCBI GI	g3522943
BLAST score	1700
E value	0.0e+00
Match length	513
% identity	33
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	271698
Contig ID	33966_2.R1011
5'-most EST	uC-zmflmo17203b08a1

Seq. No.	271699
Contig ID	33973_1.R1011
5'-most EST	afb700381147.h1
Method	BLASTX
NCBI GI	g4163997
BLAST score	419
E value	8.0e-41
Match length	182
% identity	49
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis

thaliana]

Seq. No.	271700
Contig ID	33980_1.R1011
5'-most EST	LIB3068-048-Q1-K1-C10

Seq. No.	271701
Contig ID	33984_1.R1011
5'-most EST	uC-zmflb73215h03a2

Seq. No.	271702
Contig ID	33997_1.R1011
5'-most EST	uC-zmflmo17054f11a1
Method	BLASTN
NCBI GI	g927571
BLAST score	326
E value	0.0e+00
Match length	406
% identity	94
NCBI Description	Z.mays mRNA for calreticulin precursor

Seq. No.	271703
Contig ID	33999_1.R1011
5'-most EST	LIB3157-017-Q1-K1-C1

Seq. No.	271704
Contig ID	34005_1.R1011
5'-most EST	LIB3157-017-Q1-K1-D12
Method	BLASTX
NCBI GI	g1742953
BLAST score	509
E value	1.0e-51
Match length	148
% identity	64
NCBI Description	(Z71445) CLC-a chloride channel protein [Arabidopsis thaliana]

Seq. No.	271705
Contig ID	34011_1.R1011
5'-most EST	rvl700456807.h1
Method	BLASTX
NCBI GI	g2330651
BLAST score	179
E value	2.0e-12
Match length	198
% identity	34
NCBI Description	(Y14559) topoisomerase II [Pisum sativum]

Seq. No.	271706
Contig ID	34014_1.R1011
5'-most EST	uC-zmflb73112d04a1

Seq. No.	271707
Contig ID	34014_2.R1011
5'-most EST	uC-zmflmo17227e03a1

Seq. No.	271708

Contig ID	34030_1.R1011
5'-most EST	fwa70̄0097985.h1
Method	BLASTX
NCBI GI	g121341
BLAST score	678
E value	3.0e-71
Match length	126
% identity	100
NCBI Description	GLUTAMINE SYNTHETASE, CHLOROPLAST PRECURSOR (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_539063_pir__S39482 glutamate--ammonia ligase (EC 6.3.1.2̄) 1 precursor, chloroplast - maize >gi_434334_emb_CAA46724_ (X65931) glutamine synthetase [Zea mays]

Seq. No.	271709
Contig ID	34034_1.R1011
5'-most EST	afb70̄0380861.h1

Seq. No.	271710
Contig ID	34034_3.R1011
5'-most EST	tfd70̄0574514.h1

Seq. No.	271711
Contig ID	34046_1.R1011
5'-most EST	nbm70̄0475923.h1
Method	BLASTX
NCBI GI	g3461817
BLAST score	361
E value	2.0e-34
Match length	126
% identity	52
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	271712
Contig ID	34053_1.R1011
5'-most EST	xmt70̄0264276.h1

Seq. No.	271713
Contig ID	34058_1.R1011
5'-most EST	wty70̄0172918.h1
Method	BLASTX
NCBI GI	g2708741
BLAST score	738
E value	3.0e-78
Match length	188
% identity	73
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271714
Contig ID	34069_1.R1011
5'-most EST	cat70̄0018157.r1

Seq. No.	271715
Contig ID	34073_1.R1011
5'-most EST	LIB315̄7-018-Q1-K1-F1

Seq. No.	271716

Contig ID	34077_1.R1011
5'-most EST	uC-zmf1b73225h03b1
Seq. No.	271717
Contig ID	34079_1.R1011
5'-most EST	LIB3062-002-Q1-K2-E12
Method	BLASTX
NCBI GI	g4263704
BLAST score	222
E value	7.0e-25
Match length	161
% identity	40
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]
Seq. No.	271718
Contig ID	34092_1.R1011
5'-most EST	LIB143-012-Q1-E1-B10
Method	BLASTX
NCBI GI	g3152598
BLAST score	158
E value	3.0e-10
Match length	176
% identity	27
NCBI Description	(AC002986) Contains similarity to C2-HC type zinc finger protein C.e-MyT1 gb_U67079 from C. elegans and to hypersensitivity-related gene 201 isolog T28M21.14 from A. thaliana BAC gb_AF002109. [Arabidopsis thaliana]
Seq. No.	271719
Contig ID	34095_1.R1011
5'-most EST	xjt700093856.h1
Method	BLASTX
NCBI GI	g4314378
BLAST score	516
E value	6.0e-52
Match length	339
% identity	36
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.	271720
Contig ID	34098_1.R1011
5'-most EST	LIB3068-025-Q1-K1-C2
Method	BLASTX
NCBI GI	g560610
BLAST score	161
E value	7.0e-11
Match length	48
% identity	52
NCBI Description	trypsin inhibitor, WTI [Triticum aestivum=wheat, variety San Pastore, endosperm, Peptide, 71 aa]
Seq. No.	271721
Contig ID	34098_2.R1011
5'-most EST	LIB3137-021-Q1-K1-A11
Method	BLASTX
NCBI GI	g560610

BLAST score	207
E value	3.0e-16
Match length	71
% identity	51
NCBI Description	trypsin inhibitor, WTI [Triticum aestivum=wheat, variety San Pastore, endosperm, Peptide, 71 aa]

Seq. No.	271722
Contig ID	34102_1.R1011
5'-most EST	ymt700219154.h1

Seq. No.	271723
Contig ID	34106_1.R1011
5'-most EST	wty700163594.h1
Method	BLASTN
NCBI GI	g507844
BLAST score	45
E value	5.0e-16
Match length	49
% identity	49
NCBI Description	Zea mays A188 retrotransposon gag gene, complete cds

Seq. No.	271724
Contig ID	34106_2.R1011
5'-most EST	tzu700201904.h1
Method	BLASTN
NCBI GI	g312178
BLAST score	52
E value	3.0e-20
Match length	84
% identity	90
NCBI Description	Z.mays GapC2 gene

Seq. No.	271725
Contig ID	34108_1.R1011
5'-most EST	LIB3136-037-P1-K1-B12
Method	BLASTX
NCBI GI	g4584255
BLAST score	1049
E value	1.0e-115
Match length	205
% identity	90
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	271726
Contig ID	34113_1.R1011
5'-most EST	clt700044761.f1
Method	BLASTX
NCBI GI	g4538992
BLAST score	166
E value	3.0e-11
Match length	49
% identity	57
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	271727
Contig ID	34118_1.R1011

5'-most EST	LIB3182-009-P2-M1-F5
Method	BLASTX
NCBI GI	g2827528
BLAST score	194
E value	1.0e-14
Match length	48
% identity	73
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	271728
Contig ID	34119_1.R1011
5'-most EST	uC-zmflmo17289g05a1

Seq. No.	271729
Contig ID	34121_1.R1011
5'-most EST	LIB3157-019-Q1-K1-F3

Seq. No.	271730
Contig ID	34124_1.R1011
5'-most EST	cat700016789.r1

Seq. No.	271731
Contig ID	34126_1.R1011
5'-most EST	uC-zmflmo17371d12a1

Seq. No.	271732
Contig ID	34142_1.R1011
5'-most EST	dyk700102047.h1
Method	BLASTX
NCBI GI	g1362103
BLAST score	279
E value	1.0e-24
Match length	81
% identity	67
NCBI Description	ubiquitin conjugating enzyme - tomato >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating enzyme [Lycopersicon esculentum]

Seq. No.	271733
Contig ID	34145_1.R1011
5'-most EST	LIB3067-026-Q1-K1-H9
Method	BLASTX
NCBI GI	g2944417
BLAST score	221
E value	8.0e-18
Match length	93
% identity	53
NCBI Description	(AF049881) peroxidase FLXPER4 [Linum usitatissimum]

Seq. No.	271734
Contig ID	34145_2.R1011
5'-most EST	uC-zmflb73325b01a1
Method	BLASTX
NCBI GI	g129805
BLAST score	178
E value	7.0e-13
Match length	64

% identity	58
NCBI Description	CATIONIC PEROXIDASE 1 PRECURSOR >gi_99872_pir__A38265 peroxidase (EC 1.11.1.7) precursor, cationic (clone PNC1) - peanut

Seq. No.	271735
Contig ID	34151_1.R1011
5'-most EST	rvt700550328.h1

Seq. No.	271736
Contig ID	34153_1.R1011
5'-most EST	LIB3136-035-Q1-K1-E9

Seq. No.	271737
Contig ID	34174_1.R1011
5'-most EST	xyt700343072.h1

Seq. No.	271738
Contig ID	34186_1.R1011
5'-most EST	LIB3060-027-Q1-K1-B9
Method	BLASTX
NCBI GI	g3874991
BLAST score	155
E value	1.0e-15
Match length	191
% identity	32
NCBI Description	(Z81449) UNC-93 protein [Caenorhabditis elegans]

Seq. No.	271739
Contig ID	34192_1.R1011
5'-most EST	LIB3069-049-Q1-K1-F5
Method	BLASTX
NCBI GI	g3702319
BLAST score	150
E value	5.0e-09
Match length	150
% identity	27
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271740
Contig ID	34192_2.R1011
5'-most EST	LIB3136-014-Q1-K1-H1

Seq. No.	271741
Contig ID	34197_1.R1011
5'-most EST	cjh700197264.h1
Method	BLASTN
NCBI GI	g2326786
BLAST score	105
E value	7.0e-52
Match length	237
% identity	86
NCBI Description	O.sativa mRNA for SEB1 protein

Seq. No.	271742
Contig ID	34205_1.R1011
5'-most EST	LIB3157-020-Q1-K1-G5

Seq. No.	271743
Contig ID	34210_1.R1011
5'-most EST	uC-zmflMo17085g11b1

Seq. No.	271744
Contig ID	34217_1.R1011
5'-most EST	xyt700342662.h1
Method	BLASTX
NCBI GI	g100535
BLAST score	212
E value	2.0e-16
Match length	78
% identity	58
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	271745
Contig ID	34217_2.R1011
5'-most EST	vux700157378.h1

Seq. No.	271746
Contig ID	34217_3.R1011
5'-most EST	cyk700049917.f1

Seq. No.	271747
Contig ID	34223_1.R1011
5'-most EST	cyk700047920.f1
Method	BLASTX
NCBI GI	g2832783
BLAST score	753
E value	1.0e-161
Match length	328
% identity	86
NCBI Description	(AJ225806) potassium channel beta subunit [Egeria densa]

Seq. No.	271748
Contig ID	34223_2.R1011
5'-most EST	LIB3069-031-Q1-K1-F1
Method	BLASTX
NCBI GI	g1197587
BLAST score	252
E value	2.0e-21
Match length	57
% identity	93
NCBI Description	(U46758) potassium channel beta subunit protein [Oryza sativa]

Seq. No.	271749
Contig ID	34225_1.R1011
5'-most EST	hbs701186145.h1

Seq. No.	271750
Contig ID	34239_1.R1011
5'-most EST	pmx700090237.h1
Method	BLASTX

NCBI GI	g4218120
BLAST score	687
E value	2.0e-72
Match length	186
% identity	69
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	271751
Contig ID	34245_1.R1011
5'-most EST	LIB143-016-Q1-E1-B9
Method	BLASTX
NCBI GI	g3242705
BLAST score	486
E value	8.0e-49
Match length	107
% identity	82
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	271752
Contig ID	34246_1.R1011
5'-most EST	LIB3157-021-Q1-K1-E1

Seq. No.	271753
Contig ID	34248_1.R1011
5'-most EST	LIB3157-021-Q1-K1-E12

Seq. No.	271754
Contig ID	34251_1.R1011
5'-most EST	uC-zmroteosinte041g11b1
Method	BLASTX
NCBI GI	g2662310
BLAST score	527
E value	1.0e-53
Match length	113
% identity	89
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]

Seq. No.	271755
Contig ID	34256_1.R1011
5'-most EST	uC-zmf1b73130a02b2
Method	BLASTX
NCBI GI	g2697103
BLAST score	177
E value	4.0e-12
Match length	128
% identity	35
NCBI Description	(AF000364) heterogeneous nuclear ribonucleoprotein R [Homo sapiens]

Seq. No.	271756
Contig ID	34256_2.R1011
5'-most EST	kem700612212.h1
Method	BLASTX
NCBI GI	g2697103
BLAST score	280

E value	2.0e-24
Match length	211
% identity	36
NCBI Description	(AF000364) heterogeneous nuclear ribonucleoprotein R [Homo sapiens]

Seq. No.	271757
Contig ID	34258_1.R1011
5'-most EST	uC-zmroteosinte046d07b1
Method	BLASTX
NCBI GI	g3193303
BLAST score	240
E value	8.0e-20
Match length	100
% identity	50
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	271758
Contig ID	34262_1.R1011
5'-most EST	wty700172144.h1

Seq. No.	271759
Contig ID	34266_1.R1011
5'-most EST	hbs701181948.h1

Seq. No.	271760
Contig ID	34268_1.R1011
5'-most EST	uC-zmflb73276d02b1
Method	BLASTX
NCBI GI	g1407705
BLAST score	930
E value	1.0e-162
Match length	800
% identity	42
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	271761
Contig ID	34274_1.R1011
5'-most EST	LIB3136-049-Q1-K1-G12
Method	BLASTX
NCBI GI	g4335763
BLAST score	408
E value	2.0e-39
Match length	170
% identity	49
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	271762
Contig ID	34276_1.R1011
5'-most EST	xsy700209329.h1
Method	BLASTX
NCBI GI	g3250697
BLAST score	254
E value	1.0e-21

Match length	75
% identity	67
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	271763
Contig ID	34284_1.R1011
5'-most EST	LIB3158-001-Q1-K1-D5

Seq. No.	271764
Contig ID	34286_1.R1011
5'-most EST	nbm700466170.h1

Seq. No.	271765
Contig ID	34288_1.R1011
5'-most EST	uC-zmrob73050b04b1
Method	BLASTX
NCBI GI	g4204263
BLAST score	213
E value	7.0e-17
Match length	134
% identity	40
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	271766
Contig ID	34290_1.R1011
5'-most EST	LIB3158-001-Q1-K1-E12
Method	BLASTX
NCBI GI	g2262159
BLAST score	889
E value	9.0e-96
Match length	262
% identity	63
NCBI Description	(AC002329) predicted protein similar to S.pombe protein C5H10.03 [Arabidopsis thaliana]

Seq. No.	271767
Contig ID	34293_1.R1011
5'-most EST	uC-zmflb73196f02b1
Method	BLASTX
NCBI GI	g4584685
BLAST score	427
E value	5.0e-42
Match length	117
% identity	68
NCBI Description	(AJ237754) putative lectin [Hordeum vulgare]

Seq. No.	271768
Contig ID	34297_1.R1011
5'-most EST	LIB143-022-Q1-E1-D3
Method	BLASTX
NCBI GI	g2501555
BLAST score	1165
E value	1.0e-128
Match length	300
% identity	72
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	271769
Contig ID	34297_2.R1011
5'-most EST	LIB3137-014-Q1-K1-F8
Method	BLASTX
NCBI GI	g2501555
BLAST score	523
E value	5.0e-53
Match length	193
% identity	56
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	271770
Contig ID	34298_1.R1011
5'-most EST	LIB3158-001-Q1-K1-A11
Method	BLASTX
NCBI GI	g4107276
BLAST score	266
E value	3.0e-23
Match length	61
% identity	79
NCBI Description	(X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No.	271771
Contig ID	34301_1.R1011
5'-most EST	uC-zmflmo17053b06b1

Seq. No.	271772
Contig ID	34303_1.R1011
5'-most EST	xsy700207483.h1
Method	BLASTX
NCBI GI	g170131
BLAST score	389
E value	2.0e-37
Match length	99
% identity	70
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	271773
Contig ID	34309_1.R1011
5'-most EST	LIB83-015-Q1-E1-D2
Method	BLASTX
NCBI GI	g3687235
BLAST score	588
E value	2.0e-60
Match length	147
% identity	80
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	271774
Contig ID	34313_1.R1011
5'-most EST	uC-zmflmo17164e05b1

Seq. No.	271775
Contig ID	34322_2.R1011

5'-most EST	uC-zmflmo17199g01b1
Seq. No.	271776
Contig ID	34340_1.R1011
5'-most EST	vux700159287.h1
Method	BLASTX
NCBI GI	g4376650
BLAST score	308
E value	5.0e-28
Match length	102
% identity	56
NCBI Description	(AE001621) GcpE Protein [Chlamydia pneumoniae]
Seq. No.	271777
Contig ID	34344_1.R1011
5'-most EST	uC-zmflb73020g08b1
Seq. No.	271778
Contig ID	34344_2.R1011
5'-most EST	LIB3179-002-P1-K2-F9
Seq. No.	271779
Contig ID	34344_3.R1011
5'-most EST	ymt700224237.h1
Seq. No.	271780
Contig ID	34350_1.R1011
5'-most EST	LIB3158-003-Q1-K1-E12
Seq. No.	271781
Contig ID	34377_1.R1011
5'-most EST	LIB3158-003-Q1-K1-H10
Method	BLASTX
NCBI GI	g4469025
BLAST score	343
E value	4.0e-32
Match length	78
% identity	81
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	271782
Contig ID	34377_2.R1011
5'-most EST	tfd700571124.h1
Method	BLASTX
NCBI GI	g4469025
BLAST score	278
E value	8.0e-25
Match length	64
% identity	80
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	271783
Contig ID	34378_1.R1011
5'-most EST	uC-zmflb73091f11a1
Method	BLASTN
NCBI GI	g313135
BLAST score	363

E value	0.0e+00
Match length	379
% identity	99
NCBI Description	Z.mays mRNA for porin

Seq. No.	271784
Contig ID	34378_2.R1011
5'-most EST	tfd700575765.h1
Method	BLASTN
NCBI GI	g313135
BLAST score	276
E value	1.0e-154
Match length	319
% identity	97
NCBI Description	Z.mays mRNA for porin

Seq. No.	271785
Contig ID	34379_1.R1011
5'-most EST	LIB3158-003-Q1-K1-H5
Method	BLASTX
NCBI GI	g3241944
BLAST score	295
E value	2.0e-26
Match length	65
% identity	78
NCBI Description	(AC004625) DNA-(apurinic or apyrimidinic site) lyase, ARP [Arabidopsis thaliana]

Seq. No.	271786
Contig ID	34380_1.R1011
5'-most EST	LIB3136-002-P1-K1-A7

Seq. No.	271787
Contig ID	34384_1.R1011
5'-most EST	uC-zmflb73060d02b1
Method	BLASTX
NCBI GI	g3687235
BLAST score	486
E value	1.0e-48
Match length	135
% identity	65
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	271788
Contig ID	34384_2.R1011
5'-most EST	fdz701158410.h1

Seq. No.	271789
Contig ID	34391_1.R1011
5'-most EST	LIB3136-025-Q1-K1-C3

Seq. No.	271790
Contig ID	34392_1.R1011
5'-most EST	uC-zmroteosinte061b02b2
Method	BLASTX
NCBI GI	g2947064

BLAST score	561
E value	2.0e-57
Match length	196
% identity	56
NCBI Description	(AC002521) unknown protein [Arabidopsis thaliana]

Seq. No.	271791
Contig ID	34402_1.R1011
5'-most EST	LIB3158-004-Q1-K1-D2
Method	BLASTX
NCBI GI	g2459408
BLAST score	478
E value	8.0e-48
Match length	157
% identity	61
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana] >gi_2924769 (AC002334) unknown protein [Arabidopsis thaliana]

Seq. No.	271792
Contig ID	34404_1.R1011
5'-most EST	LIB3158-004-Q1-K1-D4
Method	BLASTX
NCBI GI	g4454567
BLAST score	193
E value	4.0e-14
Match length	144
% identity	35
NCBI Description	(AF128407) lipase homolog [Arabidopsis thaliana]

Seq. No.	271793
Contig ID	34408_1.R1011
5'-most EST	LIB3158-004-Q1-K1-E2
Method	BLASTX
NCBI GI	g407942
BLAST score	560
E value	3.0e-57
Match length	250
% identity	46
NCBI Description	(U02496) epoxide hydrolase [Solanum tuberosum]

Seq. No.	271794
Contig ID	34409_1.R1011
5'-most EST	uC-zmrob73059g12a1

Seq. No.	271795
Contig ID	34415_1.R1011
5'-most EST	uC-zmflmo17159a07b1

Seq. No.	271796
Contig ID	34422_1.R1011
5'-most EST	LIB3158-004-Q1-K1-G4

Seq. No.	271797
Contig ID	34432_1.R1011
5'-most EST	hbs701185720.h1
Method	BLASTX

NCBI GI	g3522941
BLAST score	196
E value	2.0e-19
Match length	63
% identity	77
NCBI Description	(AC004411) putative peptide chain release factor [Arabidopsis thaliana]

Seq. No.	271798
Contig ID	34434_1.R1011
5'-most EST	LIB3158-004-Q1-K1-H9

Seq. No.	271799
Contig ID	34445_1.R1011
5'-most EST	ceu700429004.h1
Method	BLASTX
NCBI GI	g4582470
BLAST score	471
E value	3.0e-47
Match length	147
% identity	28
NCBI Description	(AC007071) unknown protein [Arabidopsis thaliana]

Seq. No.	271800
Contig ID	34452_1.R1011
5'-most EST	LIB3158-005-Q1-K1-B9
Method	BLASTX
NCBI GI	g2245118
BLAST score	609
E value	5.0e-63
Match length	154
% identity	69
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271801
Contig ID	34459_1.R1011
5'-most EST	uC-zmflmo17075h06a1
Method	BLASTX
NCBI GI	g1402918
BLAST score	245
E value	2.0e-20
Match length	89
% identity	56
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	271802
Contig ID	34459_2.R1011
5'-most EST	ntr700074921.h1
Method	BLASTX
NCBI GI	g1402918
BLAST score	1115
E value	1.0e-122
Match length	331
% identity	66
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana]

	>gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]
Seq. No.	271803
Contig ID	34459_3.R1011
5'-most EST	wyr700240850.h1
Method	BLASTX
NCBI GI	g1402918
BLAST score	305
E value	8.0e-28
Match length	81
% identity	68
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]
Seq. No.	271804
Contig ID	34459_4.R1011
5'-most EST	uC-zmroteosinte064g01b1
Method	BLASTX
NCBI GI	g1402918
BLAST score	223
E value	2.0e-18
Match length	55
% identity	75
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]
Seq. No.	271805
Contig ID	34463_1.R1011
5'-most EST	gct701178895.h1
Seq. No.	271806
Contig ID	34468_1.R1011
5'-most EST	wen700335894.h1
Seq. No.	271807
Contig ID	34476_1.R1011
5'-most EST	uC-zmflb73180d01b1
Method	BLASTX
NCBI GI	g1708924
BLAST score	2245
E value	0.0e+00
Match length	530
% identity	79
NCBI Description	MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate dehydrogenase (NADP+) [Vitis vinifera]
Seq. No.	271808
Contig ID	34476_2.R1011
5'-most EST	uC-zmflmo17297e12b1
Method	BLASTX
NCBI GI	g1708924
BLAST score	511
E value	8.0e-52

Match length	133
% identity	75
NCBI Description	MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate dehydrogenase (NADP+) [Vitis vinifera]

Seq. No.	271809
Contig ID	34476_3.R1011
5'-most EST	uC-zmroteosinte075e11b1
Method	BLASTX
NCBI GI	g1561774
BLAST score	504
E value	4.0e-63
Match length	162
% identity	72
NCBI Description	(U67426) malate dehydrogenase [Vitis vinifera]

Seq. No.	271810
Contig ID	34477_1.R1011
5'-most EST	LIB3137-033-Q1-K1-H3

Seq. No.	271811
Contig ID	34477_2.R1011
5'-most EST	uC-zmroteosinte047h09b1

Seq. No.	271812
Contig ID	34478_1.R1011
5'-most EST	uC-zmflmo17046g12b1

Seq. No.	271813
Contig ID	34478_2.R1011
5'-most EST	LIB3137-018-Q1-K1-G1
Method	BLASTX
NCBI GI	g3068705
BLAST score	315
E value	2.0e-28
Match length	204
% identity	35
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	271814
Contig ID	34478_3.R1011
5'-most EST	LIB3137-030-Q1-K1-D2
Method	BLASTX
NCBI GI	g3068705
BLAST score	191
E value	3.0e-14
Match length	116
% identity	36
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	271815
Contig ID	34479_1.R1011
5'-most EST	uC-zmflb73066b09b1
Method	BLASTX
NCBI GI	g4427003
BLAST score	559

E value	1.0e-70
Match length	187
% identity	74
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No.	271816
Contig ID	34479_2.R1011
5'-most EST	xmt700259067.h1
Method	BLASTX
NCBI GI	g4427003
BLAST score	602
E value	1.0e-62
Match length	139
% identity	83
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No.	271817
Contig ID	34481_1.R1011
5'-most EST	LIB3136-024-Q1-K1-D3
Method	BLASTX
NCBI GI	g3355480
BLAST score	218
E value	2.0e-17
Match length	154
% identity	32
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	271818
Contig ID	34487_1.R1011
5'-most EST	uC-zmroteosinte090g05b2
Method	BLASTX
NCBI GI	g2880047
BLAST score	447
E value	4.0e-44
Match length	189
% identity	49
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	271819
Contig ID	34496_1.R1011
5'-most EST	LIB3158-005-Q1-K1-G4
Method	BLASTX
NCBI GI	g4538959
BLAST score	360
E value	4.0e-34
Match length	123
% identity	55
NCBI Description	(AL049488) putative protein [Arabidopsis thaliana]

Seq. No.	271820
Contig ID	34500_1.R1011
5'-most EST	wen700333235.h1

Seq. No.	271821
Contig ID	34502_1.R1011
5'-most EST	LIB3158-005-Q1-K1-H1

Method	BLASTX
NCBI GI	g345829
BLAST score	477
E value	2.0e-47
Match length	254
% identity	43
NCBI Description	ubiquitin carrier protein E2 - human

Seq. No.	271822
Contig ID	34507_1.R1011
5'-most EST	nbm700464778.h1
Method	BLASTX
NCBI GI	g4539465
BLAST score	350
E value	4.0e-42
Match length	371
% identity	37
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	271823
Contig ID	34507_2.R1011
5'-most EST	arm700460754.h1

Seq. No.	271824
Contig ID	34510_1.R1011
5'-most EST	uC-zmflb73272d06b1

Seq. No.	271825
Contig ID	34510_2.R1011
5'-most EST	uC-zmflb73055d11b1

Seq. No.	271826
Contig ID	34513_1.R1011
5'-most EST	LIB84-026-Q1-E1-B11

Seq. No.	271827
Contig ID	34513_2.R1011
5'-most EST	uC-zmflmo17239d02a1

Seq. No.	271828
Contig ID	34513_3.R1011
5'-most EST	zuv700356259.h1

Seq. No.	271829
Contig ID	34516_1.R1011
5'-most EST	LIB3137-033-Q1-K1-F5
Method	BLASTX
NCBI GI	g2493809
BLAST score	475
E value	1.0e-47
Match length	135
% identity	74
NCBI Description	COPROPORPHYRINOGEN III OXIDASE PRECURSOR (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) >gi_1212994_emb_CAA58037_ (X82830) coproporphyrinogen oxidase [Hordeum vulgare]

Seq. No.	271830
Contig ID	34519_1.R1011
5'-most EST	LIB3279-059-P1-K1-H9

Seq. No.	271831
Contig ID	34533_1.R1011
5'-most EST	LIB3067-036-Q1-K1-F5
Method	BLASTX
NCBI GI	g2285792
BLAST score	218
E value	6.0e-26
Match length	78
% identity	76
NCBI Description	(AB004568) cyanase [Arabidopsis thaliana] >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]

Seq. No.	271832
Contig ID	34536_1.R1011
5'-most EST	LIB3158-006-Q1-K1-C11
Method	BLASTX
NCBI GI	g1621268
BLAST score	400
E value	1.0e-54
Match length	154
% identity	68
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	271833
Contig ID	34538_1.R1011
5'-most EST	LIB3279-053-P1-K1-B6

Seq. No.	271834
Contig ID	34542_1.R1011
5'-most EST	uC-zmrob73054h07a1
Method	BLASTX
NCBI GI	g3395432
BLAST score	1065
E value	0.0e+00
Match length	437
% identity	75
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	271835
Contig ID	34542_2.R1011
5'-most EST	LIB3279-055-P1-K1-H7
Method	BLASTX
NCBI GI	g3395432
BLAST score	223
E value	5.0e-18
Match length	59
% identity	63
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	271836
Contig ID	34542_3.R1011
5'-most EST	LIB143-040-Q1-E1-D12

Seq. No.	271837
Contig ID	34542_5.R1011
5'-most EST	xmt700259064.h1
Method	BLASTX
NCBI GI	g3395432
BLAST score	389
E value	1.0e-37
Match length	140
% identity	57
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	271838
Contig ID	34543_1.R1011
5'-most EST	LIB3069-040-Q1-K1-G9

Seq. No.	271839
Contig ID	34543_2.R1011
5'-most EST	pmx700086724.h1
Method	BLASTX
NCBI GI	g4432846
BLAST score	206
E value	3.0e-16
Match length	119
% identity	53
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	271840
Contig ID	34550_1.R1011
5'-most EST	LIB148-041-Q1-E1-G1
Method	BLASTN
NCBI GI	g2801535
BLAST score	51
E value	1.0e-19
Match length	91
% identity	89
NCBI Description	Oryza sativa lysophospholipase homolog (LPL1) mRNA, complete cds

Seq. No.	271841
Contig ID	34553_1.R1011
5'-most EST	mwy700442678.h1
Method	BLASTX
NCBI GI	g3820648
BLAST score	229
E value	1.0e-18
Match length	90
% identity	51
NCBI Description	(Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	271842
Contig ID	34556_1.R1011
5'-most EST	LIB3136-056-Q1-K1-H8
Method	BLASTX
NCBI GI	g4455232
BLAST score	682
E value	9.0e-72

Match length	188
% identity	66
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	271843
Contig ID	34559_1.R1011
5'-most EST	pwr700450184.h1
Method	BLASTX
NCBI GI	g3941480
BLAST score	572
E value	8.0e-59
Match length	179
% identity	63
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	271844
Contig ID	34559_2.R1011
5'-most EST	fwa700098560.h1
Method	BLASTX
NCBI GI	g3941480
BLAST score	397
E value	1.0e-42
Match length	99
% identity	82
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	271845
Contig ID	34569_1.R1011
5'-most EST	pmx700085510.h1
Method	BLASTX
NCBI GI	g3395938
BLAST score	741
E value	3.0e-78
Match length	237
% identity	45
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	271846
Contig ID	34569_2.R1011
5'-most EST	kem700611292.h1

Seq. No.	271847
Contig ID	34573_2.R1011
5'-most EST	cyk700051736.f1

Seq. No.	271848
Contig ID	34577_1.R1011
5'-most EST	LIB3137-001-Q1-K1-B5
Method	BLASTX
NCBI GI	g2959370
BLAST score	158
E value	2.0e-10
Match length	82
% identity	38

NCBI Description	(AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	271849
Contig ID	34577_2.R1011
5'-most EST	cjh700196809.h1
Method	BLASTN
NCBI GI	g3510343
BLAST score	38
E value	6.0e-12
Match length	38
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	271850
Contig ID	34584_1.R1011
5'-most EST	ymt700223675.h1
Method	BLASTN
NCBI GI	g563633
BLAST score	90
E value	7.0e-43
Match length	98
% identity	98
NCBI Description	Z.mays (MU141B) mRNA for U14 small nucleolar RNA

Seq. No.	271851
Contig ID	34599_1.R1011
5'-most EST	mwy700439179.h1

Seq. No.	271852
Contig ID	34626_1.R1011
5'-most EST	LIB3062-024-Q1-K1-F6
Method	BLASTX
NCBI GI	g119791
BLAST score	613
E value	1.0e-104
Match length	245
% identity	78
NCBI Description	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE) >gi_1084385_pir__S22450 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor - Cuphea lanceolata >gi_18046_emb_CAA45866_ (X64566) 3-oxoacyl-[acyl-carrier protein] reductase [Cuphea lanceolata] >gi_228929_prf__1814446A beta ketoacyl-ACP reductase [Cuphea lanceolata]

Seq. No.	271853
Contig ID	34637_1.R1011
5'-most EST	LIB3136-049-Q1-K1-A5

Seq. No.	271854
Contig ID	34638_1.R1011
5'-most EST	LIB3158-010-Q1-K1-A9

Seq. No.	271855
Contig ID	34640_1.R1011

5'-most EST	LIB3158-010-Q1-K1-B11
Seq. No.	271856
Contig ID	34642_1.R1011
5'-most EST	uwc700154871.h1
Method	BLASTX
NCBI GI	g3860008
BLAST score	490
E value	3.0e-49
Match length	189
% identity	50
NCBI Description	(AF091085) unknown [Homo sapiens]
Seq. No.	271857
Contig ID	34642_2.R1011
5'-most EST	wyr700238545.h1
Method	BLASTX
NCBI GI	g3878494
BLAST score	201
E value	3.0e-15
Match length	103
% identity	41
NCBI Description	(Z79602) predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2 (SW:YAE2_YEAST); cDNA EST EMBL:T01631 comes from this gene; cDNA EST EMBL:M88949 comes from this gene [Caenorhabditis elegans]
Seq. No.	271858
Contig ID	34648_1.R1011
5'-most EST	LIB143-055-Q1-E1-F2
Method	BLASTX
NCBI GI	g3212862
BLAST score	529
E value	1.0e-53
Match length	184
% identity	58
NCBI Description	(AC004005) putative riboflavin synthase [Arabidopsis thaliana]
Seq. No.	271859
Contig ID	34648_4.R1011
5'-most EST	LIB143-012-Q1-E1-E2
Method	BLASTX
NCBI GI	g3212862
BLAST score	150
E value	1.0e-09
Match length	54
% identity	63
NCBI Description	(AC004005) putative riboflavin synthase [Arabidopsis thaliana]
Seq. No.	271860
Contig ID	34655_1.R1011
5'-most EST	uC-zmf1b73061b02b1
Seq. No.	271861
Contig ID	34655_2.R1011

5'-most EST	LIB3137-020-Q1-K1-A5
Seq. No.	271862
Contig ID	34671_1.R1011
5'-most EST	wyr700237746.h1
Method	BLASTX
NCBI GI	g4581203
BLAST score	264
E value	8.0e-23
Match length	68
% identity	75
NCBI Description	(Y17912) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]
Seq. No.	271863
Contig ID	34674_1.R1011
5'-most EST	LIB3158-010-Q1-K1-F11
Seq. No.	271864
Contig ID	34683_1.R1011
5'-most EST	LIB3158-010-Q1-K1-G1
Seq. No.	271865
Contig ID	34693_1.R1011
5'-most EST	uC-zmroteosinte008e12b1
Method	BLASTX
NCBI GI	g2119757
BLAST score	591
E value	6.0e-61
Match length	113
% identity	94
NCBI Description	glucose starvation-induced protein precursor (clone pZSS2) - maize >gi_559534_emb_CAA57674_ (X82184) defence-related protein [Zea mays]
Seq. No.	271866
Contig ID	34693_2.R1011
5'-most EST	ntr700075615.h1
Method	BLASTX
NCBI GI	g442693
BLAST score	524
E value	3.0e-53
Match length	117
% identity	80
NCBI Description	Barwin, Basic Barley Seed Protein (Nmr, 20 Structures) >gi_442694_pdb_1BW4_ Barwin, Basic Barley Seed Protein (Nmr, 20 Structures)
Seq. No.	271867
Contig ID	34693_3.R1011
5'-most EST	LIB143-050-Q1-E1-D2
Method	BLASTX
NCBI GI	g2119757
BLAST score	360
E value	3.0e-34
Match length	72
% identity	89

NCBI Description	glucose starvation-induced protein precursor (clone pZSS2) - maize >gi_559534_emb_CAA57674_ (X82184) defence-related protein [Zea mays]
Seq. No.	271868
Contig ID	34693_4.R1011
5'-most EST	dyk700102825.h1
Method	BLASTN
NCBI GI	g559533
BLAST score	62
E value	2.0e-26
Match length	126
% identity	99
NCBI Description	Z.mays mRNA for defense-related protein
Seq. No.	271869
Contig ID	34696_1.R1011
5'-most EST	LIB189-013-Q1-E1-G8
Method	BLASTX
NCBI GI	g4512122
BLAST score	492
E value	3.0e-49
Match length	256
% identity	39
NCBI Description	(AF131219) chorismate mutase 3 [Arabidopsis thaliana]
Seq. No.	271870
Contig ID	34696_2.R1011
5'-most EST	LIB3158-010-Q1-K1-H6
Seq. No.	271871
Contig ID	34696_3.R1011
5'-most EST	uC-zmflmo17140h02a1
Method	BLASTX
NCBI GI	g4512122
BLAST score	165
E value	3.0e-11
Match length	70
% identity	51
NCBI Description	(AF131219) chorismate mutase 3 [Arabidopsis thaliana]
Seq. No.	271872
Contig ID	34701_1.R1011
5'-most EST	LIB3158-011-Q1-K1-A10
Seq. No.	271873
Contig ID	34705_1.R1011
5'-most EST	uC-zmroteosinte061d05b2
Method	BLASTX
NCBI GI	g2897942
BLAST score	342
E value	1.0e-31
Match length	166
% identity	43
NCBI Description	(AF003938) thioredoxin-like protein [Homo sapiens] >gi_2961254 (AF051896) thioredoxin homolog [Homo sapiens] >gi_2970689 (AF052659) thioredoxin-related protein [Homo

	sapiens]
Seq. No.	271874
Contig ID	34705_2.R1011
5'-most EST	pmx700084218.h1
Method	BLASTX
NCBI GI	g2970691
BLAST score	185
E value	1.0e-13
Match length	85
% identity	46
NCBI Description	(AF052660) thioredoxin-related protein [Mus musculus]
Seq. No.	271875
Contig ID	34711_1.R1011
5'-most EST	ymt700219955.h1
Method	BLASTX
NCBI GI	g1653953
BLAST score	338
E value	4.0e-31
Match length	167
% identity	42
NCBI Description	(D90917) hypothetical protein [Synechocystis sp.]
Seq. No.	271876
Contig ID	34711_2.R1011
5'-most EST	xsy700208171.h1
Method	BLASTX
NCBI GI	g1653953
BLAST score	155
E value	2.0e-22
Match length	145
% identity	43
NCBI Description	(D90917) hypothetical protein [Synechocystis sp.]
Seq. No.	271877
Contig ID	34722_1.R1011
5'-most EST	hbs701183642.h1
Method	BLASTX
NCBI GI	g585661
BLAST score	211
E value	1.0e-16
Match length	65
% identity	69
NCBI Description	PEROXIDASE PRECURSOR >gi_287401_dbj_BAA03644_ (D14997) peroxidase [Oryza sativa]
Seq. No.	271878
Contig ID	34741_1.R1011
5'-most EST	wyr700243745.h1
Method	BLASTX
NCBI GI	g3738302
BLAST score	867
E value	4.0e-93
Match length	362
% identity	51
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana]

>gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	271879
Contig ID	34741_3.R1011
5'-most EST	uC-zmrob73050h10b1
Method	BLASTX
NCBI GI	g3738302
BLAST score	254
E value	8.0e-22
Match length	89
% identity	56
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	271880
Contig ID	34751_1.R1011
5'-most EST	LIB3158-011-Q1-K1-F6
Method	BLASTX
NCBI GI	g2245030
BLAST score	211
E value	4.0e-20
Match length	81
% identity	56
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]

Seq. No.	271881
Contig ID	34751_2.R1011
5'-most EST	ceu700432352.h1

Seq. No.	271882
Contig ID	34757_1.R1011
5'-most EST	uC-zmflb73152a07b1

Seq. No.	271883
Contig ID	34766_1.R1011
5'-most EST	gct701177951.h1
Method	BLASTX
NCBI GI	g3136033
BLAST score	150
E value	2.0e-09
Match length	76
% identity	45
NCBI Description	(AL023590) putative metallopeptidase [Schizosaccharomyces pombe]

Seq. No.	271884
Contig ID	34768_1.R1011
5'-most EST	gwl700614220.h1

Seq. No.	271885
Contig ID	34768_2.R1011
5'-most EST	uC-zmroteosinte115f05b1
Method	BLASTX
NCBI GI	g4511988

BLAST score	401
E value	6.0e-62
Match length	249
% identity	52
NCBI Description	(AF088896) ubiquinone methyltransferase [Zymomonas mobilis]

Seq. No.	271886
Contig ID	34768_3.R1011
5'-most EST	LIB3059-045-Q1-K1-C7

Seq. No.	271887
Contig ID	34768_4.R1011
5'-most EST	uC-zmflb73066d10b1
Method	BLASTX
NCBI GI	g4511988
BLAST score	194
E value	2.0e-14
Match length	139
% identity	40
NCBI Description	(AF088896) ubiquinone methyltransferase [Zymomonas mobilis]

Seq. No.	271888
Contig ID	34775_1.R1011
5'-most EST	pmx700083617.h1

Seq. No.	271889
Contig ID	34781_1.R1011
5'-most EST	uC-zmflmo17022d12b1
Method	BLASTX
NCBI GI	g4262149
BLAST score	540
E value	5.0e-55
Match length	142
% identity	66
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	271890
Contig ID	34786_1.R1011
5'-most EST	uer700579247.h1
Method	BLASTX
NCBI GI	g3242659
BLAST score	279
E value	5.0e-27
Match length	99
% identity	59
NCBI Description	(AB015599) spermidine synthase [Coffea arabica]

Seq. No.	271891
Contig ID	34794_1.R1011
5'-most EST	LIB3158-012-Q1-K1-C10
Method	BLASTX
NCBI GI	g4544369
BLAST score	258
E value	6.0e-25
Match length	124
% identity	52

NCBI Description	(AC006920) hypothetical protein [Arabidopsis thaliana]
Seq. No.	271892
Contig ID	34809_1.R1011
5'-most EST	LIB3158-012-Q1-K1-D7
Seq. No.	271893
Contig ID	34810_1.R1011
5'-most EST	wyr700243290.h1
Seq. No.	271894
Contig ID	34810_2.R1011
5'-most EST	uC-zmflmo17168h03b1
Seq. No.	271895
Contig ID	34822_1.R1011
5'-most EST	uC-zmroteosinte013d06b1
Method	BLASTX
NCBI GI	g2832686
BLAST score	330
E value	3.0e-30
Match length	212
% identity	36
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]
Seq. No.	271896
Contig ID	34838_1.R1011
5'-most EST	LIB3158-012-Q1-K1-H11
Method	BLASTX
NCBI GI	g2982431
BLAST score	255
E value	1.0e-21
Match length	128
% identity	5
NCBI Description	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
Seq. No.	271897
Contig ID	34853_1.R1011
5'-most EST	xjt700092786.h1
Seq. No.	271898
Contig ID	34854_1.R1011
5'-most EST	yyf700351336.h1
Method	BLASTX
NCBI GI	g3004552
BLAST score	358
E value	7.0e-34
Match length	190
% identity	43
NCBI Description	(AC003673) unknown protein [Arabidopsis thaliana]
Seq. No.	271899
Contig ID	34857_1.R1011
5'-most EST	uC-zmflb73067e04b1
Seq. No.	271900

Contig ID	34877_1.R1011
5'-most EST	xjt700094160.h1

Seq. No.	271901
Contig ID	34878_1.R1011
5'-most EST	uC-zmrob73039b10a1
Method	BLASTX
NCBI GI	g4185136
BLAST score	1373
E value	1.0e-152
Match length	396
% identity	64
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	271902
Contig ID	34890_1.R1011
5'-most EST	LIB3158-014-Q1-K1-E2
Method	BLASTX
NCBI GI	g4468990
BLAST score	465
E value	3.0e-46
Match length	177
% identity	57
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	271903
Contig ID	34900_1.R1011
5'-most EST	uC-zmflb73135h06b2

Seq. No.	271904
Contig ID	34902_1.R1011
5'-most EST	LIB3158-014-Q1-K1-F2

Seq. No.	271905
Contig ID	34903_1.R1011
5'-most EST	uC-zmflmo17268c01b1
Method	BLASTX
NCBI GI	g124021
BLAST score	266
E value	3.0e-23
Match length	64
% identity	66
NCBI Description	BOWMAN-BIRK TYPE TRYPSIN INHIBITOR TI1 >gi_68814_pir__TIOAB trypsin inhibitor (Bowman-Birk) - Job's tears

Seq. No.	271906
Contig ID	34903_2.R1011
5'-most EST	LIB3158-014-Q1-K1-F3
Method	BLASTX
NCBI GI	g124021
BLAST score	248
E value	7.0e-21
Match length	64
% identity	59
NCBI Description	BOWMAN-BIRK TYPE TRYPSIN INHIBITOR TI1 >gi_68814_pir__TIOAB trypsin inhibitor (Bowman-Birk) - Job's tears

Seq. No.	271907
Contig ID	34903_3.R1011
5'-most EST	wty700170169.h1

Seq. No.	271908
Contig ID	34919_2.R1011
5'-most EST	wty700172413.h1

Seq. No.	271909
Contig ID	34919_3.R1011
5'-most EST	pmx700089123.h1

Seq. No.	271910
Contig ID	34931_1.R1011
5'-most EST	LIB3069-009-Q1-K1-B2

Seq. No.	271911
Contig ID	34931_2.R1011
5'-most EST	uwc700151082.h1

Seq. No.	271912
Contig ID	34939_1.R1011
5'-most EST	LIB3158-015-Q1-K1-B4
Method	BLASTX
NCBI GI	g129021
BLAST score	528
E value	2.0e-53
Match length	290
% identity	41
NCBI Description	SPO0B-ASSOCIATED GTP-BINDING PROTEIN >gi_98326_pir__B32804 GTP-binding protein, spo0B 3'-region - Bacillus subtilis >gi_508979 (M24537) GTP-binding protein [Bacillus subtilis] >gi_2635257_emb_CAB14752_ (Z99118) GTPase activity [Bacillus subtilis]

Seq. No.	271913
Contig ID	34939_2.R1011
5'-most EST	xjt700092228.h1

Seq. No.	271914
Contig ID	34941_1.R1011
5'-most EST	uC-zmroteosinte053h06b2
Method	BLASTX
NCBI GI	g3152660
BLAST score	298
E value	2.0e-26
Match length	270
% identity	29
NCBI Description	(AF064603) GA17 protein [Homo sapiens]

Seq. No.	271915
Contig ID	34941_2.R1011
5'-most EST	LIB3061-057-Q1-K1-C7

Seq. No.	271916
Contig ID	34942_1.R1011

5'-most EST	wyr700240249.h1
Method	BLASTX
NCBI GI	g4206122
BLAST score	1592
E value	1.0e-178
Match length	377
% identity	79
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	271917
Contig ID	34942_2.R1011
5'-most EST	uC-zmflb73119f01b1
Method	BLASTX
NCBI GI	g4206122
BLAST score	399
E value	1.0e-38
Match length	94
% identity	81
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	271918
Contig ID	34942_3.R1011
5'-most EST	uC-zmflb73182d12b1
Method	BLASTX
NCBI GI	g4206122
BLAST score	167
E value	1.0e-11
Match length	45
% identity	67
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	271919
Contig ID	34942_4.R1011
5'-most EST	uer700579626.h1
Method	BLASTX
NCBI GI	g4206122
BLAST score	329
E value	5.0e-31
Match length	91
% identity	79
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	271920
Contig ID	34951_1.R1011
5'-most EST	pmx700082508.h1
Method	BLASTX
NCBI GI	g4314391
BLAST score	672
E value	2.0e-70
Match length	227
% identity	57
NCBI Description	(AC006232) unknown protein [Arabidopsis thaliana]

Seq. No.	271921
Contig ID	34953_1.R1011
5'-most EST	tzu700206755.h1

Seq. No.	271922
Contig ID	34960_1.R1011
5'-most EST	uC-zmflmo17023f02b1
Method	BLASTX
NCBI GI	g3063392
BLAST score	1256
E value	1.0e-138
Match length	424
% identity	61
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	271923
Contig ID	34960_4.R1011
5'-most EST	xjt700094573.h1
Method	BLASTX
NCBI GI	g3063392
BLAST score	208
E value	2.0e-16
Match length	76
% identity	59
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	271924
Contig ID	34961_1.R1011
5'-most EST	uC-zmflmo17244g02a1
Method	BLASTX
NCBI GI	g3602942
BLAST score	226
E value	1.0e-18
Match length	64
% identity	64
NCBI Description	(AF041468) PSII protein W [Guillardia theta]

Seq. No.	271925
Contig ID	34966_1.R1011
5'-most EST	uC-zmflmo17222c08b1
Method	BLASTX
NCBI GI	g283004
BLAST score	621
E value	2.0e-64
Match length	228
% identity	42
NCBI Description	DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328_ (X68261) gt-2 [Oryza sativa]

Seq. No.	271926
Contig ID	34966_2.R1011
5'-most EST	LIB3068-006-Q1-K1-A4
Method	BLASTX
NCBI GI	g100673
BLAST score	460
E value	8.0e-46
Match length	110

% identity	77
NCBI Description	DNA-binding protein GT-2 - rice (fragment)

Seq. No.	271927
Contig ID	34967_1.R1011
5'-most EST	LIB3137-038-Q1-K1-B5
Method	BLASTX
NCBI GI	g2792155
BLAST score	268
E value	2.0e-23
Match length	114
% identity	45
NCBI Description	(AJ223291) chalcone reductase [Sesbania rostrata]

Seq. No.	271928
Contig ID	34969_1.R1011
5'-most EST	uC-zmflmo17341d03a1
Method	BLASTX
NCBI GI	g4455336
BLAST score	280
E value	1.0e-24
Match length	74
% identity	61
NCBI Description	(AL035525) pectinesterase-like protein [Arabidopsis thaliana]

Seq. No.	271929
Contig ID	34975_1.R1011
5'-most EST	nbm700468110.h1

Seq. No.	271930
Contig ID	34975_2.R1011
5'-most EST	xyt700346854.h1

Seq. No.	271931
Contig ID	34975_3.R1011
5'-most EST	tzu700204231.h1

Seq. No.	271932
Contig ID	34981_1.R1011
5'-most EST	uC-zmrob73066b08b1

Seq. No.	271933
Contig ID	34981_2.R1011
5'-most EST	LIB3158-015-Q1-K1-F7
Method	BLASTX
NCBI GI	g3643088
BLAST score	217
E value	2.0e-17
Match length	62
% identity	65
NCBI Description	(AF075581) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	271934
Contig ID	34981_3.R1011
5'-most EST	LIB3067-009-Q1-K1-E2

Seq. No.	271935
Contig ID	34987_1.R1011
5'-most EST	LIB3067-033-Q1-K1-B6

Seq. No.	271936
Contig ID	34996_1.R1011
5'-most EST	tfd700570053.h1
Method	BLASTX
NCBI GI	g1770214
BLAST score	209
E value	3.0e-16
Match length	119
% identity	34
NCBI Description	(X99207) smallminded [Drosophila melanogaster]

Seq. No.	271937
Contig ID	35001_1.R1011
5'-most EST	uC-zmflb73286f04b1

Seq. No.	271938
Contig ID	35001_2.R1011
5'-most EST	xsy700213209.h1

Seq. No.	271939
Contig ID	35002_1.R1011
5'-most EST	nbm700476183.h1
Method	BLASTN
NCBI GI	g1628481
BLAST score	769
E value	0.0e+00
Match length	850
% identity	98
NCBI Description	Z.mays dek34 gene

Seq. No.	271940
Contig ID	35010_1.R1011
5'-most EST	uC-zmflb73047h06b1

Seq. No.	271941
Contig ID	35012_1.R1011
5'-most EST	uC-zmflb73279a07a2

Seq. No.	271942
Contig ID	35021_1.R1011
5'-most EST	nwy700444341.h1
Method	BLASTX
NCBI GI	g4512667
BLAST score	1547
E value	0.0e+00
Match length	517
% identity	67
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	271943
Contig ID	35022_1.R1011
5'-most EST	uC-zmroteosinte024a09b1

Method	BLASTX
NCBI GI	g2462757
BLAST score	151
E value	2.0e-09
Match length	125
% identity	33
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	271944
Contig ID	35032_1.R1011
5'-most EST	gct701178481.h1

Seq. No.	271945
Contig ID	35048_1.R1011
5'-most EST	LIB3059-030-Q1-K1-H12

Seq. No.	271946
Contig ID	35049_1.R1011
5'-most EST	uC-zmflb73214h10a1

Seq. No.	271947
Contig ID	35055_1.R1011
5'-most EST	LIB3158-016-Q1-K1-G5
Method	BLASTX
NCBI GI	g1495366
BLAST score	306
E value	1.0e-50
Match length	175
% identity	59
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	271948
Contig ID	35079_1.R1011
5'-most EST	fwa700098870.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	271949
Contig ID	35079_2.R1011
5'-most EST	LIB83-006-Q1-E1-D4

Seq. No.	271950
Contig ID	35081_1.R1011
5'-most EST	rvt700550874.h1
Method	BLASTX
NCBI GI	g1532165
BLAST score	498
E value	4.0e-50
Match length	227
% identity	47
NCBI Description	(U63815) similar to dehydrogenase encoded by GenBank Accession Number S39508; localized according to blastn

similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop

Seq. No.	271951
Contig ID	35087_1.R1011
5'-most EST	cjh700194501.h1
Method	BLASTX
NCBI GI	g3132478
BLAST score	219
E value	3.0e-17
Match length	192
% identity	32
NCBI Description	(AC003096) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	271952
Contig ID	35087_2.R1011
5'-most EST	uC-zmflb73168c05a1

Seq. No.	271953
Contig ID	35088_1.R1011
5'-most EST	uC-zmflmo17116g04a1

Seq. No.	271954
Contig ID	35088_2.R1011
5'-most EST	uC-zmflmo17116h06a1

Seq. No.	271955
Contig ID	35092_1.R1011
5'-most EST	gwl700616764.h1
Method	BLASTX
NCBI GI	g4559387
BLAST score	232
E value	7.0e-19
Match length	167
% identity	38
NCBI Description	(AC006526) putative oxa1 protein [Arabidopsis thaliana]

Seq. No.	271956
Contig ID	35116_1.R1011
5'-most EST	hbs701183682.h1
Method	BLASTX
NCBI GI	g3135264
BLAST score	411
E value	7.0e-40
Match length	177
% identity	49
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	271957
Contig ID	35123_1.R1011
5'-most EST	LIB3062-021-Q1-K1-H2

Seq. No.	271958
Contig ID	35123_2.R1011
5'-most EST	kem700610922.h1
Method	BLASTN

NCBI GI	g206371
BLAST score	71
E value	4.0e-31
Match length	95
% identity	94
NCBI Description	Rat(Sprague-Dawley) prolactin gene:exons IV,V and flanks

Seq. No.	271959
Contig ID	35136_1.R1011
5'-most EST	uC-zmflmo17281g01b1
Method	BLASTX
NCBI GI	g3822223
BLAST score	1471
E value	1.0e-164
Match length	392
% identity	69
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	271960
Contig ID	35136_2.R1011
5'-most EST	wty700167537.h1
Method	BLASTX
NCBI GI	g1945277
BLAST score	184
E value	2.0e-13
Match length	62
% identity	55
NCBI Description	(Z94180) branched chain alpha-keto acid dehydrogenase E1-alpha subunit [Lycopersicon esculentum]

Seq. No.	271961
Contig ID	35136_3.R1011
5'-most EST	LIB3060-054-Q1-K1-B8
Method	BLASTX
NCBI GI	g3822223
BLAST score	530
E value	4.0e-54
Match length	128
% identity	77
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	271962
Contig ID	35141_1.R1011
5'-most EST	LIB3069-053-Q1-K1-A5
Method	BLASTX
NCBI GI	g629592
BLAST score	827
E value	2.0e-88
Match length	302
% identity	53
NCBI Description	hypothetical protein - rape

Seq. No.	271963
Contig ID	35143_1.R1011
5'-most EST	uC-zmflb73061g05a2

Seq. No.	271964
Contig ID	35147_1.R1011
5'-most EST	uC-zmroteosinte010b12b1

Seq. No.	271965
Contig ID	35150_1.R1011
5'-most EST	LIB3136-001-P1-K1-C11
Method	BLASTN
NCBI GI	g3282393
BLAST score	42
E value	2.0e-14
Match length	122
% identity	84
NCBI Description	Oryza sativa aie2 mRNA, partial cds

Seq. No.	271966
Contig ID	35151_2.R1011
5'-most EST	clt700044572.f1

Seq. No.	271967
Contig ID	35152_1.R1011
5'-most EST	LIB3068-058-Q1-K1-E2
Method	BLASTX
NCBI GI	g3850579
BLAST score	223
E value	5.0e-18
Match length	144
% identity	36
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an

Seq. No.	271968
Contig ID	35155_1.R1011
5'-most EST	wyr700240075.h1

Seq. No.	271969
Contig ID	35157_1.R1011
5'-most EST	nbm700468059.h1

Seq. No.	271970
Contig ID	35167_1.R1011
5'-most EST	LIB3136-059-Q1-K1-C6
Method	BLASTX
NCBI GI	g3298547
BLAST score	393
E value	6.0e-38
Match length	189
% identity	46
NCBI Description	(AC004681) putative condensin protein [Arabidopsis thaliana]

Seq. No.	271971
Contig ID	35169_1.R1011

5'-most EST	LIB143-019-Q1-E1-G9
Method	BLASTX
NCBI GI	g2832898
BLAST score	1339
E value	1.0e-148
Match length	320
% identity	76
NCBI Description	(AJ000886) Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]

Seq. No.	271972
Contig ID	35169_2.R1011
5'-most EST	LIB3062-015-Q1-K1-A5
Method	BLASTX
NCBI GI	g4337027
BLAST score	686
E value	4.0e-72
Match length	185
% identity	69
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	271973
Contig ID	35169_3.R1011
5'-most EST	ntr700074190.h1
Method	BLASTX
NCBI GI	g4337027
BLAST score	583
E value	5.0e-61
Match length	151
% identity	78
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	271974
Contig ID	35173_1.R1011
5'-most EST	uC-zmroteosinte016b01b1

Seq. No.	271975
Contig ID	35177_1.R1011
5'-most EST	LIB3061-010-Q1-K1-A10
Method	BLASTX
NCBI GI	g1262756
BLAST score	160
E value	2.0e-10
Match length	81
% identity	37
NCBI Description	(X97022) lamin [Brassica oleracea]

Seq. No.	271976
Contig ID	35179_1.R1011
5'-most EST	LIB3158-018-Q1-K1-D11

Seq. No.	271977
Contig ID	35184_1.R1011
5'-most EST	uC-zmroteosinte010b02b1
Method	BLASTX
NCBI GI	g4557349
BLAST score	171

E value	6.0e-15
Match length	130
% identity	38
NCBI Description	BRCA1 associated RING domain 1 >gi_1710175 (U76638) BRCA1-associated RING domain protein [Homo sapiens]

Seq. No.	271978
Contig ID	35187_1.R1011
5'-most EST	fxb700397449.h1
Method	BLASTX
NCBI GI	g2244846
BLAST score	406
E value	2.0e-39
Match length	104
% identity	72
NCBI Description	(Z97337) ferredoxin [Arabidopsis thaliana]

Seq. No.	271979
Contig ID	35190_1.R1011
5'-most EST	wty700169383.h1
Method	BLASTX
NCBI GI	g4580455
BLAST score	415
E value	4.0e-77
Match length	200
% identity	76
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	271980
Contig ID	35201_1.R1011
5'-most EST	ceu700431146.h1
Method	BLASTX
NCBI GI	g2435518
BLAST score	295
E value	3.0e-26
Match length	105
% identity	48
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	271981
Contig ID	35201_2.R1011
5'-most EST	uC-zmflb73300g12b1

Seq. No.	271982
Contig ID	35214_1.R1011
5'-most EST	uC-zmrob73054a08a1
Method	BLASTX
NCBI GI	g4584539
BLAST score	436
E value	6.0e-43
Match length	153
% identity	52
NCBI Description	(AL049608) extensin-like protein [Arabidopsis thaliana]

Seq. No.	271983
Contig ID	35217_1.R1011

5'-most EST	LIB3158-018-Q1-K1-G6
Method	BLASTX
NCBI GI	g3661541
BLAST score	226
E value	1.0e-18
Match length	105
% identity	13
NCBI Description	(AF091396) poly-zinc finger protein [Trypanosoma cruzi]

Seq. No.	271984
Contig ID	35222_1.R1011
5'-most EST	xjt70̄0094352.h1

Seq. No.	271985
Contig ID	35222_3.R1011
5'-most EST	xjt70̄0092796.h1

Seq. No.	271986
Contig ID	35222_4.R1011
5'-most EST	xjt70̄0094695.h1

Seq. No.	271987
Contig ID	35229_1.R1011
5'-most EST	ntr70̄0074242.h1
Method	BLASTX
NCBI GI	g3176687
BLAST score	1035
E value	1.0e-113
Match length	296
% identity	63
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	271988
Contig ID	35232_1.R1011
5'-most EST	cjh70̄0194183.h1
Method	BLASTX
NCBI GI	g4220527
BLAST score	449
E value	1.0e-44
Match length	111
% identity	73
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	271989
Contig ID	35234_1.R1011
5'-most EST	rvl70̄0457259.h1
Method	BLASTX
NCBI GI	g4467130
BLAST score	947
E value	1.0e-102
Match length	278
% identity	70
NCBI Description	(AL035538) glycosyltransferase like protein [Arabidopsis thaliana]

Seq. No.	271990
Contig ID	35234_2.R1011
5'-most EST	uC-zmflmo17174a09a1

Seq. No.	271991
Contig ID	35235_1.R1011
5'-most EST	uC-zmroteosinte002d08b1

Seq. No.	271992
Contig ID	35236_1.R1011
5'-most EST	LIB3159-002-Q1-K1-G7
Method	BLASTX
NCBI GI	g1169228
BLAST score	420
E value	3.0e-41
Match length	142
% identity	62
NCBI Description	RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir__S42639 helicase-like protein - Wood tobacco >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein DB10 [Nicotiana sylvestris]

Seq. No.	271993
Contig ID	35238_1.R1011
5'-most EST	rv1700455239.h1
Method	BLASTX
NCBI GI	g4097561
BLAST score	813
E value	7.0e-87
Match length	210
% identity	77
NCBI Description	(U64918) ATGP1 [Arabidopsis thaliana]

Seq. No.	271994
Contig ID	35238_2.R1011
5'-most EST	LIB3159-002-Q1-K1-H1
Method	BLASTX
NCBI GI	g4097561
BLAST score	221
E value	4.0e-18
Match length	77
% identity	65
NCBI Description	(U64918) ATGP1 [Arabidopsis thaliana]

Seq. No.	271995
Contig ID	35243_1.R1011
5'-most EST	LIB3159-021-Q1-K1-E5

Seq. No.	271996
Contig ID	35255_1.R1011
5'-most EST	LIB3159-002-Q1-K1-E5

Seq. No.	271997
Contig ID	35260_1.R1011
5'-most EST	uC-zmflmo17116d03b1

Seq. No.	271998
Contig ID	35268_1.R1011
5'-most EST	uC-zmroteosinte006e06b1

Seq. No.	271999
Contig ID	35274_1.R1011
5'-most EST	rvt700549875.h1
Method	BLASTX
NCBI GI	g3643611
BLAST score	426
E value	5.0e-60
Match length	140
% identity	83
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	272000
Contig ID	35280_1.R1011
5'-most EST	LIB3159-002-Q1-K1-C6
Method	BLASTX
NCBI GI	g4415934
BLAST score	355
E value	1.0e-63
Match length	188
% identity	60
NCBI Description	(AC006418) putative auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	272001
Contig ID	35282_1.R1011
5'-most EST	uC-zmrob73050d04b1

Seq. No.	272002
Contig ID	35284_1.R1011
5'-most EST	cyk700051223.f1
Method	BLASTX
NCBI GI	g2462838
BLAST score	242
E value	1.0e-20
Match length	82
% identity	56
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	272003
Contig ID	35312_1.R1011
5'-most EST	LIB3062-019-Q1-K1-E8

Seq. No.	272004
Contig ID	35321_1.R1011
5'-most EST	LIB3159-003-Q1-K1-B4
Method	BLASTX
NCBI GI	g3413706
BLAST score	336
E value	2.0e-31
Match length	76
% identity	74
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272005
Contig ID	35322_1.R1011
5'-most EST	LIB3159-003-Q1-K1-B5
Method	BLASTX
NCBI GI	g4415925
BLAST score	172
E value	2.0e-14
Match length	102
% identity	43
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	272006
Contig ID	35325_1.R1011
5'-most EST	rvt700552648.h1
Method	BLASTX
NCBI GI	g2765140
BLAST score	1290
E value	1.0e-142
Match length	400
% identity	65
NCBI Description	(Y11931) 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase [Nicotiana rustica]

Seq. No.	272007
Contig ID	35341_1.R1011
5'-most EST	LIB3159-004-Q1-K1-A2

Seq. No.	272008
Contig ID	35341_2.R1011
5'-most EST	xsy700211614.h1
Method	BLASTX
NCBI GI	g4490325
BLAST score	270
E value	1.0e-34
Match length	118
% identity	61
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272009
Contig ID	35344_1.R1011
5'-most EST	uer700582864.h1

Seq. No.	272010
Contig ID	35345_1.R1011
5'-most EST	uC-zmf1b73015d07b1
Method	BLASTX
NCBI GI	g1617268
BLAST score	1402
E value	1.0e-156
Match length	400
% identity	64
NCBI Description	(Z72153) acyl CoA synthetase [Brassica napus]

Seq. No.	272011
Contig ID	35346_1.R1011
5'-most EST	uC-zmf1B73022d05b1

Method	BLASTX
NCBI GI	g2746826
BLAST score	156
E value	5.0e-10
Match length	118
% identity	32
NCBI Description	(AF040646) No definition line found [Caenorhabditis elegans]

Seq. No.	272012
Contig ID	35350_1.R1011
5'-most EST	uC-zmflb73296d12b2
Method	BLASTX
NCBI GI	g1001631
BLAST score	236
E value	3.0e-19
Match length	161
% identity	34
NCBI Description	(D64002) integral membrane protein [Synechocystis sp.]

Seq. No.	272013
Contig ID	35351_1.R1011
5'-most EST	uC-zmroB73001b11b1
Method	BLASTX
NCBI GI	g3522950
BLAST score	959
E value	1.0e-104
Match length	345
% identity	51
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272014
Contig ID	35358_1.R1011
5'-most EST	ypc700805413.h1
Method	BLASTX
NCBI GI	g4160292
BLAST score	532
E value	1.0e-68
Match length	160
% identity	73
NCBI Description	(Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]

Seq. No.	272015
Contig ID	35360_1.R1011
5'-most EST	LIB3159-004-Q1-K1-D4

Seq. No.	272016
Contig ID	35372_1.R1011
5'-most EST	uer700577462.h1
Method	BLASTN
NCBI GI	g22466
BLAST score	36
E value	9.0e-11
Match length	48
% identity	94
NCBI Description	Zea mays rcy:Mu7 Cy transposable element system

Seq. No.	272017
Contig ID	35374_1.R1011
5'-most EST	LIB3069-043-Q1-K1-H5
Method	BLASTX
NCBI GI	g3193285
BLAST score	377
E value	5.0e-36
Match length	131
% identity	57
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	272018
Contig ID	35374_2.R1011
5'-most EST	LIB84-008-Q1-E1-G6

Seq. No.	272019
Contig ID	35378_1.R1011
5'-most EST	LIB3159-004-Q1-K1-H1

Seq. No.	272020
Contig ID	35380_1.R1011
5'-most EST	pwr700449896.h2
Method	BLASTX
NCBI GI	g2213601
BLAST score	989
E value	1.0e-107
Match length	343
% identity	53
NCBI Description	(AC000348) T7N9.21 [Arabidopsis thaliana]

Seq. No.	272021
Contig ID	35392_1.R1011
5'-most EST	wyr700242527.h1
Method	BLASTX
NCBI GI	g3482919
BLAST score	648
E value	1.0e-67
Match length	194
% identity	66
NCBI Description	(AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	272022
Contig ID	35395_1.R1011
5'-most EST	LIB3159-005-Q1-K1-C4
Method	BLASTX
NCBI GI	g1617268
BLAST score	240
E value	3.0e-24
Match length	123
% identity	54
NCBI Description	(Z72153) acyl CoA synthetase [Brassica napus]

Seq. No.	272023
Contig ID	35397_1.R1011
5'-most EST	LIB3159-005-Q1-K1-D2
Method	BLASTX
NCBI GI	g1931649

BLAST score	238
E value	4.0e-20
Match length	90
% identity	57
NCBI Description	(U95973) DNA helicase isolog [Arabidopsis thaliana]

Seq. No.	272024
Contig ID	35407_1.R1011
5'-most EST	LIB3159-005-Q1-K1-G5
Method	BLASTX
NCBI GI	g1076758
BLAST score	562
E value	6.0e-58
Match length	129
% identity	85
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir__S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]

Seq. No.	272025
Contig ID	35407_2.R1011
5'-most EST	ntr700077122.h1
Method	BLASTX
NCBI GI	g1076758
BLAST score	433
E value	6.0e-43
Match length	115
% identity	77
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir__S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]

Seq. No.	272026
Contig ID	35419_1.R1011
5'-most EST	uC-zmflb73380f06a1

Seq. No.	272027
Contig ID	35429_1.R1011
5'-most EST	clt700044014.f1
Method	BLASTX
NCBI GI	g2494264
BLAST score	300
E value	7.0e-27
Match length	132
% identity	48
NCBI Description	HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105 >gi_1651837_dbj_BAA16764_ (D90900) elongation factor EF-G [Synechocystis sp.]

Seq. No.	272028
Contig ID	35432_1.R1011
5'-most EST	LIB3066-036-Q1-K1-E1

Seq. No.	272029
Contig ID	35436_1.R1011

5'-most EST	cyk700050856.f1
Seq. No.	272030
Contig ID	35443_1.R1011
5'-most EST	uC-zmroteosinte066g04b1
Seq. No.	272031
Contig ID	35443_2.R1011
5'-most EST	LIB3159-007-Q1-K1-A1
Method	BLASTX
NCBI GI	g1703012
BLAST score	237
E value	2.0e-19
Match length	246
% identity	30
NCBI Description	CYTOSOLIC PURINE 5'-NUCLEOTIDASE >gi_1079484_pir__JC2436 5'-nucleotidase (EC 3.1.3.5) - human >gi_633071_dbj_BAA07529_ (D38524) 5'-nucleotidase [Homo sapiens]
Seq. No.	272032
Contig ID	35462_1.R1011
5'-most EST	LIB3159-007-Q1-K1-B5
Seq. No.	272033
Contig ID	35472_1.R1011
5'-most EST	LIB3159-007-Q1-K1-C7
Method	BLASTX
NCBI GI	g2961345
BLAST score	348
E value	2.0e-32
Match length	82
% identity	82
NCBI Description	(AL022140) hypothetical protein [Arabidopsis thaliana]
Seq. No.	272034
Contig ID	35472_2.R1011
5'-most EST	LIB3062-023-Q1-K1-E4
Method	BLASTX
NCBI GI	g2961345
BLAST score	184
E value	2.0e-13
Match length	47
% identity	77
NCBI Description	(AL022140) hypothetical protein [Arabidopsis thaliana]
Seq. No.	272035
Contig ID	35473_1.R1011
5'-most EST	xsy700208631.h1
Seq. No.	272036
Contig ID	35473_2.R1011
5'-most EST	LIB3159-007-Q1-K1-C9
Seq. No.	272037
Contig ID	35478_1.R1011
5'-most EST	pmx700082613.h1

Seq. No.	272038
Contig ID	35480_1.R1011
5'-most EST	uC-zmflMo17089g03b1
Method	BLASTX
NCBI GI	g3980412
BLAST score	911
E value	3.0e-98
Match length	368
% identity	31
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	272039
Contig ID	35480_2.R1011
5'-most EST	LIB3159-007-Q1-K1-D7
Method	BLASTX
NCBI GI	g4539306
BLAST score	205
E value	5.0e-16
Match length	72
% identity	53
NCBI Description	(AL049480) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	272040
Contig ID	35482_1.R1011
5'-most EST	uC-zmroteosinte001d09b1
Method	BLASTN
NCBI GI	g577818
BLAST score	197
E value	1.0e-106
Match length	262
% identity	94
NCBI Description	Z.mays gene for H2B histone (gH2B4)

Seq. No.	272041
Contig ID	35482_2.R1011
5'-most EST	pmx700081960.h1
Method	BLASTN
NCBI GI	g4234845
BLAST score	425
E value	0.0e+00
Match length	457
% identity	98
NCBI Description	Zea mays copia-like retrotransposon Sto-17, partial sequence

Seq. No.	272042
Contig ID	35494_1.R1011
5'-most EST	LIB3159-007-Q1-K1-F1

Seq. No.	272043
Contig ID	35494_2.R1011
5'-most EST	hvj700620332.h1

Seq. No.	272044
Contig ID	35506_1.R1011
5'-most EST	ntr700075931.h1

Method	BLASTX
NCBI GI	g3293547
BLAST score	233
E value	5.0e-19
Match length	246
% identity	33
NCBI Description	(AF072709) putative oxidoreductase [Streptomyces lividans]

Seq. No.	272045
Contig ID	35512_1.R1011
5'-most EST	ntr700075953.h1
Method	BLASTX
NCBI GI	g4200044
BLAST score	201
E value	1.0e-15
Match length	128
% identity	35
NCBI Description	(AB022732) cytochrome P450 [Glycyrrhiza echinata]

Seq. No.	272046
Contig ID	35525_1.R1011
5'-most EST	LIB3159-008-Q1-K1-A2

Seq. No.	272047
Contig ID	35564_1.R1011
5'-most EST	uwc700153820.h1
Method	BLASTX
NCBI GI	g2541876
BLAST score	448
E value	4.0e-44
Match length	257
% identity	38
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	272048
Contig ID	35566_1.R1011
5'-most EST	LIB3159-008-Q1-K1-F11
Method	BLASTX
NCBI GI	g4490317
BLAST score	157
E value	8.0e-10
Match length	68
% identity	50
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	272049
Contig ID	35567_1.R1011
5'-most EST	LIB84-025-Q1-E1-H9

Seq. No.	272050
Contig ID	35571_1.R1011
5'-most EST	uC-zmflmo17303e12b1

Seq. No.	272051
Contig ID	35571_2.R1011
5'-most EST	LIB84-001-Q1-E1-F6

Seq. No.	272052
Contig ID	35571_3.R1011
5'-most EST	uC-zmroteosinte080h09b1

Seq. No.	272053
Contig ID	35574_1.R1011
5'-most EST	pmx700087470.h1
Method	BLASTX
NCBI GI	g2160177
BLAST score	816
E value	6.0e-87
Match length	444
% identity	50
NCBI Description	(AC000132) EST gb_R64758 comes from this gene. [Arabidopsis thaliana]

Seq. No.	272054
Contig ID	35575_1.R1011
5'-most EST	uC-zmflb73194a08b2
Method	BLASTX
NCBI GI	g1653291
BLAST score	482
E value	2.0e-62
Match length	251
% identity	49
NCBI Description	(D90912) hypothetical protein [Synechocystis sp.]

Seq. No.	272055
Contig ID	35579_1.R1011
5'-most EST	kem700610923.h1

Seq. No.	272056
Contig ID	35583_1.R1011
5'-most EST	LIB3070-008-Q1-N1-H8
Method	BLASTX
NCBI GI	g3157934
BLAST score	868
E value	2.0e-93
Match length	201
% identity	82
NCBI Description	(AC002131) Similar to hypothetical protein F09E5.8 gb_U37429 from C. elegans. ESTs gb_T42019 and gb_N97000 come from this gene. [Arabidopsis thaliana]

Seq. No.	272057
Contig ID	35596_1.R1011
5'-most EST	uC-zmroteosinte082a05b2
Method	BLASTX
NCBI GI	g421989
BLAST score	1081
E value	1.0e-118
Match length	273
% identity	77
NCBI Description	serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx [Hordeum vulgare]

Seq. No.	272058
Contig ID	35599_1.R1011
5'-most EST	LIB3066-047-Q1-K1-C1

Seq. No.	272059
Contig ID	35611_1.R1011
5'-most EST	LIB3159-009-Q1-K1-E12
Method	BLASTX
NCBI GI	g2288988
BLAST score	297
E value	2.0e-26
Match length	120
% identity	43
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272060
Contig ID	35615_1.R1011
5'-most EST	gwl700615538.h1

Seq. No.	272061
Contig ID	35633_1.R1011
5'-most EST	wen700332785.h1
Method	BLASTX
NCBI GI	g4406764
BLAST score	559
E value	2.0e-57
Match length	177
% identity	64
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	272062
Contig ID	35640_1.R1011
5'-most EST	uC-zmflb73172g06a1

Seq. No.	272063
Contig ID	35646_1.R1011
5'-most EST	LIB3159-010-Q1-K1-A7

Seq. No.	272064
Contig ID	35664_1.R1011
5'-most EST	dyk700103120.h1
Method	BLASTX
NCBI GI	g2465923
BLAST score	741
E value	2.0e-78
Match length	325
% identity	48
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	272065
Contig ID	35675_1.R1011
5'-most EST	uer700582208.h1

Seq. No.	272066

Contig ID	35681_1.R1011
5'-most EST	tfd70̄0570193.h1
Method	BLASTX
NCBI GI	g3746071
BLAST score	741
E value	2.0e-78
Match length	197
% identity	70
NCBI Description	(AC005311) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No.	272067
Contig ID	35682_1.R1011
5'-most EST	cyk70̄0051102.f1
Method	BLASTX
NCBI GI	g3482978
BLAST score	375
E value	3.0e-36
Match length	103
% identity	74
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	272068
Contig ID	35700_1.R1011
5'-most EST	uC-zmf̄lmo17160a08b1
Method	BLASTX
NCBI GI	g2262105
BLAST score	551
E value	3.0e-56
Match length	220
% identity	50
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	272069
Contig ID	35704_1.R1011
5'-most EST	uC-zmf̄lmo17168c04b1

Seq. No.	272070
Contig ID	35711_1.R1011
5'-most EST	vux70̄0161738.h1
Method	BLASTX
NCBI GI	g1707008
BLAST score	220
E value	1.0e-17
Match length	113
% identity	42
NCBI Description	(U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]

Seq. No.	272071
Contig ID	35716_1.R1011
5'-most EST	LIB315̄9-011-Q1-K1-B8

Seq. No.	272072
Contig ID	35722_1.R1011
5'-most EST	LIB306̄9-036-Q1-K1-F1

Seq. No.	272073
Contig ID	35733_1.R1011
5'-most EST	LIB3159-011-Q1-K1-D6
Seq. No.	272074
Contig ID	35735_2.R1011
5'-most EST	ymt70_0223623.h1
Seq. No.	272075
Contig ID	35741_1.R1011
5'-most EST	LIB189-002-Q1-E1-A2
Seq. No.	272076
Contig ID	35743_1.R1011
5'-most EST	uC-zmflmo17038a09b1
Method	BLASTX
NCBI GI	g2213626
BLAST score	303
E value	3.0e-27
Match length	125
% identity	50
NCBI Description	(AC000103) F21J9.18 [Arabidopsis thaliana]
Seq. No.	272077
Contig ID	35749_1.R1011
5'-most EST	LIB3137-040-Q1-K1-E12
Method	BLASTN
NCBI GI	g2198852
BLAST score	40
E value	6.0e-13
Match length	84
% identity	87
NCBI Description	Zea mays cystathionine gamma-synthase (CGS1) gene, complete cds
Seq. No.	272078
Contig ID	35759_1.R1011
5'-most EST	LIB3159-011-Q1-K1-G9
Seq. No.	272079
Contig ID	35763_2.R1011
5'-most EST	nbm70_0467252.h1
Seq. No.	272080
Contig ID	35772_1.R1011
5'-most EST	uC-zmflmo17278g09b1
Seq. No.	272081
Contig ID	35781_1.R1011
5'-most EST	LIB3159-012-Q1-K1-B2
Seq. No.	272082
Contig ID	35786_1.R1011
5'-most EST	LIB3159-012-Q1-K1-B9
Seq. No.	272083
Contig ID	35799_1.R1011

5'-most EST	qmh700029801.f1
Method	BLASTX
NCBI GI	g3461835
BLAST score	774
E value	1.0e-82
Match length	188
% identity	77
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No.	272084
Contig ID	35804_1.R1011
5'-most EST	uC-zmflb73135a12b2

Seq. No.	272085
Contig ID	35805_1.R1011
5'-most EST	LIB143-014-Q1-E1-D7

Seq. No.	272086
Contig ID	35810_1.R1011
5'-most EST	uC-zmflmo17113d07a1
Method	BLASTX
NCBI GI	g2760317
BLAST score	201
E value	1.0e-15
Match length	59
% identity	63
NCBI Description	(AC002130) F1N21.1 [Arabidopsis thaliana]

Seq. No.	272087
Contig ID	35810_2.R1011
5'-most EST	rvl700456526.h1
Method	BLASTX
NCBI GI	g3341697
BLAST score	486
E value	7.0e-49
Match length	158
% identity	57
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272088
Contig ID	35815_1.R1011
5'-most EST	uC-zmflb73158f08b2

Seq. No.	272089
Contig ID	35815_2.R1011
5'-most EST	uC-zmrob73079b06b1

Seq. No.	272090
Contig ID	35815_3.R1011
5'-most EST	uC-zmflb73017h01b1
Method	BLASTX
NCBI GI	g3258575
BLAST score	248
E value	7.0e-21
Match length	66

% identity	70
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	272091
Contig ID	35816_1.R1011
5'-most EST	LIB3159-012-Q1-K1-F8

Seq. No.	272092
Contig ID	35818_1.R1011
5'-most EST	LIB3136-003-Q1-K1-H8
Method	BLASTX
NCBI GI	g115815
BLAST score	596
E value	7.0e-62
Match length	126
% identity	89
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll a/b-binding protein precursor - maize >gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

Seq. No.	272093
Contig ID	35821_1.R1011
5'-most EST	LIB189-025-Q1-E1-B10
Method	BLASTX
NCBI GI	g2760830
BLAST score	532
E value	3.0e-54
Match length	111
% identity	86
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	272094
Contig ID	35821_2.R1011
5'-most EST	LIB3159-012-Q1-K1-G2
Method	BLASTX
NCBI GI	g4544399
BLAST score	265
E value	1.0e-25
Match length	91
% identity	73
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	272095
Contig ID	35824_1.R1011
5'-most EST	uC-zmroteosinte021g05b1
Method	BLASTX
NCBI GI	g3367571
BLAST score	316
E value	8.0e-29
Match length	167
% identity	43
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	272096
Contig ID	35824_2.R1011
5'-most EST	rvl700456346.h1
Seq. No.	272097
Contig ID	35829_1.R1011
5'-most EST	LIB3159-012-Q1-K1-H3
Seq. No.	272098
Contig ID	35830_1.R1011
5'-most EST	LIB3066-019-Q1-K1-H10
Method	BLASTX
NCBI GI	g2827664
BLAST score	175
E value	2.0e-12
Match length	42
% identity	71
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana] >gi_2982427_emb_CAA18236_ (AL022224) hypothetical protein [Arabidopsis thaliana]
Seq. No.	272099
Contig ID	35833_1.R1011
5'-most EST	LIB3159-013-Q1-K1-A11
Method	BLASTX
NCBI GI	g3183106
BLAST score	491
E value	4.0e-49
Match length	258
% identity	42
NCBI Description	PROBABLE OXALYL-COA DECARBOXYLASE >gi_1788716 (AE000325) putative enzyme [Escherichia coli]
Seq. No.	272100
Contig ID	35843_1.R1011
5'-most EST	LIB3159-013-Q1-K1-B12
Seq. No.	272101
Contig ID	35844_1.R1011
5'-most EST	LIB3159-013-Q1-K1-B2
Seq. No.	272102
Contig ID	35846_1.R1011
5'-most EST	LIB3159-013-Q1-K1-B4
Seq. No.	272103
Contig ID	35847_1.R1011
5'-most EST	sem700930110.h1
Method	BLASTX
NCBI GI	g2738996
BLAST score	867
E value	2.0e-93
Match length	248
% identity	65
NCBI Description	(AF022457) CYP97B2p [Glycine max]
Seq. No.	272104

Contig ID	35856_1.R1011
5'-most EST	LIB3159-013-Q1-K1-C6

Seq. No.	272105
Contig ID	35860_1.R1011
5'-most EST	uC-zmroteosinte034h04b1
Method	BLASTX
NCBI GI	g4455360
BLAST score	154
E value	8.0e-15
Match length	157
% identity	9
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	272106
Contig ID	35862_1.R1011
5'-most EST	LIB3159-013-Q1-K1-D3
Method	BLASTX
NCBI GI	g986969
BLAST score	387
E value	2.0e-37
Match length	150
% identity	53
NCBI Description	(L28005) TGACG-motif-binding protein [Glycine max]

Seq. No.	272107
Contig ID	35866_1.R1011
5'-most EST	LIB84-024-Q1-E1-F6
Method	BLASTX
NCBI GI	g2130023
BLAST score	204
E value	1.0e-15
Match length	105
% identity	41
NCBI Description	DNA-binding protein ABF1 - wild oat (fragment) >gi_1159877_emb_CAA88326_ (Z48429) DNA-binding protein [Avena fatua]

Seq. No.	272108
Contig ID	35878_1.R1011
5'-most EST	mwy700441373.h1
Method	BLASTX
NCBI GI	g3252807
BLAST score	489
E value	3.0e-49
Match length	171
% identity	58
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272109
Contig ID	35884_1.R1011
5'-most EST	LIB3159-013-Q1-K1-F7

Seq. No.	272110
Contig ID	35885_1.R1011
5'-most EST	LIB3159-013-Q1-K1-F8

Seq. No.	272111
Contig ID	35891_1.R1011
5'-most EST	pmx700083227.h1
Method	BLASTX
NCBI GI	g2827711
BLAST score	1600
E value	1.0e-179
Match length	354
% identity	81
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	272112
Contig ID	35899_1.R1011
5'-most EST	LIB3159-013-Q1-K1-H12

Seq. No.	272113
Contig ID	35901_1.R1011
5'-most EST	tfd700575753.h1

Seq. No.	272114
Contig ID	35901_2.R1011
5'-most EST	fdz701160778.h1

Seq. No.	272115
Contig ID	35911_1.R1011
5'-most EST	uC-zmflmo17340h10b1
Method	BLASTX
NCBI GI	g1223579
BLAST score	221
E value	1.0e-17
Match length	185
% identity	34
NCBI Description	(X96481) cDNA101 [Arabidopsis thaliana]

Seq. No.	272116
Contig ID	35912_1.R1011
5'-most EST	ntr700073337.h1
Method	BLASTX
NCBI GI	g3859696
BLAST score	144
E value	7.0e-09
Match length	144
% identity	27
NCBI Description	(AL033497) unknown hypothetical protein [Candida albicans]

Seq. No.	272117
Contig ID	35919_1.R1011
5'-most EST	uC-zmflmo17113h11b1
Method	BLASTX
NCBI GI	g2924247
BLAST score	1142
E value	1.0e-125
Match length	233
% identity	89
NCBI Description	(Y07782) expansin [Oryza sativa]

Seq. No.	272118
Contig ID	35919_3.R1011
5'-most EST	uC-zmflb73124c05a1
Method	BLASTX
NCBI GI	g2924247
BLAST score	424
E value	9.0e-42
Match length	91
% identity	88
NCBI Description	(Y07782) expansin [Oryza sativa]

Seq. No.	272119
Contig ID	35927_1.R1011
5'-most EST	LIB3067-059-Q1-K1-H3
Method	BLASTX
NCBI GI	g2129851
BLAST score	416
E value	2.0e-40
Match length	219
% identity	39
NCBI Description	tRNA adenylyltransferase (EC 2.7.7.25) - white lupine >gi_1139585 (U15930) tRNA nucleotidyltransferase [Lupinus albus]

Seq. No.	272120
Contig ID	35930_1.R1011
5'-most EST	LIB189-034-Q1-E1-H1
Method	BLASTX
NCBI GI	g4103635
BLAST score	227
E value	2.0e-18
Match length	113
% identity	42
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	272121
Contig ID	35940_1.R1011
5'-most EST	ymt700220233.h1
Method	BLASTX
NCBI GI	g4336205
BLAST score	584
E value	5.0e-60
Match length	256
% identity	48
NCBI Description	(AF077372) cytochrome b5 reductase [Zea mays]

Seq. No.	272122
Contig ID	35941_2.R1011
5'-most EST	ymt700219961.h1

Seq. No.	272123
Contig ID	35966_1.R1011
5'-most EST	LIB3159-016-Q1-K1-B2

Seq. No.	272124
Contig ID	35972_1.R1011
5'-most EST	LIB3159-016-Q1-K1-B4

Seq. No.	272125
Contig ID	35973_1.R1011
5'-most EST	xmt700267968.h1
Method	BLASTX
NCBI GI	g1168750
BLAST score	303
E value	3.0e-27
Match length	172
% identity	36
NCBI Description	CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) >gi_458230 (U04380) calcineurin B [Naegleria gruberi]

Seq. No.	272126
Contig ID	35974_1.R1011
5'-most EST	nwy700443423.h1
Method	BLASTX
NCBI GI	g1330343
BLAST score	361
E value	3.0e-34
Match length	113
% identity	60
NCBI Description	(U58755) C34D4.12 gene product [Caenorhabditis elegans]

Seq. No.	272127
Contig ID	35980_1.R1011
5'-most EST	clt700044849.f1
Method	BLASTX
NCBI GI	g3386548
BLAST score	248
E value	6.0e-21
Match length	184
% identity	35
NCBI Description	(AF079504) H-protein promoter binding factor-2b [Arabidopsis thaliana]

Seq. No.	272128
Contig ID	35985_2.R1011
5'-most EST	LIB3159-016-Q1-K1-C9
Method	BLASTX
NCBI GI	g1296805
BLAST score	394
E value	5.0e-67
Match length	163
% identity	82
NCBI Description	(X90929) C-terminal peptidase of the D1 protein [Hordeum vulgare]

Seq. No.	272129
Contig ID	35998_1.R1011
5'-most EST	LIB3159-016-Q1-K1-F1

Seq. No.	272130
Contig ID	36008_1.R1011
5'-most EST	LIB3159-016-Q1-K1-G1

Seq. No.	272131
Contig ID	36008_2.R1011
5'-most EST	uC-zmflmo17220f12b1
Seq. No.	272132
Contig ID	36019_1.R1011
5'-most EST	uC-zmflm017086c01b1
Seq. No.	272133
Contig ID	36019_2.R1011
5'-most EST	dyk700104408.h1
Method	BLASTX
NCBI GI	g1352057
BLAST score	252
E value	2.0e-21
Match length	88
% identity	59
NCBI Description	AUXIN-INDUCED PROTEIN IAA4 >gi_629633_pir__S39075 auxin-induced protein - garden pea >gi_414181_emb_CAA48297_ (X68215) auxin-induced protein [Pisum sativum]
Seq. No.	272134
Contig ID	36033_1.R1011
5'-most EST	LIB3059-040-Q1-K1-G3
Method	BLASTX
NCBI GI	g3805770
BLAST score	228
E value	1.0e-18
Match length	102
% identity	44
NCBI Description	(U78721) ETTIN protein [Arabidopsis thaliana]
Seq. No.	272135
Contig ID	36034_1.R1011
5'-most EST	LIB3060-015-Q1-K1-E9
Seq. No.	272136
Contig ID	36037_1.R1011
5'-most EST	LIB3159-017-Q1-K1-B2
Seq. No.	272137
Contig ID	36038_1.R1011
5'-most EST	LIB3180-045-P2-M2-H5
Seq. No.	272138
Contig ID	36044_1.R1011
5'-most EST	uC-zmflmo17131h02a1
Seq. No.	272139
Contig ID	36044_2.R1011
5'-most EST	uC-zmromo17026h07a1
Seq. No.	272140
Contig ID	36044_3.R1011
5'-most EST	uC-zmflb73076e06b2
Seq. No.	272141

Contig ID	36052_1.R1011
5'-most EST	LIB3159-017-Q1-K1-D1
Seq. No.	272142
Contig ID	36052_2.R1011
5'-most EST	cjh700196148.h1
Method	BLASTX
NCBI GI	g3461820
BLAST score	256
E value	4.0e-24
Match length	158
% identity	45
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.	272143
Contig ID	36052_3.R1011
5'-most EST	uC-zmflb73151d08a2
Seq. No.	272144
Contig ID	36064_1.R1011
5'-most EST	uC-zmflb73017d10b1
Method	BLASTX
NCBI GI	g2244866
BLAST score	847
E value	9.0e-91
Match length	247
% identity	65
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	272145
Contig ID	36064_2.R1011
5'-most EST	uC-zmroteosinte020f06b1
Method	BLASTX
NCBI GI	g2244866
BLAST score	270
E value	1.0e-23
Match length	89
% identity	54
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	272146
Contig ID	36064_3.R1011
5'-most EST	uwc700150844.h1
Method	BLASTX
NCBI GI	g2244866
BLAST score	185
E value	5.0e-14
Match length	57
% identity	61
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	272147
Contig ID	36066_1.R1011
5'-most EST	ypc700800741.h1
Method	BLASTX
NCBI GI	g4325339
BLAST score	1315

E value	1.0e-145
Match length	348
% identity	65
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	272148
Contig ID	36087_1.R1011
5'-most EST	uC-zmflb73264e09b1
Method	BLASTX
NCBI GI	g3395758
BLAST score	461
E value	8.0e-46
Match length	164
% identity	55
NCBI Description	(U76300) unknown [Arabidopsis thaliana]

Seq. No.	272149
Contig ID	36092_1.R1011
5'-most EST	uC-zmflmo17263f05b1
Method	BLASTX
NCBI GI	g3128218
BLAST score	1274
E value	1.0e-140
Match length	378
% identity	67
NCBI Description	(AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No.	272150
Contig ID	36095_1.R1011
5'-most EST	LIB3059-036-Q1-K1-B5

Seq. No.	272151
Contig ID	36102_1.R1011
5'-most EST	xtd700282282.h2

Seq. No.	272152
Contig ID	36105_1.R1011
5'-most EST	hvj700620740.h1
Method	BLASTX
NCBI GI	g3138972
BLAST score	631
E value	1.0e-108
Match length	360
% identity	60
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	272153
Contig ID	36105_2.R1011
5'-most EST	fC-zmro700571675a1
Method	BLASTX
NCBI GI	g3138972
BLAST score	436
E value	3.0e-43
Match length	137
% identity	66

NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	272154
Contig ID	36105_3.R1011
5'-most EST	uC-zmflb73098a11b1
Method	BLASTX
NCBI GI	g3138972
BLAST score	380
E value	8.0e-46
Match length	146
% identity	68
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	272155
Contig ID	36111_1.R1011
5'-most EST	LIB3159-018-Q1-K1-B8

Seq. No.	272156
Contig ID	36123_1.R1011
5'-most EST	LIB3159-018-Q1-K1-D1

Seq. No.	272157
Contig ID	36137_1.R1011
5'-most EST	LIB3069-009-Q1-K1-C4
Method	BLASTX
NCBI GI	g3858935
BLAST score	823
E value	5.0e-88
Match length	220
% identity	72
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	272158
Contig ID	36139_1.R1011
5'-most EST	uC-zmflb73262b03b3
Method	BLASTX
NCBI GI	g4512649
BLAST score	1036
E value	1.0e-113
Match length	261
% identity	71
NCBI Description	(AC007048) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272159
Contig ID	36140_1.R1011
5'-most EST	xyt700346830.h1
Method	BLASTX
NCBI GI	g2842648
BLAST score	216
E value	4.0e-17

Match length	94
% identity	46
NCBI Description	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KD SUBUNIT RELATED-PROTEIN 2 >gi_2137782_pir__A57120 small nuclear ribonucleoprotein auxiliary factor U2 - mouse >gi_927659_dbj_BAA08143_ (D45205) U2af1-rs2 [Mus musculus]

Seq. No.	272160
Contig ID	36146_1.R1011
5'-most EST	LIB3159-018-Q1-K1-G1

Seq. No.	272161
Contig ID	36148_1.R1011
5'-most EST	LIB3159-018-Q1-K1-G4

Seq. No.	272162
Contig ID	36152_1.R1011
5'-most EST	uC-zmflb73136d03b1

Seq. No.	272163
Contig ID	36154_1.R1011
5'-most EST	cat700020395.r1

Seq. No.	272164
Contig ID	36155_1.R1011
5'-most EST	LIB3060-013-Q1-K1-B12

Seq. No.	272165
Contig ID	36174_1.R1011
5'-most EST	LIB3159-019-Q1-K1-C10

Seq. No.	272166
Contig ID	36187_1.R1011
5'-most EST	uC-zmflb73040b02b1
Method	BLASTX
NCBI GI	g1871192
BLAST score	330
E value	4.0e-54
Match length	243
% identity	51
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	272167
Contig ID	36191_1.R1011
5'-most EST	LIB3159-019-Q1-K1-E3
Method	BLASTX
NCBI GI	g168445
BLAST score	297
E value	7.0e-27
Match length	97
% identity	60
NCBI Description	(L00973) acidic class I chitinase [Zea mays]

Seq. No.	272168
Contig ID	36202_1.R1011
5'-most EST	clt700041638.f1

Seq. No.	272169
Contig ID	36203_1.R1011
5'-most EST	LIB3067-034-Q1-K1-F5
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	272170
Contig ID	36203_2.R1011
5'-most EST	cat700019373.r1
Method	BLASTX
NCBI GI	g4056428
BLAST score	222
E value	4.0e-18
Match length	78
% identity	63
NCBI Description	(AC005322) Similar to gb_U43629 integral membrane protein from Beta vulgaris and a member of sugar transporter family PF_00083. [Arabidopsis thaliana]

Seq. No.	272171
Contig ID	36204_1.R1011
5'-most EST	wyr700237333.h1
Method	BLASTX
NCBI GI	g3377822
BLAST score	543
E value	3.0e-55
Match length	243
% identity	51
NCBI Description	(AF076275) contains similarity to Caenorhabditis elegans MEL-26 (GB:U67737) [Arabidopsis thaliana]

Seq. No.	272172
Contig ID	36213_1.R1011
5'-most EST	LIB3068-059-Q1-K1-A10

Seq. No.	272173
Contig ID	36213_2.R1011
5'-most EST	ymt700218955.h1
Method	BLASTX
NCBI GI	g1171747
BLAST score	685
E value	6.0e-72
Match length	194
% identity	65
NCBI Description	PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120) >gi_482505_pir__A48168 proliferating-cell nucleolar antigen P120 - human >gi_287723_emb_CAA39119_ (X55504) P120 antigen [Homo sapiens]

Seq. No. 272174

Contig ID	36214_1.R1011
5'-most EST	LIB143-020-Q1-E1-A10
Seq. No.	272175
Contig ID	36218_1.R1011
5'-most EST	uC-zmflmo17202c03b1
Method	BLASTN
NCBI GI	g902585
BLAST score	40
E value	1.0e-12
Match length	72
% identity	89
NCBI Description	Zea mays clone MubG9 ubiquitin gene, complete cds
Seq. No.	272176
Contig ID	36225_1.R1011
5'-most EST	xmt700262525.h1
Seq. No.	272177
Contig ID	36226_1.R1011
5'-most EST	wyr700240804.h1
Seq. No.	272178
Contig ID	36227_1.R1011
5'-most EST	LIB3159-020-Q1-K1-A3
Method	BLASTX
NCBI GI	g4006886
BLAST score	406
E value	2.0e-39
Match length	210
% identity	59
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	272179
Contig ID	36230_1.R1011
5'-most EST	LIB3159-020-Q1-K1-A6
Seq. No.	272180
Contig ID	36234_1.R1011
5'-most EST	xjt700096110.h1
Method	BLASTX
NCBI GI	g2791278
BLAST score	626
E value	6.0e-65
Match length	377
% identity	36
NCBI Description	(Z69257) beta-xylosidase [Hypocrea jecorina]
Seq. No.	272181
Contig ID	36239_1.R1011
5'-most EST	xjt700095668.h1
Method	BLASTX
NCBI GI	g3136313
BLAST score	1190
E value	1.0e-131
Match length	242
% identity	89

NCBI Description	(AF062735) soluble acid invertase [Saccharum officinarum]

Seq. No.	272182
Contig ID	36248_1.R1011
5'-most EST	LIB3059-044-Q1-K1-H7

Seq. No.	272183
Contig ID	36248_2.R1011
5'-most EST	LIB3137-013-Q1-K1-D9
Method	BLASTX
NCBI GI	g3702343
BLAST score	602
E value	5.0e-62
Match length	336
% identity	41
NCBI Description	(AC005397) putative homeotic gene regulator [Arabidopsis thaliana]

Seq. No.	272184
Contig ID	36254_1.R1011
5'-most EST	uwc700151624.h1
Method	BLASTX
NCBI GI	g4512263
BLAST score	1001
E value	1.0e-109
Match length	267
% identity	74
NCBI Description	(AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]

Seq. No.	272185
Contig ID	36268_1.R1011
5'-most EST	LIB3159-020-Q1-K1-F7
Method	BLASTX
NCBI GI	g731485
BLAST score	484
E value	2.0e-48
Match length	251
% identity	40
NCBI Description	HYPOTHETICAL 62.3 KD PROTEIN IN PTP3-ILV1 INTERGENIC REGION >gi_1077677_pir__S50585 hypothetical protein YER082c - yeast (Saccharomyces cerevisiae) >gi_603320 (U18839) Yer082cp [Saccharomyces cerevisiae]

Seq. No.	272186
Contig ID	36281_1.R1011
5'-most EST	LIB3159-020-Q1-K1-H2

Seq. No.	272187
Contig ID	36283_1.R1011
5'-most EST	uC-zmrob73019a01b1
Method	BLASTX
NCBI GI	g2813966
BLAST score	435
E value	2.0e-42
Match length	337
% identity	34
NCBI Description	(Z97053) placental protein Diff33 [Homo sapiens]

>gi_4545219_gb_AAD22448.1_ (AF112227) TDE homolog [Homo sapiens]

Seq. No.	272188
Contig ID	36296_1.R1011
5'-most EST	uC-zmflm017205h10b1
Method	BLASTX
NCBI GI	g4262234
BLAST score	692
E value	6.0e-73
Match length	210
% identity	60
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	272189
Contig ID	36296_2.R1011
5'-most EST	wty700164341.h1
Method	BLASTX
NCBI GI	g4262234
BLAST score	159
E value	3.0e-16
Match length	59
% identity	62
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	272190
Contig ID	36307_1.R1011
5'-most EST	tfd700572370.h1
Method	BLASTX
NCBI GI	g3834323
BLAST score	240
E value	5.0e-20
Match length	154
% identity	35
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	272191
Contig ID	36308_1.R1011
5'-most EST	xsy700217478.h1
Method	BLASTX
NCBI GI	g2182029
BLAST score	1891
E value	0.0e+00
Match length	399
% identity	91
NCBI Description	(Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No.	272192
Contig ID	36309_1.R1011
5'-most EST	LIB3159-021-Q1-K1-C5

Seq. No.	272193
Contig ID	36312_1.R1011
5'-most EST	gct701176853.h1
Method	BLASTX
NCBI GI	g3924604
BLAST score	429

E value	3.0e-42
Match length	167
% identity	53
NCBI Description	(AF069442) putative leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	272194
Contig ID	36315_1.R1011
5'-most EST	LIB3159-021-Q1-K1-D3

Seq. No.	272195
Contig ID	36320_1.R1011
5'-most EST	LIB3159-021-Q1-K1-E10
Method	BLASTX
NCBI GI	g3445204
BLAST score	585
E value	3.0e-60
Match length	173
% identity	64
NCBI Description	(AC004786) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No.	272196
Contig ID	36341_1.R1011
5'-most EST	uC-zmflmo17181d06b1

Seq. No.	272197
Contig ID	36348_1.R1011
5'-most EST	wen700333103.h1
Method	BLASTX
NCBI GI	g4522009
BLAST score	753
E value	4.0e-82
Match length	275
% identity	60
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	272198
Contig ID	36349_1.R1011
5'-most EST	rvl700454585.h1
Method	BLASTX
NCBI GI	g550542
BLAST score	1551
E value	1.0e-173
Match length	316
% identity	96
NCBI Description	(X81831) cytochrome P450 [Zea mays] >gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea mays]

Seq. No.	272199
Contig ID	36349_2.R1011
5'-most EST	LIB3136-023-Q1-K1-H9
Method	BLASTX
NCBI GI	g550542
BLAST score	335
E value	6.0e-59

Match length	139
% identity	90
NCBI Description	(X81831) cytochrome P450 [Zea mays] >gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea mays]

Seq. No.	272200
Contig ID	36357_1.R1011
5'-most EST	uC-zmflb73142d05b1
Method	BLASTX
NCBI GI	g2827631
BLAST score	746
E value	5.0e-79
Match length	254
% identity	57
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	272201
Contig ID	36357_2.R1011
5'-most EST	fC-zmle700444014a1
Method	BLASTX
NCBI GI	g2827631
BLAST score	208
E value	2.0e-16
Match length	79
% identity	52
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	272202
Contig ID	36357_3.R1011
5'-most EST	rvl700456423.h1
Method	BLASTX
NCBI GI	g2827631
BLAST score	180
E value	2.0e-24
Match length	106
% identity	58
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	272203
Contig ID	36363_1.R1011
5'-most EST	LIB3179-001-P1-K1-B4
Method	BLASTX
NCBI GI	g2460203
BLAST score	156
E value	2.0e-10
Match length	73
% identity	47
NCBI Description	(AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]

Seq. No.	272204
Contig ID	36364_1.R1011
5'-most EST	tfd700572187.h1

Seq. No.	272205
Contig ID	36367_1.R1011

5'-most EST	LIB3179-001-P1-K2-D1
Seq. No.	272206
Contig ID	36370_1.R1011
5'-most EST	nwy700443859.h1
Method	BLASTX
NCBI GI	g2118425
BLAST score	221
E value	6.0e-18
Match length	63
% identity	71
NCBI Description	subtilisin/chymotrypsin inhibitor - maize >gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea mays] >gi_475922_emb_CAA49593_ (X69972) proteinase inhibitor [Zea mays] >gi_559538_emb_CAA57677_ (X82187) substilin /chymotrypsin-like inhibitor [Zea mays]
Seq. No.	272207
Contig ID	36384_1.R1011
5'-most EST	xsy700217778.h1
Seq. No.	272208
Contig ID	36387_1.R1011
5'-most EST	LIB3060-006-Q1-K1-B12
Method	BLASTX
NCBI GI	g4206195
BLAST score	401
E value	1.0e-38
Match length	162
% identity	52
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana]
Seq. No.	272209
Contig ID	36396_1.R1011
5'-most EST	uC-zmflMo17013f07b1
Method	BLASTX
NCBI GI	g1723125
BLAST score	362
E value	3.0e-34
Match length	121
% identity	60
NCBI Description	HYPOTHETICAL 27.8 KD PROTEIN SLL0194 >gi_1001604_dbj_BAA10232_ (D64000) hypothetical protein [Synechocystis sp.]
Seq. No.	272210
Contig ID	36396_2.R1011
5'-most EST	uC-zmflb73057a02b1
Seq. No.	272211
Contig ID	36410_1.R1011
5'-most EST	uC-zmflmo17377b08a1
Seq. No.	272212
Contig ID	36486_1.R1011

5'-most EST	LIB3179-002-P1-K2-A10
Seq. No.	272213
Contig ID	36489_1.R1011
5'-most EST	cjh700193217.h1
Seq. No.	272214
Contig ID	36503_1.R1011
5'-most EST	nbm700471422.h1
Seq. No.	272215
Contig ID	36504_1.R1011
5'-most EST	nbm700466555.h1
Method	BLASTX
NCBI GI	g3287494
BLAST score	465
E value	2.0e-46
Match length	135
% identity	73
NCBI Description	(D78504) similar to yeast SRP1 [Oryza sativa]
Seq. No.	272216
Contig ID	36509_1.R1011
5'-most EST	LIB3179-002-P1-K2-E8
Method	BLASTX
NCBI GI	g298750
BLAST score	921
E value	1.0e-100
Match length	171
% identity	99
NCBI Description	photosystem I reaction center protein psaA product [Sorghum bicolor, Qiuji No. 5, Peptide Chloroplast, 750 aa]
Seq. No.	272217
Contig ID	36511_1.R1011
5'-most EST	LIB3179-002-P1-K2-E3
Method	BLASTX
NCBI GI	g2058313
BLAST score	334
E value	4.0e-31
Match length	100
% identity	62
NCBI Description	(X97433) cinnamoyl-CoA reductase [Eucalyptus gunnii]
Seq. No.	272218
Contig ID	36514_1.R1011
5'-most EST	LIB3060-054-Q1-K1-F4
Seq. No.	272219
Contig ID	36514_2.R1011
5'-most EST	LIB3060-002-Q1-K2-G8
Method	BLASTX
NCBI GI	g3643602
BLAST score	223
E value	4.0e-18
Match length	131
% identity	40

NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	272220
Contig ID	36515_1.R1011
5'-most EST	LIB36-009-Q1-E1-C1
Method	BLASTX
NCBI GI	g560610
BLAST score	191
E value	3.0e-14
Match length	55
% identity	58
NCBI Description	trypsin inhibitor, WTI [Triticum aestivum=wheat, variety San Pastore, endosperm, Peptide, 71 aa]

Seq. No.	272221
Contig ID	36525_1.R1011
5'-most EST	LIB3179-002-P1-K2-H2

Seq. No.	272222
Contig ID	36527_1.R1011
5'-most EST	wty700165231.h1

Seq. No.	272223
Contig ID	36527_2.R1011
5'-most EST	wty700163559.h1

Seq. No.	272224
Contig ID	36527_3.R1011
5'-most EST	wty700171522.h1

Seq. No.	272225
Contig ID	36527_4.R1011
5'-most EST	wty700163175.h1

Seq. No.	272226
Contig ID	36558_1.R1011
5'-most EST	uC-zmflb73131a10b2
Method	BLASTX
NCBI GI	g3046815
BLAST score	511
E value	9.0e-52
Match length	149
% identity	61
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	272227
Contig ID	36558_2.R1011
5'-most EST	uC-zmflb73018g07b1
Method	BLASTX
NCBI GI	g3080353
BLAST score	619
E value	4.0e-64
Match length	177
% identity	64
NCBI Description	(AL022580) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	272228
Contig ID	36558_3.R1011
5'-most EST	LIB3069-002-Q1-K1-D10
Method	BLASTX
NCBI GI	g3461849
BLAST score	212
E value	8.0e-17
Match length	120
% identity	42
NCBI Description	(AC005315) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	272229
Contig ID	36632_1.R1011
5'-most EST	LIB3179-019-P1-K1-B4

Seq. No.	272230
Contig ID	36633_1.R1011
5'-most EST	LIB83-007-Q1-E1-F11
Method	BLASTN
NCBI GI	g1935046
BLAST score	35
E value	5.0e-10
Match length	99
% identity	84
NCBI Description	Zea mays helix-loop-helix type transcription factor R (R-d:Catspaw allele) gene, exon 1, inverted repeat, partial cds

Seq. No.	272231
Contig ID	36634_1.R1011
5'-most EST	LIB3117-013-Q1-K1-D1

Seq. No.	272232
Contig ID	36637_1.R1011
5'-most EST	LIB3179-019-P1-K1-C8
Method	BLASTX
NCBI GI	g4006881
BLAST score	157
E value	7.0e-17
Match length	60
% identity	75
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	272233
Contig ID	36648_1.R1011
5'-most EST	pmx700082112.h1
Method	BLASTX
NCBI GI	g2736186
BLAST score	1288
E value	1.0e-142
Match length	355
% identity	72
NCBI Description	(AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No.	272234
Contig ID	36649_1.R1011
5'-most EST	LIB3179-019-P1-K1-H9

Seq. No.	272235
Contig ID	36652_1.R1011
5'-most EST	tzu700203042.h1

Seq. No.	272236
Contig ID	36652_2.R1011
5'-most EST	wyr700236381.h1
Method	BLASTX
NCBI GI	g2618699
BLAST score	187
E value	6.0e-14
Match length	143
% identity	29
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	272237
Contig ID	36652_3.R1011
5'-most EST	LIB3136-044-P1-K1-C5

Seq. No.	272238
Contig ID	36664_1.R1011
5'-most EST	LIB3179-020-P1-K1-E12
Method	BLASTX
NCBI GI	g2499613
BLAST score	304
E value	2.0e-27
Match length	90
% identity	62
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2 >gi_1204129_emb_CAA57719_ (X82268) protein kinase [Medicago sativa]

Seq. No.	272239
Contig ID	36689_1.R1011
5'-most EST	LIB3137-058-Q1-K1-G10
Method	BLASTX
NCBI GI	g1206013
BLAST score	614
E value	9.0e-77
Match length	193
% identity	69
NCBI Description	(U44087) beta-D-glucosidase precursor [Zea mays]

Seq. No.	272240
Contig ID	36694_1.R1011
5'-most EST	LIB3060-025-Q1-K1-D6
Method	BLASTX
NCBI GI	g3033382
BLAST score	449
E value	2.0e-44
Match length	145
% identity	59
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	272241
Contig ID	36698_1.R1011

5'-most EST	LIB3179-022-P1-K1-C9
Seq. No.	272242
Contig ID	36710_1.R1011
5'-most EST	uC-zmflb73226a11b1
Seq. No.	272243
Contig ID	36729_1.R1011
5'-most EST	LIB3180-001-P1-M1-B11
Seq. No.	272244
Contig ID	36731_1.R1011
5'-most EST	LIB3180-001-P1-M1-B2
Seq. No.	272245
Contig ID	36735_1.R1011
5'-most EST	LIB3180-043-P2-M2-B10
Seq. No.	272246
Contig ID	36737_1.R1011
5'-most EST	LIB3180-001-P1-M1-B9
Method	BLASTX
NCBI GI	g2160694
BLAST score	638
E value	1.0e-66
Match length	213
% identity	57
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
Seq. No.	272247
Contig ID	36743_1.R1011
5'-most EST	LIB3180-001-P1-M1-C3
Seq. No.	272248
Contig ID	36745_1.R1011
5'-most EST	LIB3180-001-P1-M1-C5
Method	BLASTX
NCBI GI	g3258571
BLAST score	198
E value	1.0e-25
Match length	93
% identity	68
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	272249
Contig ID	36748_1.R1011
5'-most EST	LIB3180-001-P1-M1-C8
Method	BLASTX
NCBI GI	g3015488
BLAST score	152
E value	1.0e-09
Match length	110
% identity	39
NCBI Description	(U58474) receptor-like protein kinase [Lycopersicon esculentum]

Seq. No.	272250
Contig ID	36749_1.R1011
5'-most EST	LIB3180-001-P1-M1-C9
Method	BLASTX
NCBI GI	g283035
BLAST score	392
E value	6.0e-38
Match length	95
% identity	84
NCBI Description	chaperonin hsp60 - maize >gi_22248_emb_CAA78100_ (Z12114) mitochondrial chaperonin-60 [Zea mays]

Seq. No.	272251
Contig ID	36752_1.R1011
5'-most EST	vvh700281961.h2
Method	BLASTX
NCBI GI	g4469012
BLAST score	152
E value	1.0e-09
Match length	58
% identity	53
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272252
Contig ID	36756_1.R1011
5'-most EST	uC-zmflMo17005b07b1

Seq. No.	272253
Contig ID	36760_1.R1011
5'-most EST	uC-zmflb73011c07b1

Seq. No.	272254
Contig ID	36760_2.R1011
5'-most EST	LIB3068-028-Q1-K1-H11

Seq. No.	272255
Contig ID	36766_1.R1011
5'-most EST	LIB3180-001-P1-M1-E6

Seq. No.	272256
Contig ID	36790_1.R1011
5'-most EST	LIB143-018-Q1-E1-A7
Method	BLASTX
NCBI GI	g4008339
BLAST score	190
E value	3.0e-14
Match length	92
% identity	46
NCBI Description	(Z19152) similar to Hydrolase; cDNA EST EMBL:T00652 comes from this gene; cDNA EST EMBL:T00998 comes from this gene; cDNA EST yk217d2.5 comes from this gene; cDNA EST yk282g2.3 comes from this gene; cDNA EST yk282g2.5 comes fro

Seq. No.	272257
Contig ID	36791_1.R1011
5'-most EST	LIB3180-001-P1-M1-H12

Seq. No.	272258
Contig ID	36795_1.R1011
5'-most EST	LIB3180-001-P1-M1-H9

Seq. No.	272259
Contig ID	36804_1.R1011
5'-most EST	LIB3180-002-P1-M1-A5

Seq. No.	272260
Contig ID	36809_1.R1011
5'-most EST	uC-zmflmo17317f04a1
Method	BLASTX
NCBI GI	g3914212
BLAST score	199
E value	4.0e-15
Match length	102
% identity	41
NCBI Description	5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE) >gi_1732065 (U70825) 5-oxo-L-prolinase [Rattus norvegicus]

Seq. No.	272261
Contig ID	36816_1.R1011
5'-most EST	LIB143-062-Q1-E1-D3

Seq. No.	272262
Contig ID	36818_1.R1011
5'-most EST	uC-zmflb73205c12b2
Method	BLASTX
NCBI GI	g2708750
BLAST score	187
E value	9.0e-14
Match length	169
% identity	34
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	272263
Contig ID	36826_1.R1011
5'-most EST	ceu700429627.h1
Method	BLASTX
NCBI GI	g2204242
BLAST score	171
E value	6.0e-12
Match length	114
% identity	39
NCBI Description	(Z69999) lectin 3 [Phaseolus lunatus]

Seq. No.	272264
Contig ID	36831_1.R1011
5'-most EST	yne700379438.h1
Method	BLASTX
NCBI GI	g3184098
BLAST score	601
E value	4.0e-77
Match length	321
% identity	50

NCBI Description	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]

Seq. No.	272265
Contig ID	36842_1.R1011
5'-most EST	qmh70O028034.f1

Seq. No.	272266
Contig ID	36846_1.R1011
5'-most EST	LIB3180-002-P1-M1-E8
Method	BLASTX
NCBI GI	g2129656
BLAST score	437
E value	2.0e-43
Match length	124
% identity	70
NCBI Description	OBP33pep protein - Arabidopsis thaliana (fragment) >gi_1022801 (U37699) OBP33pep [Arabidopsis thaliana]

Seq. No.	272267
Contig ID	36848_1.R1011
5'-most EST	wyr70O236144.h1
Method	BLASTX
NCBI GI	g2341032
BLAST score	424
E value	3.0e-41
Match length	181
% identity	45
NCBI Description	(AC000104) EST gb_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No.	272268
Contig ID	36851_1.R1011
5'-most EST	LIB3180-002-P1-M1-F2
Method	BLASTX
NCBI GI	g4063752
BLAST score	301
E value	3.0e-27
Match length	110
% identity	58
NCBI Description	(AC005851) unknown protein [Arabidopsis thaliana] >gi_4510410_gb_AAD21496.1_ (AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	272269
Contig ID	36857_1.R1011
5'-most EST	uC-zmrob73019e04b1
Method	BLASTX
NCBI GI	g1688072
BLAST score	185
E value	2.0e-13
Match length	44
% identity	77
NCBI Description	(U41369) biotin holocarboxylase synthetase [Arabidopsis thaliana]

Seq. No.	272270

Contig ID	36867_1.R1011
5'-most EST	LIB3067-053-Q1-K1-D8
Seq. No.	272271
Contig ID	36867_2.R1011
5'-most EST	rvt700549602.h1
Seq. No.	272272
Contig ID	36867_3.R1011
5'-most EST	LIB3068-051-Q1-K1-E12
Seq. No.	272273
Contig ID	36868_1.R1011
5'-most EST	LIB3180-002-P1-M1-H1
Method	BLASTX
NCBI GI	g3023436
BLAST score	340
E value	7.0e-32
Match length	116
% identity	58
NCBI Description	CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA 3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT) >gi_857578 (U27116) caffeoyl-CoA 3-O-methyltransferase [Populus tremuloides]
Seq. No.	272274
Contig ID	36870_1.R1011
5'-most EST	LIB3180-002-P1-M1-H12
Seq. No.	272275
Contig ID	36874_1.R1011
5'-most EST	zla700379671.h1
Seq. No.	272276
Contig ID	36880_1.R1011
5'-most EST	uC-zmroteosinte072e05b2
Seq. No.	272277
Contig ID	36880_2.R1011
5'-most EST	uC-zmflb73208d03b1
Seq. No.	272278
Contig ID	36888_1.R1011
5'-most EST	LIB36-022-Q1-E1-A1
Seq. No.	272279
Contig ID	36888_2.R1011
5'-most EST	tzu700204703.h1
Seq. No.	272280
Contig ID	36898_1.R1011
5'-most EST	uC-zmflmo17195h12b1
Method	BLASTX
NCBI GI	g2244835
BLAST score	1259
E value	1.0e-139
Match length	364

% identity	65
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	272281
Contig ID	36898_2.R1011
5'-most EST	uC-zmflmo17161b07b1
Method	BLASTX
NCBI GI	g2244835
BLAST score	256
E value	3.0e-41
Match length	191
% identity	70
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	272282
Contig ID	36901_1.R1011
5'-most EST	LIB3180-003-P2-M1-C8
Method	BLASTX
NCBI GI	g3860256
BLAST score	246
E value	6.0e-21
Match length	120
% identity	47
NCBI Description	(AC005824) putative tRNA isopentenylpyrophosphate transferase [Arabidopsis thaliana]

Seq. No.	272283
Contig ID	36921_1.R1011
5'-most EST	xmt700262123.h1
Method	BLASTX
NCBI GI	g4103324
BLAST score	815
E value	2.0e-87
Match length	178
% identity	88
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No.	272284
Contig ID	36921_2.R1011
5'-most EST	LIB3180-013-P2-M1-D5
Method	BLASTX
NCBI GI	g4103324
BLAST score	340
E value	9.0e-32
Match length	77
% identity	88
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No.	272285
Contig ID	36937_1.R1011
5'-most EST	gwl700613187.h1
Method	BLASTX
NCBI GI	g113178
BLAST score	267
E value	2.0e-25

Match length	204
% identity	38
NCBI Description	ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE) (APH) (ACYLAMINOACYL-PEPTIDASE) >gi_91923_pir__S07624 acylaminoacyl-peptidase (EC 3.4.19.1) - rat >gi_202932 (J04733) acyl-peptide hydrolase [Rattus norvegicus]

Seq. No.	272286
Contig ID	36953_1.R1011
5'-most EST	xsy700217178.h1

Seq. No.	272287
Contig ID	36954_1.R1011
5'-most EST	ntr700073252.h1

Seq. No.	272288
Contig ID	36958_1.R1011
5'-most EST	ntr700073158.h1
Method	BLASTX
NCBI GI	g4586253
BLAST score	147
E value	9.0e-09
Match length	196
% identity	29
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	272289
Contig ID	36973_1.R1011
5'-most EST	xyt700343036.h1

Seq. No.	272290
Contig ID	36992_1.R1011
5'-most EST	uC-zmflb73068b11b1
Method	BLASTX
NCBI GI	g3820531
BLAST score	345
E value	2.0e-32
Match length	95
% identity	63
NCBI Description	(AF072736) beta-glucosidase [Pinus contorta]

Seq. No.	272291
Contig ID	36995_1.R1011
5'-most EST	uC-zmflmo17175a03b1
Method	BLASTX
NCBI GI	g1903034
BLAST score	696
E value	4.0e-73
Match length	342
% identity	42
NCBI Description	(X94625) amp-binding protein [Brassica napus]

Seq. No.	272292
Contig ID	36995_2.R1011
5'-most EST	LIB3180-004-P2-M1-G6
Method	BLASTX
NCBI GI	g1903034

BLAST score	178
E value	7.0e-13
Match length	91
% identity	42
NCBI Description	(X94625) amp-binding protein [Brassica napus]

Seq. No.	272293
Contig ID	37019_1.R1011
5'-most EST	uC-zmroteosinte051e04b2
Method	BLASTX
NCBI GI	g1220453
BLAST score	312
E value	7.0e-42
Match length	194
% identity	44
NCBI Description	(M79328) alpha-amylase [Solanum tuberosum]

Seq. No.	272294
Contig ID	37042_1.R1011
5'-most EST	ymt700220693.h1
Method	BLASTX
NCBI GI	g3935168
BLAST score	638
E value	2.0e-66
Match length	253
% identity	53
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	272295
Contig ID	37043_1.R1011
5'-most EST	LIB3180-005-P2-M1-D6
Method	BLASTX
NCBI GI	g435805
BLAST score	183
E value	1.0e-13
Match length	73
% identity	48
NCBI Description	(S66176) UNC-18=vesicle transport protein [Caenorhabditis elegans, Peptide, 591 aa] [Caenorhabditis elegans]

Seq. No.	272296
Contig ID	37048_1.R1011
5'-most EST	uwc700152164.h1

Seq. No.	272297
Contig ID	37049_1.R1011
5'-most EST	LIB3067-059-Q1-K1-C3
Method	BLASTX
NCBI GI	g4512659
BLAST score	460
E value	2.0e-45
Match length	164
% identity	61
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	272298
Contig ID	37050_1.R1011
5'-most EST	LIB3180-005-P2-M1-E3
Method	BLASTX
NCBI GI	g2934902
BLAST score	292
E value	2.0e-26
Match length	104
% identity	58
NCBI Description	(AF039304) cpSecY [Zea mays]

Seq. No.	272299
Contig ID	37068_1.R1011
5'-most EST	LIB3067-047-Q1-K1-G4
Method	BLASTX
NCBI GI	g4587987
BLAST score	593
E value	1.0e-61
Match length	141
% identity	77
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No.	272300
Contig ID	37088_1.R1011
5'-most EST	LIB3180-007-P2-M1-B2

Seq. No.	272301
Contig ID	37096_1.R1011
5'-most EST	LIB3180-007-P2-M1-C12

Seq. No.	272302
Contig ID	37137_1.R1011
5'-most EST	LIB3180-007-P2-M1-G8

Seq. No.	272303
Contig ID	37165_1.R1011
5'-most EST	uC-zmflmo17076b01b1
Method	BLASTX
NCBI GI	g4539453
BLAST score	240
E value	4.0e-20
Match length	65
% identity	65
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	272304
Contig ID	37206_1.R1011
5'-most EST	LIB3180-008-P2-M1-H9

Seq. No.	272305
Contig ID	37229_1.R1011
5'-most EST	pwr700453694.h1

Seq. No.	272306
Contig ID	37231_1.R1011
5'-most EST	uwc700153575.h1

Method	BLASTX
NCBI GI	g3184283
BLAST score	762
E value	3.0e-81
Match length	207
% identity	71
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	272307
Contig ID	37237_1.R1011
5'-most EST	xsy700212263.h1

Seq. No.	272308
Contig ID	37247_1.R1011
5'-most EST	uC-zmflB73046f12b1
Method	BLASTX
NCBI GI	g1084442
BLAST score	723
E value	2.0e-76
Match length	202
% identity	64
NCBI Description	cellulase (EC 3.2.1.4) - European elder >gi_575404_emb_CAA52343_ (X74290) cellulase [Sambucus nigra]

Seq. No.	272309
Contig ID	37259_1.R1011
5'-most EST	uC-zmroteosinte092h09b2

Seq. No.	272310
Contig ID	37262_1.R1011
5'-most EST	LIB3180-009-P2-M1-G3

Seq. No.	272311
Contig ID	37280_1.R1011
5'-most EST	LIB3180-010-P2-M1-A6

Seq. No.	272312
Contig ID	37309_1.R1011
5'-most EST	uC-zmroteosinte108b01b3
Method	BLASTX
NCBI GI	g3093294
BLAST score	409
E value	6.0e-40
Match length	139
% identity	54
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	272313
Contig ID	37314_1.R1011
5'-most EST	nbm700468075.h1

Seq. No.	272314
Contig ID	37320_1.R1011
5'-most EST	LIB3180-010-P2-M1-E9
Method	BLASTX

NCBI GI	g4309728
BLAST score	571
E value	5.0e-59
Match length	126
% identity	88
NCBI Description	(AC006439) putative ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	272315
Contig ID	37339_1.R1011
5'-most EST	uC-zmflb73226g03b1
Method	BLASTX
NCBI GI	g3786011
BLAST score	250
E value	3.0e-36
Match length	186
% identity	49
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	272316
Contig ID	37339_3.R1011
5'-most EST	pmx700084340.h1
Method	BLASTX
NCBI GI	g2160184
BLAST score	183
E value	2.0e-13
Match length	82
% identity	55
NCBI Description	(AC000132) ESTs gb_H37208,gb_H36853 come from this gene. [Arabidopsis thaliana]

Seq. No.	272317
Contig ID	37345_1.R1011
5'-most EST	LIB3180-011-P2-M1-B12

Seq. No.	272318
Contig ID	37354_1.R1011
5'-most EST	LIB3180-011-P2-M1-C1

Seq. No.	272319
Contig ID	37356_1.R1011
5'-most EST	LIB3180-011-P2-M1-C11
Method	BLASTX
NCBI GI	g3953465
BLAST score	295
E value	8.0e-27
Match length	97
% identity	65
NCBI Description	(AC002328) F20N2.10 [Arabidopsis thaliana]

Seq. No.	272320
Contig ID	37370_1.R1011
5'-most EST	LIB3180-011-P2-M1-D4
Method	BLASTX
NCBI GI	g3859116
BLAST score	395

E value	3.0e-38
Match length	115
% identity	64
NCBI Description	(AF031609) unknown [Oryza sativa]

Seq. No.	272321
Contig ID	37374_1.R1011
5'-most EST	uer700577927.h1
Method	BLASTX
NCBI GI	g4503375
BLAST score	430
E value	3.0e-42
Match length	182
% identity	46
NCBI Description	dihydropyrimidinase >gi_3122049_sp_Q14117_DPYS_HUMAN DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP) >gi_1330236_dbj_BAA11189_ (D78011) dihydropyrimidinase [Homo sapiens] >gi_3608122_dbj_BAA33067_ (AB004678) dihydropyrimidinase [Homo sapiens]

Seq. No.	272322
Contig ID	37379_1.R1011
5'-most EST	uC-zmflb73278d09b1

Seq. No.	272323
Contig ID	37384_1.R1011
5'-most EST	LIB3117-007-Q1-K1-C11

Seq. No.	272324
Contig ID	37390_1.R1011
5'-most EST	LIB3180-011-P2-M1-F7

Seq. No.	272325
Contig ID	37395_1.R1011
5'-most EST	uC-zmflb73066b10b1
Method	BLASTX
NCBI GI	g4521249
BLAST score	509
E value	1.0e-51
Match length	129
% identity	75
NCBI Description	(AB013912) DNA helicase [Mus musculus]

Seq. No.	272326
Contig ID	37395_2.R1011
5'-most EST	uC-zmrob73077d12b1
Method	BLASTX
NCBI GI	g4521249
BLAST score	429
E value	2.0e-42
Match length	118
% identity	69
NCBI Description	(AB013912) DNA helicase [Mus musculus]

Seq. No.	272327
Contig ID	37411_1.R1011
5'-most EST	LIB3180-023-P2-M1-E10

Method	BLASTX
NCBI GI	g4056421
BLAST score	686
E value	2.0e-72
Match length	178
% identity	74
NCBI Description	(AC005322) Similar to gb_Z30094 basic transcripion factor 2, 44 kD subunit from Homo sapiens. EST gb_W43325 comes from this gene. [Arabidopsis thaliana]

Seq. No.	272328
Contig ID	37444_1.R1011
5'-most EST	uC-zmflb73053b08b2

Seq. No.	272329
Contig ID	37451_1.R1011
5'-most EST	LIB3069-021-Q1-K1-C10
Method	BLASTX
NCBI GI	g3063453
BLAST score	237
E value	2.0e-22
Match length	226
% identity	38
NCBI Description	(AC003981) F22O13.15 [Arabidopsis thaliana]

Seq. No.	272330
Contig ID	37464_1.R1011
5'-most EST	ymt700220649.h1
Method	BLASTX
NCBI GI	g2253010
BLAST score	1097
E value	1.0e-120
Match length	298
% identity	69
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	272331
Contig ID	37465_1.R1011
5'-most EST	LIB3180-012-P2-M1-H5
Method	BLASTX
NCBI GI	g4454467
BLAST score	627
E value	4.0e-65
Match length	263
% identity	48
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	272332
Contig ID	37465_2.R1011
5'-most EST	LIB3069-017-Q1-K1-F6
Method	BLASTX
NCBI GI	g4454467
BLAST score	551
E value	1.0e-56
Match length	142
% identity	65

NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	272333
Contig ID	37465_3.R1011
5'-most EST	ymt700218857.h1
Method	BLASTX
NCBI GI	g4454467
BLAST score	539
E value	3.0e-55
Match length	161
% identity	60
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	272334
Contig ID	37466_1.R1011
5'-most EST	xyt700343416.h1
Method	BLASTX
NCBI GI	g1841468
BLAST score	1158
E value	1.0e-127
Match length	271
% identity	77
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No.	272335
Contig ID	37466_2.R1011
5'-most EST	xyt700347052.h1
Method	BLASTX
NCBI GI	g1841468
BLAST score	235
E value	2.0e-19
Match length	73
% identity	58
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No.	272336
Contig ID	37478_1.R1011
5'-most EST	LIB3180-013-P2-M1-B12

Seq. No.	272337
Contig ID	37478_2.R1011
5'-most EST	LIB3069-030-Q1-K1-B5

Seq. No.	272338
Contig ID	37483_1.R1011
5'-most EST	pmx700087862.h1

Seq. No.	272339
Contig ID	37483_2.R1011
5'-most EST	xjt700096891.h1

Seq. No.	272340
Contig ID	37496_1.R1011
5'-most EST	uC-zmflmo17137b09b1
Method	BLASTX
NCBI GI	g2829918
BLAST score	781

E value	4.0e-83
Match length	254
% identity	64
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	272341
Contig ID	37501_1.R1011
5'-most EST	LIB3069-031-Q1-K1-C2

Seq. No.	272342
Contig ID	37501_2.R1011
5'-most EST	LIB3180-049-P2-M1-B6

Seq. No.	272343
Contig ID	37506_1.R1011
5'-most EST	LIB3180-013-P2-M1-F1
Method	BLASTX
NCBI GI	g1825766
BLAST score	323
E value	2.0e-29
Match length	278
% identity	32
NCBI Description	(U88314) similar to flavin-containing monooxygenases [Caenorhabditis elegans]

Seq. No.	272344
Contig ID	37506_2.R1011
5'-most EST	wty700172642.h1

Seq. No.	272345
Contig ID	37507_1.R1011
5'-most EST	tfd700571250.h1
Method	BLASTX
NCBI GI	g3023947
BLAST score	695
E value	2.0e-73
Match length	133
% identity	94
NCBI Description	PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi_2665840 (AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No.	272346
Contig ID	37511_1.R1011
5'-most EST	LIB3180-013-P2-M1-F3
Method	BLASTX
NCBI GI	g3212854
BLAST score	152
E value	2.0e-09
Match length	149
% identity	36
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	272347
Contig ID	37513_1.R1011
5'-most EST	xjt700093789.h1
Method	BLASTX

NCBI GI	g3451072
BLAST score	238
E value	4.0e-20
Match length	71
% identity	59
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	272348
Contig ID	37516_1.R1011
5'-most EST	LIB3180-013-P2-M1-F9

Seq. No.	272349
Contig ID	37526_1.R1011
5'-most EST	nbm700468260.h1
Method	BLASTX
NCBI GI	g283966
BLAST score	179
E value	3.0e-13
Match length	46
% identity	70
NCBI Description	activator 1 37K chain - human

Seq. No.	272350
Contig ID	37527_1.R1011
5'-most EST	LIB3180-013-P2-M1-H3

Seq. No.	272351
Contig ID	37529_1.R1011
5'-most EST	wty700169029.h1

Seq. No.	272352
Contig ID	37529_2.R1011
5'-most EST	LIB3180-013-P2-M1-H4

Seq. No.	272353
Contig ID	37531_1.R1011
5'-most EST	ymt700223067.h1

Seq. No.	272354
Contig ID	37531_2.R1011
5'-most EST	LIB3061-018-Q1-K1-B11

Seq. No.	272355
Contig ID	37535_1.R1011
5'-most EST	LIB3180-014-P2-M1-A1

Seq. No.	272356
Contig ID	37540_1.R1011
5'-most EST	LIB3180-014-P2-M1-A7

Seq. No.	272357
Contig ID	37548_1.R1011
5'-most EST	LIB3180-014-P2-M1-B9
Method	BLASTX
NCBI GI	g4567095
BLAST score	472
E value	3.0e-48

Match length	119
% identity	78
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	272358
Contig ID	37550_1.R1011
5'-most EST	ymt700223860.h1

Seq. No.	272359
Contig ID	37555_1.R1011
5'-most EST	uC-zmflB73106h01b1
Method	BLASTX
NCBI GI	g3687237
BLAST score	575
E value	1.0e-58
Match length	158
% identity	67
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	272360
Contig ID	37555_3.R1011
5'-most EST	uC-zmflmo17045a02b1
Method	BLASTX
NCBI GI	g3687237
BLAST score	432
E value	6.0e-47
Match length	190
% identity	55
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	272361
Contig ID	37555_4.R1011
5'-most EST	uC-zmflb73091f05b2
Method	BLASTX
NCBI GI	g3643609
BLAST score	202
E value	9.0e-16
Match length	37
% identity	86
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No.	272362
Contig ID	37555_5.R1011
5'-most EST	uC-zmflmo17013d04b1
Method	BLASTX
NCBI GI	g3687237
BLAST score	332
E value	7.0e-31
Match length	131
% identity	55
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	272363
Contig ID	37557_1.R1011
5'-most EST	LIB3180-014-P2-M1-C7
Method	BLASTX
NCBI GI	g3135493
BLAST score	248
E value	4.0e-21
Match length	110
% identity	55
NCBI Description	(AF060248) unknown [Arabidopsis thaliana]

Seq. No.	272364
Contig ID	37566_1.R1011
5'-most EST	uC-zmflmo17223b01b1
Method	BLASTX
NCBI GI	g2130150
BLAST score	656
E value	1.0e-68
Match length	136
% identity	90
NCBI Description	hypothetical protein 137 - maize chloroplast >gi_902263_emb_CAA60328_ (X86563) ORF137 [Zea mays] >gi_902308_emb_CAA60372_ (X86563) ORF137 [Zea mays]

Seq. No.	272365
Contig ID	37566_2.R1011
5'-most EST	uC-zmflb73258f05b3
Method	BLASTX
NCBI GI	g132857
BLAST score	718
E value	1.0e-100
Match length	224
% identity	85
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_71089_pir__R5ZM2 ribosomal protein L2 - maize chloroplast >gi_2673858_emb_CAA60329_ (X86563) ribosomal protein L2 [Zea mays] >gi_2673859_emb_CAA60371_ (X86563) ribosomal protein L2 [Zea mays]

Seq. No.	272366
Contig ID	37579_1.R1011
5'-most EST	LIB143-052-Q1-E1-H10
Method	BLASTX
NCBI GI	g3096935
BLAST score	562
E value	3.0e-57
Match length	310
% identity	45
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	272367
Contig ID	37583_1.R1011
5'-most EST	rvt700549551.h1

Seq. No.	272368
Contig ID	37592_1.R1011
5'-most EST	fdz701160476.h1

Method	BLASTX
NCBI GI	g2655029
BLAST score	861
E value	6.0e-93
Match length	163
% identity	99
NCBI Description	(AF019296) starch synthase isoform zSTSII-1 [Zea mays]

Seq. No.	272369
Contig ID	37605_1.R1011
5'-most EST	LIB3180-015-P2-M1-C1

Seq. No.	272370
Contig ID	37620_1.R1011
5'-most EST	ntr700075261.h1
Method	BLASTX
NCBI GI	g3024764
BLAST score	390
E value	1.0e-37
Match length	168
% identity	50
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (UBIQUITIN THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T) (DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) >gi_3287373 (AC002397) ISOT [Mus musculus]

Seq. No.	272371
Contig ID	37623_1.R1011
5'-most EST	uC-zmflmo17076d02b1
Method	BLASTX
NCBI GI	g4160518
BLAST score	332
E value	8.0e-31
Match length	101
% identity	60
NCBI Description	(AJ131346) beta-glucosidase [Caldicellulosiruptor sp. 14B]

Seq. No.	272372
Contig ID	37623_2.R1011
5'-most EST	wty700172681.h1
Method	BLASTX
NCBI GI	g4160518
BLAST score	146
E value	1.0e-09
Match length	45
% identity	58
NCBI Description	(AJ131346) beta-glucosidase [Caldicellulosiruptor sp. 14B]

Seq. No.	272373
Contig ID	37624_1.R1011
5'-most EST	uC-zmflmo17198f02b1
Method	BLASTX
NCBI GI	g4115931
BLAST score	357
E value	8.0e-34
Match length	91
% identity	76

NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	272374
Contig ID	37624_2.R1011
5'-most EST	LIB3180-015-P2-M1-D8

Seq. No.	272375
Contig ID	37633_1.R1011
5'-most EST	uC-zmflb73245h04b2
Method	BLASTX
NCBI GI	g4538939
BLAST score	1595
E value	1.0e-178
Match length	473
% identity	66
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	272376
Contig ID	37633_4.R1011
5'-most EST	LIB3180-015-P2-M1-F1
Method	BLASTX
NCBI GI	g4538939
BLAST score	515
E value	1.0e-78
Match length	191
% identity	79
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	272377
Contig ID	37645_1.R1011
5'-most EST	xmt700265079.h1

Seq. No.	272378
Contig ID	37665_1.R1011
5'-most EST	LIB3180-016-P2-M1-A3

Seq. No.	272379
Contig ID	37669_1.R1011
5'-most EST	wty700169546.h1
Method	BLASTX
NCBI GI	g4406132
BLAST score	468
E value	8.0e-47
Match length	103
% identity	88
NCBI Description	(AF077760) MADS box protein [Oryza sativa]

Seq. No.	272380
Contig ID	37672_2.R1011
5'-most EST	tzu700204076.h1

Seq. No.	272381
Contig ID	37679_1.R1011
5'-most EST	pmx700087455.h1

Method	BLASTX
NCBI GI	g4567283
BLAST score	1494
E value	1.0e-166
Match length	525
% identity	57
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	272382
Contig ID	37683_1.R1011
5'-most EST	LIB3180-016-P2-M1-C3
Method	BLASTX
NCBI GI	g4539351
BLAST score	310
E value	5.0e-29
Match length	76
% identity	82
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	272383
Contig ID	37684_1.R1011
5'-most EST	uC-zmroteosinte103b12b2
Method	BLASTX
NCBI GI	g3834302
BLAST score	787
E value	6.0e-84
Match length	166
% identity	92
NCBI Description	(AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis thaliana]

Seq. No.	272384
Contig ID	37684_2.R1011
5'-most EST	uC-zmflb73191a04b1
Method	BLASTX
NCBI GI	g3834302
BLAST score	862
E value	8.0e-93
Match length	191
% identity	86
NCBI Description	(AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis thaliana]

Seq. No.	272385
Contig ID	37691_1.R1011
5'-most EST	uC-zmflmo17289f02b1

Seq. No.	272386
Contig ID	37692_1.R1011
5'-most EST	LIB3180-016-P2-M1-D8

Seq. No.	272387
Contig ID	37693_1.R1011
5'-most EST	yyf700352077.h1
Method	BLASTX

NCBI GI	g2388585
BLAST score	511
E value	5.0e-75
Match length	221
% identity	69
NCBI Description	(AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No.	272388
Contig ID	37694_1.R1011
5'-most EST	fwa700099855.h1
Method	BLASTX
NCBI GI	g4309698
BLAST score	1304
E value	1.0e-144
Match length	498
% identity	65
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	272389
Contig ID	37694_2.R1011
5'-most EST	xsy700209420.h1
Method	BLASTX
NCBI GI	g4309698
BLAST score	404
E value	1.0e-39
Match length	108
% identity	70
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	272390
Contig ID	37702_1.R1011
5'-most EST	LIB3180-016-P2-M1-F10

Seq. No.	272391
Contig ID	37719_1.R1011
5'-most EST	yyf700350962.h1

Seq. No.	272392
Contig ID	37729_1.R1011
5'-most EST	LIB3180-017-P2-M1-B1
Method	BLASTX
NCBI GI	g4099482
BLAST score	195
E value	6.0e-15
Match length	136
% identity	32
NCBI Description	(U87791) eRFS [Homo sapiens]

Seq. No.	272393
Contig ID	37764_2.R1011
5'-most EST	LIB3180-019-P2-M1-D2
Method	BLASTX
NCBI GI	g3372518
BLAST score	230

E value	4.0e-35
Match length	94
% identity	74
NCBI Description	(AF050631) invertase [Zea mays]

Seq. No.	272394
Contig ID	37772_2.R1011
5'-most EST	xmt700262651.h1

Seq. No.	272395
Contig ID	37773_1.R1011
5'-most EST	LIB3180-017-P2-M1-F9

Seq. No.	272396
Contig ID	37773_2.R1011
5'-most EST	gct701173983.h1

Seq. No.	272397
Contig ID	37779_1.R1011
5'-most EST	ypc700799524.h1
Method	BLASTX
NCBI GI	g1808686
BLAST score	533
E value	2.0e-54
Match length	180
% identity	64
NCBI Description	(Y10783) hypothetical protein [Sporobolus stapfianus]

Seq. No.	272398
Contig ID	37787_1.R1011
5'-most EST	LIB3180-017-P2-M1-H2

Seq. No.	272399
Contig ID	37792_1.R1011
5'-most EST	xmt700266176.h1
Method	BLASTX
NCBI GI	g2832620
BLAST score	341
E value	1.0e-32
Match length	123
% identity	57
NCBI Description	(AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272400
Contig ID	37806_1.R1011
5'-most EST	LIB3180-018-P2-M1-C3
Method	BLASTX
NCBI GI	g1788469
BLAST score	212
E value	2.0e-16
Match length	119
% identity	41
NCBI Description	(AE000303) putative oxidoreductase [Escherichia coli]

Seq. No.	272401
Contig ID	37817_1.R1011
5'-most EST	LIB3180-018-P2-M1-E12

Seq. No.	272402
Contig ID	37817_2.R1011
5'-most EST	LIB3059-020-Q1-K1-E1

Seq. No.	272403
Contig ID	37822_1.R1011
5'-most EST	LIB3180-018-P2-M1-F1
Method	BLASTX
NCBI GI	g4582459
BLAST score	457
E value	7.0e-46
Match length	107
% identity	75
NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No.	272404
Contig ID	37845_1.R1011
5'-most EST	nbm700467318.h1

Seq. No.	272405
Contig ID	37847_1.R1011
5'-most EST	LIB3180-018-P2-M1-H9
Method	BLASTX
NCBI GI	g4006905
BLAST score	275
E value	2.0e-32
Match length	202
% identity	47
NCBI Description	(Z99708) ATPase-like protein [Arabidopsis thaliana]

Seq. No.	272406
Contig ID	37855_1.R1011
5'-most EST	uC-zmf1B73025e02b2
Method	BLASTX
NCBI GI	g399854
BLAST score	276
E value	2.0e-24
Match length	61
% identity	92
NCBI Description	HISTONE H2B.2 >gi_283042_pir__S28049 histone H2B - maize >gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]

Seq. No.	272407
Contig ID	37855_2.R1011
5'-most EST	wyr700241119.h1
Method	BLASTX
NCBI GI	g1708107
BLAST score	229
E value	7.0e-19
Match length	57
% identity	81
NCBI Description	HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]

Seq. No.	272408
Contig ID	37867_1.R1011

5'-most EST	LIB3180-019-P2-M1-C12
Seq. No.	272409
Contig ID	37875_1.R1011
5'-most EST	uC-zmromo17107a08a1
Method	BLASTX
NCBI GI	g3377843
BLAST score	557
E value	1.0e-56
Match length	266
% identity	48
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]
Seq. No.	272410
Contig ID	37875_2.R1011
5'-most EST	LIB3180-019-P2-M1-D3
Seq. No.	272411
Contig ID	37877_1.R1011
5'-most EST	LIB3136-057-Q1-K1-C3
Method	BLASTX
NCBI GI	g2244902
BLAST score	332
E value	5.0e-31
Match length	126
% identity	58
NCBI Description	(Z97339) allene oxide synthase [Arabidopsis thaliana]
Seq. No.	272412
Contig ID	37878_1.R1011
5'-most EST	uC-zmflb73011a10b1
Method	BLASTX
NCBI GI	g1657619
BLAST score	218
E value	5.0e-21
Match length	145
% identity	42
NCBI Description	(U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]
Seq. No.	272413
Contig ID	37879_2.R1011
5'-most EST	cyk700052244.f1
Seq. No.	272414
Contig ID	37883_1.R1011
5'-most EST	wty700169863.h1
Method	BLASTX
NCBI GI	g2204089
BLAST score	204
E value	2.0e-16
Match length	83
% identity	51
NCBI Description	(Z82989) FCA gamma [Arabidopsis thaliana]
Seq. No.	272415

Contig ID 37886_1.R1011
5'-most EST LIB3180-019-P2-M1-F11

Seq. No. 272416
Contig ID 37888_1.R1011
5'-most EST pwr700448669.h1
Method BLASTX
NCBI GI g2252843
BLAST score 244
E value 3.0e-20
Match length 239
% identity 31
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 272417
Contig ID 37896_1.R1011
5'-most EST LIB3180-019-P2-M1-G12

Seq. No. 272418
Contig ID 37899_1.R1011
5'-most EST uC-zmflmo17281h12b1
Method BLASTX
NCBI GI g498643
BLAST score 1550
E value 1.0e-179
Match length 377
% identity 85
NCBI Description (U10270) G-box binding factor 1 [Zea mays]

Seq. No. 272419
Contig ID 37899_2.R1011
5'-most EST uC-zmflb73056b12b1
Method BLASTX
NCBI GI g498643
BLAST score 460
E value 2.0e-45
Match length 86
% identity 93
NCBI Description (U10270) G-box binding factor 1 [Zea mays]

Seq. No. 272420
Contig ID 37914_1.R1011
5'-most EST LIB3180-020-P2-M1-A3

Seq. No. 272421
Contig ID 37934_1.R1011
5'-most EST pmx700085489.h1

Seq. No. 272422
Contig ID 37949_1.R1011
5'-most EST uC-zmflmo17077b08b1

Seq. No. 272423
Contig ID 37949_2.R1011
5'-most EST uC-zmflmo17116f04b1

Seq. No. 272424

Contig ID	37972_1.R1011
5'-most EST	nbm700469321.h1
Method	BLASTX
NCBI GI	g1076715
BLAST score	540
E value	5.0e-55
Match length	139
% identity	71
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	272425
Contig ID	37972_2.R1011
5'-most EST	xmt700265529.h1
Method	BLASTX
NCBI GI	g1076715
BLAST score	371
E value	2.0e-35
Match length	100
% identity	67
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	272426
Contig ID	37976_1.R1011
5'-most EST	uC-zmflb73319h11b1

Seq. No.	272427
Contig ID	37986_1.R1011
5'-most EST	LIB3180-021-P2-M1-B2

Seq. No.	272428
Contig ID	37987_1.R1011
5'-most EST	fdz701165033.h1

Seq. No.	272429
Contig ID	37990_1.R1011
5'-most EST	uC-zmflmo17290d10b1
Method	BLASTX
NCBI GI	g2275219
BLAST score	145
E value	5.0e-09
Match length	61
% identity	56
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]

Seq. No.	272430
Contig ID	38002_1.R1011
5'-most EST	nbm700471746.h1
Method	BLASTX
NCBI GI	g3355477
BLAST score	221
E value	7.0e-26
Match length	100
% identity	63
NCBI Description	(AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No.	272431
Contig ID	38018_1.R1011
5'-most EST	uC-zmflb73045e12a2
Seq. No.	272432
Contig ID	38025_1.R1011
5'-most EST	LIB3180-055-P2-M1-D5
Seq. No.	272433
Contig ID	38028_1.R1011
5'-most EST	LIB3180-021-P2-M1-H2
Method	BLASTX
NCBI GI	g1244716
BLAST score	304
E value	8.0e-28
Match length	70
% identity	81
NCBI Description	(U42336) ACC synthase [Triticum aestivum]
Seq. No.	272434
Contig ID	38040_1.R1011
5'-most EST	LIB3068-021-Q1-K1-B9
Method	BLASTX
NCBI GI	g1169170
BLAST score	460
E value	6.0e-46
Match length	100
% identity	92
NCBI Description	APOCYTOCHROME F PRECURSOR >gi_1363527_pir__S58564 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome f - maize chloroplast >gi_902234_emb_CAA60298_ (X86563) cytochrome f [Zea mays]
Seq. No.	272435
Contig ID	38045_1.R1011
5'-most EST	tzu7000206159.h1
Seq. No.	272436
Contig ID	38045_2.R1011
5'-most EST	LIB3180-022-P2-M1-B6
Seq. No.	272437
Contig ID	38045_3.R1011
5'-most EST	xmt7000267066.h1
Seq. No.	272438
Contig ID	38074_1.R1011
5'-most EST	uC-zmflmo17258c08b1
Method	BLASTX
NCBI GI	g4001805
BLAST score	518
E value	8.0e-53
Match length	407
% identity	41
NCBI Description	(AF041476) BAF53a [Mus musculus]

Seq. No.	272439
Contig ID	38074_2.R1011
5'-most EST	xsy700214502.h1
Method	BLASTX
NCBI GI	g4001805
BLAST score	216
E value	2.0e-17
Match length	105
% identity	42
NCBI Description	(AF041476) BAF53a [Mus musculus]

Seq. No.	272440
Contig ID	38081_1.R1011
5'-most EST	LIB84-006-Q1-E1-B11
Method	BLASTX
NCBI GI	g3023951
BLAST score	165
E value	2.0e-11
Match length	98
% identity	29
NCBI Description	HISTONE TRANSCRIPTION REGULATOR 1 HOMOLOG >gi_2226424_emb_CAB10089.1_ (Z97204) putative hira protein; histone transcription regulator [Schizosaccharomyces pombe]

Seq. No.	272441
Contig ID	38082_1.R1011
5'-most EST	LIB3180-022-P2-M1-G9
Method	BLASTX
NCBI GI	g3176690
BLAST score	686
E value	3.0e-72
Match length	190
% identity	75
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	272442
Contig ID	38086_1.R1011
5'-most EST	fwa700097187.h1
Method	BLASTX
NCBI GI	g1085952
BLAST score	389
E value	1.0e-37
Match length	79
% identity	87
NCBI Description	hypothetical protein S1 - Phalaris coerulescens >gi_556831_emb_CAA57519_ (X81991) S1 [Phalaris coerulescens] >gi_1103489_emb_CAA63108_ (X92351) self-incompatibility mutant protein [Phalaris coerulescens]

Seq. No.	272443
Contig ID	38090_1.R1011
5'-most EST	uC-zmrob73076c06b1
Method	BLASTX
NCBI GI	g4249382
BLAST score	469

E value	8.0e-47
Match length	123
% identity	69
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	272444
Contig ID	38090_2.R1011
5'-most EST	LIB143-067-Q1-E1-E11
Method	BLASTX
NCBI GI	g4249382
BLAST score	480
E value	2.0e-48
Match length	130
% identity	72
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	272445
Contig ID	38092_1.R1011
5'-most EST	uC-zmf1b73038b05b1

Seq. No.	272446
Contig ID	38098_1.R1011
5'-most EST	uC-zmf1b73260h10b2
Method	BLASTX
NCBI GI	g2498882
BLAST score	231
E value	5.0e-19
Match length	61
% identity	66
NCBI Description	SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120) >gi_2146975_pir__S60735 splicing factor SF3a 120K chain - human >gi_899298_emb_CAA59494_ (X85237) human splicing factor [Homo sapiens] >gi_3212998 (AC004997) spliceosome associated protein 114 (SF3a) [Homo sapiens]

Seq. No.	272447
Contig ID	38110_1.R1011
5'-most EST	LIB3180-040-P2-M2-C9

Seq. No.	272448
Contig ID	38117_1.R1011
5'-most EST	LIB3180-023-P2-M1-E8

Seq. No.	272449
Contig ID	38125_1.R1011
5'-most EST	LIB3279-003-P1-K1-A3
Method	BLASTX
NCBI GI	g3874563
BLAST score	234
E value	2.0e-19
Match length	81
% identity	51
NCBI Description	(Z81042) similar to Yeast hypothetical protein YEY6 like;

cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi_3924825_emb_CAB05549_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA

Seq. No.	272450
Contig ID	38141_1.R1011
5'-most EST	LIB3180-024-P2-M1-B5

Seq. No.	272451
Contig ID	38154_1.R1011
5'-most EST	uC-zmflmo17078g06b1
Method	BLASTX
NCBI GI	g1871187
BLAST score	804
E value	5.0e-86
Match length	261
% identity	61
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	272452
Contig ID	38160_1.R1011
5'-most EST	LIB3180-024-P2-M1-G12

Seq. No.	272453
Contig ID	38160_2.R1011
5'-most EST	wty700170384.h1

Seq. No.	272454
Contig ID	38163_1.R1011
5'-most EST	xsy700208540.h1

Seq. No.	272455
Contig ID	38169_2.R1011
5'-most EST	nbm700474318.h1
Method	BLASTX
NCBI GI	g2275211
BLAST score	822
E value	4.0e-88
Match length	196
% identity	81
NCBI Description	(AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	272456
Contig ID	38183_1.R1011
5'-most EST	nbm700471507.h1
Method	BLASTX
NCBI GI	g507166
BLAST score	348
E value	2.0e-32
Match length	108
% identity	61
NCBI Description	(U04819) PITSLRE beta 1 [Homo sapiens]

Seq. No. 272457
Contig ID 38188_1.R1011
5'-most EST dyk700105540.h1

Seq. No. 272458
Contig ID 38191_1.R1011
5'-most EST fC-zmfl700464609a2

Seq. No. 272459
Contig ID 38191_2.R1011
5'-most EST mwy700439106.h1

Seq. No. 272460
Contig ID 38206_1.R1011
5'-most EST LIB3279-049-P1-K1-D3

Seq. No. 272461
Contig ID 38209_1.R1011
5'-most EST LIB3180-028-P2-M2-A1
Method BLASTX
NCBI GI g1778149
BLAST score 434
E value 8.0e-51
Match length 149
% identity 72
NCBI Description (U66404) phosphate/phosphoenolpyruvate translocator precursor [Zea mays]

Seq. No. 272462
Contig ID 38223_1.R1011
5'-most EST ntr700077156.h1
Method BLASTX
NCBI GI g2582971
BLAST score 217
E value 2.0e-17
Match length 73
% identity 58
NCBI Description (D83711) TKRP125 [Nicotiana tabacum]

Seq. No. 272463
Contig ID 38226_1.R1011
5'-most EST xsy700209292.h1
Method BLASTX
NCBI GI g4376650
BLAST score 222
E value 5.0e-18
Match length 102
% identity 48
NCBI Description (AE001621) GcpE Protein [Chlamydia pneumoniae]

Seq. No. 272464
Contig ID 38248_1.R1011
5'-most EST uC-zmflB73106d02b1
Method BLASTX
NCBI GI g4512705
BLAST score 748

E value	1.0e-79
Match length	188
% identity	78
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	272465
Contig ID	38252_1.R1011
5'-most EST	uC-zmflmo17257h03b1

Seq. No.	272466
Contig ID	38274_1.R1011
5'-most EST	xdb700337643.h1

Seq. No.	272467
Contig ID	38276_1.R1011
5'-most EST	LIB3180-048-P2-C9

Seq. No.	272468
Contig ID	38283_1.R1011
5'-most EST	uC-zmflb73022e03b1

Seq. No.	272469
Contig ID	38288_1.R1011
5'-most EST	uC-zmflmo17163b01b1

Seq. No.	272470
Contig ID	38293_1.R1011
5'-most EST	uC-zmflmo17076f11b1
Method	BLASTX
NCBI GI	g2655008
BLAST score	268
E value	3.0e-23
Match length	110
% identity	52
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	272471
Contig ID	38300_1.R1011
5'-most EST	uC-zmroteosinte021b05b1
Method	BLASTX
NCBI GI	g1706186
BLAST score	479
E value	8.0e-48
Match length	210
% identity	42
NCBI Description	HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR) >gi_110721_pir__A32742 murine ecotropic retrovirus receptor protein - mouse >gi_532612 (M26687) ecotropic retrovirus receptor [Mus musculus]

Seq. No.	272472
Contig ID	38301_1.R1011
5'-most EST	uC-zmflmo17138d07b1

Method	BLASTX
NCBI GI	g170962
BLAST score	152
E value	6.0e-10
Match length	110
% identity	32
NCBI Description	(M34075) ADP/ATP-translocator protein [Saccharomyces cerevisiae]

Seq. No.	272473
Contig ID	38310_1.R1011
5'-most EST	LIB3180-029-P2-M2-H10

Seq. No.	272474
Contig ID	38318_1.R1011
5'-most EST	LIB3180-030-P2-M2-A1
Method	BLASTX
NCBI GI	g2104446
BLAST score	326
E value	2.0e-30
Match length	113
% identity	58
NCBI Description	(Z95396) WD-repeat protein [Schizosaccharomyces pombe]

Seq. No.	272475
Contig ID	38322_1.R1011
5'-most EST	LIB3069-018-Q1-K1-G7

Seq. No.	272476
Contig ID	38328_1.R1011
5'-most EST	uC-zmflmo17266b02b1

Seq. No.	272477
Contig ID	38337_1.R1011
5'-most EST	yyf700352048.h1
Method	BLASTX
NCBI GI	g1669655
BLAST score	480
E value	7.0e-48
Match length	325
% identity	39
NCBI Description	(X95962) CER3 [Arabidopsis thaliana]

Seq. No.	272478
Contig ID	38344_1.R1011
5'-most EST	uwc700150887.h1
Method	BLASTX
NCBI GI	g3738297
BLAST score	687
E value	3.0e-72
Match length	294
% identity	22
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	272479
Contig ID	38349_1.R1011
5'-most EST	LIB3180-030-P2-M2-D3

Seq. No.	272480
Contig ID	38353_1.R1011
5'-most EST	LIB3279-050-P1-K1-B9

Seq. No.	272481
Contig ID	38354_1.R1011
5'-most EST	uC-zmflmo17159h02b1
Method	BLASTX
NCBI GI	g4455287
BLAST score	426
E value	1.0e-41
Match length	136
% identity	64
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	272482
Contig ID	38354_2.R1011
5'-most EST	ntr700072980.h1
Method	BLASTX
NCBI GI	g4455287
BLAST score	289
E value	7.0e-26
Match length	91
% identity	67
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	272483
Contig ID	38365_1.R1011
5'-most EST	wyr700240618.h1

Seq. No.	272484
Contig ID	38368_1.R1011
5'-most EST	LIB3180-030-P2-M2-F5

Seq. No.	272485
Contig ID	38372_1.R1011
5'-most EST	uwc700155024.h1
Method	BLASTX
NCBI GI	g3850819
BLAST score	883
E value	6.0e-95
Match length	189
% identity	83
NCBI Description	(Y18349) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	272486
Contig ID	38372_2.R1011
5'-most EST	uC-zmrob73079c05b1
Method	BLASTX
NCBI GI	g3850818
BLAST score	322
E value	6.0e-53
Match length	112
% identity	90
NCBI Description	(Y18349) U2 snRNP auxiliary factor, small subunit [Oryza

sativa]

Seq. No.	272487
Contig ID	38372_3.R1011
5'-most EST	uC-zmflb73098d08b1

Seq. No.	272488
Contig ID	38372_4.R1011
5'-most EST	uC-zmflmo17116f02b1

Seq. No.	272489
Contig ID	38372_5.R1011
5'-most EST	uC-zmflmo17417g12a1
Method	BLASTX
NCBI GI	g3850818
BLAST score	145
E value	3.0e-09
Match length	31
% identity	90
NCBI Description	(Y18349) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	272490
Contig ID	38373_1.R1011
5'-most EST	uC-zmflb73096b12b1

Seq. No.	272491
Contig ID	38373_2.R1011
5'-most EST	xsy700214908.h1

Seq. No.	272492
Contig ID	38375_1.R1011
5'-most EST	nbm700466578.h1

Seq. No.	272493
Contig ID	38375_2.R1011
5'-most EST	LIB3180-030-P2-M2-G12

Seq. No.	272494
Contig ID	38381_1.R1011
5'-most EST	LIB3180-030-P2-M2-H10

Seq. No.	272495
Contig ID	38384_1.R1011
5'-most EST	LIB3180-030-P2-M2-H3

Seq. No.	272496
Contig ID	38388_1.R1011
5'-most EST	LIB3180-030-P2-M2-H9

Seq. No.	272497
Contig ID	38398_1.R1011
5'-most EST	uC-zmflmo17097g03b1
Method	BLASTX
NCBI GI	g4467096
BLAST score	227
E value	1.0e-18

Match length	166
% identity	40
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	272498
Contig ID	38401_1.R1011
5'-most EST	LIB143-004-Q1-E1-E9
Method	BLASTX
NCBI GI	g4582460
BLAST score	160
E value	1.0e-10
Match length	115
% identity	37
NCBI Description	(AC007071) unknown protein [Arabidopsis thaliana]

Seq. No.	272499
Contig ID	38406_1.R1011
5'-most EST	LIB3180-031-P2-M2-B9

Seq. No.	272500
Contig ID	38415_1.R1011
5'-most EST	LIB3180-031-P2-M2-D1
Method	BLASTX
NCBI GI	g3047318
BLAST score	161
E value	6.0e-11
Match length	89
% identity	10
NCBI Description	(AF056625) poly-ubiquitin [Magnaporthe grisea]

Seq. No.	272501
Contig ID	38424_1.R1011
5'-most EST	LIB3180-031-P2-M2-D8

Seq. No.	272502
Contig ID	38444_1.R1011
5'-most EST	LIB3180-031-P2-M2-G4
Method	BLASTX
NCBI GI	g4490319
BLAST score	865
E value	2.0e-93
Match length	244
% identity	67
NCBI Description	(AL035678) metal-transporting P-type ATPase [Arabidopsis thaliana]

Seq. No.	272503
Contig ID	38447_1.R1011
5'-most EST	LIB3062-030-Q1-K1-G12
Method	BLASTX
NCBI GI	g3033398
BLAST score	518
E value	3.0e-89
Match length	197
% identity	84
NCBI Description	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No.	272504
Contig ID	38457_1.R1011
5'-most EST	uC-zmflb73049f09b1
Seq. No.	272505
Contig ID	38464_1.R1011
5'-most EST	LIB143-026-Q1-E1-B7
Seq. No.	272506
Contig ID	38470_1.R1011
5'-most EST	fdz701160966.h1
Seq. No.	272507
Contig ID	38473_1.R1011
5'-most EST	uC-zmroteosinte010f05b1
Seq. No.	272508
Contig ID	38477_1.R1011
5'-most EST	uC-zmflmo17310d02b1
Seq. No.	272509
Contig ID	38482_1.R1011
5'-most EST	ceu700422584.h1
Seq. No.	272510
Contig ID	38508_1.R1011
5'-most EST	uC-zmflb73309e01a1
Seq. No.	272511
Contig ID	38513_1.R1011
5'-most EST	LIB3180-033-P2-M2-C9
Seq. No.	272512
Contig ID	38520_1.R1011
5'-most EST	xyt700344110.h1
Method	BLASTX
NCBI GI	g3929368
BLAST score	715
E value	3.0e-75
Match length	187
% identity	71
NCBI Description	PRE-MRNA SPLICING FACTOR SF2 (SR1 PROTEIN) >gi_2443472 (AF001035) ASF/SF2 homolog [Arabidopsis thaliana]
Seq. No.	272513
Contig ID	38522_1.R1011
5'-most EST	LIB3137-004-Q1-K1-C1
Seq. No.	272514
Contig ID	38523_1.R1011
5'-most EST	uC-zmflmo17101f08b1
Seq. No.	272515
Contig ID	38523_2.R1011
5'-most EST	uC-zmflmo17175h03b1

Seq. No.	272516
Contig ID	38523_3.R1011
5'-most EST	uC-zmrob73080h11b1
Method	BLASTX
NCBI GI	g4539010
BLAST score	407
E value	2.0e-39
Match length	143
% identity	62
NCBI Description	(AL049481) putative DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No.	272517
Contig ID	38523_4.R1011
5'-most EST	uC-zmflmo170114b11b1

Seq. No.	272518
Contig ID	38526_1.R1011
5'-most EST	ymt700223773.h1
Method	BLASTX
NCBI GI	g4510362
BLAST score	190
E value	2.0e-14
Match length	63
% identity	63
NCBI Description	(AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272519
Contig ID	38532_1.R1011
5'-most EST	ymt700219389.h1
Method	BLASTX
NCBI GI	g4218115
BLAST score	393
E value	1.0e-37
Match length	132
% identity	61
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	272520
Contig ID	38532_2.R1011
5'-most EST	LIB3069-002-Q1-K1-G4

Seq. No.	272521
Contig ID	38551_1.R1011
5'-most EST	LIB3180-034-P2-M2-B5

Seq. No.	272522
Contig ID	38552_1.R1011
5'-most EST	nbm700476457.h1
Method	BLASTX
NCBI GI	g4522004
BLAST score	232
E value	8.0e-28
Match length	96
% identity	72
NCBI Description	(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]

Seq. No.	272523
Contig ID	38565_1.R1011
5'-most EST	uC-zmflmo17054c11b1
Method	BLASTX
NCBI GI	g2194132
BLAST score	900
E value	7.0e-97
Match length	285
% identity	64
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	272524
Contig ID	38565_2.R1011
5'-most EST	uC-zmflmo17022b05a1
Method	BLASTN
NCBI GI	g1743387
BLAST score	70
E value	7.0e-31
Match length	308
% identity	89
NCBI Description	S.bicolor mRNA for pSbaNS5 protein

Seq. No.	272525
Contig ID	38569_1.R1011
5'-most EST	uC-zmroteosinte087a08b2
Method	BLASTX
NCBI GI	g629602
BLAST score	1105
E value	1.0e-121
Match length	427
% identity	51
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	272526
Contig ID	38589_1.R1011
5'-most EST	ntr700073171.h1

Seq. No.	272527
Contig ID	38604_1.R1011
5'-most EST	mwy700442111.h1

Seq. No.	272528
Contig ID	38606_1.R1011
5'-most EST	uC-zmflb73180g11b1
Method	BLASTX
NCBI GI	g514324
BLAST score	163
E value	5.0e-11
Match length	75
% identity	43
NCBI Description	(L34773) RNA polymerase subunit [Arabidopsis thaliana] >gi_2462755 (AC002292) RNA polymerase subunit (isoform B) [Arabidopsis thaliana] >gi_1586550_prf__2204246B RNA polymerase [Arabidopsis thaliana]

Seq. No.	272529
Contig ID	38608_1.R1011
5'-most EST	uC-zmflmo17153e11b1
Method	BLASTX
NCBI GI	g4455323
BLAST score	1243
E value	1.0e-137
Match length	450
% identity	55
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	272530
Contig ID	38614_1.R1011
5'-most EST	LIB3180-035-P2-M2-D5

Seq. No.	272531
Contig ID	38620_1.R1011
5'-most EST	uC-zmflm017207g09b1
Method	BLASTX
NCBI GI	g2827552
BLAST score	223
E value	8.0e-18
Match length	48
% identity	67
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	272532
Contig ID	38620_2.R1011
5'-most EST	LIB3180-035-P2-M2-E11
Method	BLASTX
NCBI GI	g2827552
BLAST score	244
E value	2.0e-20
Match length	138
% identity	38
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	272533
Contig ID	38627_1.R1011
5'-most EST	LIB3180-035-P2-M2-F2
Method	BLASTX
NCBI GI	g4314378
BLAST score	688
E value	5.0e-72
Match length	341
% identity	42
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	272534
Contig ID	38630_1.R1011
5'-most EST	uC-zmflb73066b12b1
Method	BLASTX
NCBI GI	g3337357
BLAST score	446
E value	9.0e-44

Match length	145
% identity	54
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272535
Contig ID	38631_1.R1011
5'-most EST	uC-zmflb73053c06b2
Method	BLASTX
NCBI GI	g549060
BLAST score	1722
E value	0.0e+00
Match length	526
% identity	63
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_631656_pir__S43058 CCTeta protein eta chain - mouse >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	272536
Contig ID	38632_1.R1011
5'-most EST	uC-zmflb73239g03b2

Seq. No.	272537
Contig ID	38636_1.R1011
5'-most EST	LIB3180-035-P2-M2-G2

Seq. No.	272538
Contig ID	38646_1.R1011
5'-most EST	uC-zmflb73020g07b1

Seq. No.	272539
Contig ID	38646_2.R1011
5'-most EST	rvt700553022.h1

Seq. No.	272540
Contig ID	38648_1.R1011
5'-most EST	LIB143-040-Q1-E1-H6
Method	BLASTX
NCBI GI	g2583117
BLAST score	258
E value	1.0e-21
Match length	96
% identity	56
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272541
Contig ID	38648_2.R1011
5'-most EST	uC-zmroteosinte021c11b1

Seq. No.	272542
Contig ID	38648_3.R1011
5'-most EST	wyr700241150.h1

Seq. No.	272543
Contig ID	38650_1.R1011
5'-most EST	fwa700099377.h1
Method	BLASTX

NCBI GI	g4584346
BLAST score	380
E value	2.0e-36
Match length	128
% identity	55
NCBI Description	(AC007127) unknown protein [Arabidopsis thaliana]

Seq. No.	272544
Contig ID	38654_1.R1011
5'-most EST	LIB3180-036-P2-M2-A3

Seq. No.	272545
Contig ID	38662_1.R1011
5'-most EST	pmx700084906.h1
Method	BLASTX
NCBI GI	g3702962
BLAST score	623
E value	3.0e-86
Match length	189
% identity	84
NCBI Description	(AF079484) rac GTP binding protein Arac7 [Arabidopsis thaliana]

Seq. No.	272546
Contig ID	38662_2.R1011
5'-most EST	fdz701163970.h1
Method	BLASTX
NCBI GI	g3702962
BLAST score	413
E value	2.0e-40
Match length	82
% identity	93
NCBI Description	(AF079484) rac GTP binding protein Arac7 [Arabidopsis thaliana]

Seq. No.	272547
Contig ID	38664_1.R1011
5'-most EST	LIB3180-036-P2-M2-B4

Seq. No.	272548
Contig ID	38666_1.R1011
5'-most EST	LIB3180-036-P2-M2-B7
Method	BLASTX
NCBI GI	g4503843
BLAST score	148
E value	3.0e-09
Match length	95
% identity	36
NCBI Description	UNKNOWN >gi_3641676_dbj_BAA33390_ (AB015318) gamma2-adaptin [Homo sapiens]

Seq. No.	272549
Contig ID	38678_1.R1011
5'-most EST	pmx700082537.h1

Seq. No.	272550
Contig ID	38680_1.R1011

5'-most EST	uC-zmflMo17065f05b1
Seq. No.	272551
Contig ID	38680_2.R1011
5'-most EST	uC-zmflMo17093h03b1
Seq. No.	272552
Contig ID	38686_1.R1011
5'-most EST	uC-zmflmo17039a06b1
Method	BLASTX
NCBI GI	g3548810
BLAST score	336
E value	3.0e-31
Match length	181
% identity	42
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
Seq. No.	272553
Contig ID	38687_1.R1011
5'-most EST	uC-zmflmo17374h09a1
Seq. No.	272554
Contig ID	38688_1.R1011
5'-most EST	LIB3180-036-P2-M2-D9
Seq. No.	272555
Contig ID	38694_1.R1011
5'-most EST	xsy700209063.h1
Method	BLASTX
NCBI GI	g2851506
BLAST score	487
E value	4.0e-49
Match length	133
% identity	71
NCBI Description	DYSKERIN (NUCLEOLAR PROTEIN NAP57) >gi_2739325_emb_CAA84402_ (Z34922) NAP57 [Rattus norvegicus]
Seq. No.	272556
Contig ID	38703_1.R1011
5'-most EST	LIB3180-036-P2-M2-F3
Method	BLASTN
NCBI GI	g1737491
BLAST score	64
E value	1.0e-27
Match length	112
% identity	89
NCBI Description	Triticum aestivum poly(A)-binding protein (wheatpab) mRNA, complete cds
Seq. No.	272557
Contig ID	38705_1.R1011
5'-most EST	LIB3180-036-P2-M2-F5
Method	BLASTX
NCBI GI	g4101718
BLAST score	285

E value 5.0e-25
Match length 144
% identity 36
NCBI Description (AF006465) B cell antigen receptor Ig beta associated protein 1 [Mus musculus]

Seq. No. 272558
Contig ID 38705_2.R1011
5'-most EST xsy700208773.h1
Method BLASTX
NCBI GI g3152666
BLAST score 151
E value 1.0e-09
Match length 85
% identity 34
NCBI Description (AF064606) KB07 protein [Homo sapiens]

Seq. No. 272559
Contig ID 38711_1.R1011
5'-most EST LIB3180-036-P2-M2-G11

Seq. No. 272560
Contig ID 38713_1.R1011
5'-most EST xjt700093773.h1
Method BLASTX
NCBI GI g3399668
BLAST score 238
E value 3.0e-32
Match length 181
% identity 41
NCBI Description (AC005393) BC331004_1 [Homo sapiens]

Seq. No. 272561
Contig ID 38717_1.R1011
5'-most EST LIB3180-036-P2-M2-G8
Method BLASTX
NCBI GI g4220472
BLAST score 346
E value 1.0e-32
Match length 104
% identity 66
NCBI Description (AC006069) similar to yeast ccc1 protein [Arabidopsis thaliana]

Seq. No. 272562
Contig ID 38717_2.R1011
5'-most EST ntr700072783.h1
Method BLASTX
NCBI GI g4220472
BLAST score 206
E value 2.0e-16
Match length 52
% identity 79
NCBI Description (AC006069) similar to yeast ccc1 protein [Arabidopsis thaliana]

Seq. No. 272563

Contig ID	38724_1.R1011
5'-most EST	LIB3180-036-P2-M2-H9

Seq. No.	272564
Contig ID	38731_1.R1011
5'-most EST	wyr700237563.h1
Method	BLASTX
NCBI GI	g2388710
BLAST score	1569
E value	1.0e-175
Match length	417
% identity	68
NCBI Description	(AF017150) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No.	272565
Contig ID	38738_1.R1011
5'-most EST	LIB3180-037-P2-M2-B7
Method	BLASTX
NCBI GI	g1001257
BLAST score	228
E value	6.0e-19
Match length	60
% identity	67
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	272566
Contig ID	38740_1.R1011
5'-most EST	ntr700075879.h1
Method	BLASTX
NCBI GI	g4539335
BLAST score	274
E value	6.0e-24
Match length	135
% identity	41
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	272567
Contig ID	38740_2.R1011
5'-most EST	uC-zmflmo17021d09b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	272568
Contig ID	38742_1.R1011
5'-most EST	LIB3180-037-P2-M2-C12

Seq. No.	272569
Contig ID	38745_1.R1011
5'-most EST	uC-zmflb73013e07b1

Seq. No. 272570

Contig ID	38746_1.R1011
5'-most EST	yyf700350180.h1
Seq. No.	272571
Contig ID	38750_1.R1011
5'-most EST	LIB3180-037-P2-M2-D2
Seq. No.	272572
Contig ID	38753_1.R1011
5'-most EST	LIB3066-031-Q1-K1-E1
Seq. No.	272573
Contig ID	38758_1.R1011
5'-most EST	LIB3180-037-P2-M2-E11
Seq. No.	272574
Contig ID	38762_1.R1011
5'-most EST	xmt700257165.h1
Method	BLASTX
NCBI GI	g4531444
BLAST score	188
E value	9.0e-14
Match length	80
% identity	53
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.	272575
Contig ID	38768_1.R1011
5'-most EST	LIB189-008-Q1-E1-E8
Method	BLASTX
NCBI GI	g4567281
BLAST score	363
E value	7.0e-34
Match length	297
% identity	38
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.	272576
Contig ID	38768_2.R1011
5'-most EST	uC-zmflb73038c07b1
Method	BLASTN
NCBI GI	g3851004
BLAST score	36
E value	2.0e-10
Match length	64
% identity	89
NCBI Description	Zea mays pyruvate dehydrogenase E1 alpha subunit RNA, nuclear gene encoding mitochondrial protein, complete cds
Seq. No.	272577
Contig ID	38770_1.R1011
5'-most EST	uC-zmflm017205a10b1
Method	BLASTN
NCBI GI	g4103634
BLAST score	254
E value	1.0e-140
Match length	579

% identity	89
NCBI Description	Hordeum vulgare ABA-responsive protein mRNA, complete cds
Seq. No.	272578
Contig ID	38780_1.R1011
5'-most EST	LIB3067-043-Q1-K1-A12
Seq. No.	272579
Contig ID	38780_2.R1011
5'-most EST	LIB3180-037-P2-M2-G4
Seq. No.	272580
Contig ID	38781_1.R1011
5'-most EST	LIB3180-037-P2-M2-G5
Method	BLASTX
NCBI GI	g4038594
BLAST score	457
E value	9.0e-46
Match length	120
% identity	72
NCBI Description	(AJ222798) tDET1 protein [Lycopersicon esculentum] >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]
Seq. No.	272581
Contig ID	38790_1.R1011
5'-most EST	hbs701181085.h1
Method	BLASTX
NCBI GI	g4427003
BLAST score	178
E value	1.0e-12
Match length	66
% identity	47
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]
Seq. No.	272582
Contig ID	38797_1.R1011
5'-most EST	uC-zmflMo17003g11b1
Method	BLASTX
NCBI GI	g1175386
BLAST score	156
E value	8.0e-10
Match length	148
% identity	31
NCBI Description	HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I >gi_2130289_pir__S58305 hypothetical protein SPAC18B11.06 - fission yeast (Schizosaccharomyces pombe) >gi_929892_emb_CAA90591_ (Z50728) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	272583
Contig ID	38798_1.R1011
5'-most EST	xjt700096588.h1
Seq. No.	272584
Contig ID	38799_1.R1011
5'-most EST	LIB3067-014-Q1-K1-H2

Method	BLASTX
NCBI GI	g2736147
BLAST score	632
E value	6.0e-66
Match length	159
% identity	68
NCBI Description	(AF021804) fatty acid hydroxylase Fah1p [Arabidopsis thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase, FAH1 [Arabidopsis thaliana]

Seq. No.	272585
Contig ID	38804_1.R1011
5'-most EST	LIB3180-038-P2-M2-B4
Method	BLASTX
NCBI GI	g687844
BLAST score	551
E value	4.0e-56
Match length	281
% identity	13
NCBI Description	(U21320) contains TPR domain-like repeats [Caenorhabditis elegans]

Seq. No.	272586
Contig ID	38806_1.R1011
5'-most EST	LIB3180-038-P2-M2-B7
Method	BLASTN
NCBI GI	g22542
BLAST score	146
E value	4.0e-76
Match length	210
% identity	92
NCBI Description	Maize gene for Mr 19000 alpha zein and 5'-flanking region

Seq. No.	272587
Contig ID	38811_1.R1011
5'-most EST	LIB3180-038-P2-M2-C12
Method	BLASTX
NCBI GI	g4454032
BLAST score	780
E value	6.0e-83
Match length	266
% identity	56
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	272588
Contig ID	38812_1.R1011
5'-most EST	LIB3060-054-Q1-K1-A2
Method	BLASTX
NCBI GI	g2262105
BLAST score	608
E value	4.0e-63
Match length	199
% identity	52
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	272589
Contig ID	38815_1.R1011

5'-most EST	LIB3180-038-P2-M2-C7
Seq. No.	272590
Contig ID	38819_1.R1011
5'-most EST	LIB3180-038-P2-M2-D10
Seq. No.	272591
Contig ID	38824_2.R1011
5'-most EST	LIB3180-038-P2-M2-D4
Method	BLASTX
NCBI GI	g4262147
BLAST score	389
E value	2.0e-37
Match length	125
% identity	56
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]
Seq. No.	272592
Contig ID	38828_1.R1011
5'-most EST	pmx700081833.h1
Method	BLASTN
NCBI GI	g3819647
BLAST score	62
E value	3.0e-26
Match length	93
% identity	91
NCBI Description	Hordeum vulgare genomic DNA fragment; clone MWG2257.rev
Seq. No.	272593
Contig ID	38839_1.R1011
5'-most EST	LIB3137-002-Q1-K1-H2
Seq. No.	272594
Contig ID	38843_1.R1011
5'-most EST	uC-zmflmo17285b09b1
Method	BLASTX
NCBI GI	g2618721
BLAST score	247
E value	2.0e-42
Match length	147
% identity	65
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]
Seq. No.	272595
Contig ID	38843_4.R1011
5'-most EST	uC-zmflmo17221f02b1
Seq. No.	272596
Contig ID	38845_1.R1011
5'-most EST	pwr700450468.h1
Seq. No.	272597
Contig ID	38867_1.R1011
5'-most EST	gct701172694.h1
Seq. No.	272598

Contig ID	38873_1.R1011
5'-most EST	LIB3180-039-P2-M2-A6
Method	BLASTX
NCBI GI	g4582436
BLAST score	171
E value	3.0e-19
Match length	104
% identity	54
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	272599
Contig ID	38885_1.R1011
5'-most EST	uC-zmflb73050b04b1

Seq. No.	272600
Contig ID	38903_1.R1011
5'-most EST	ymt700223877.h1

Seq. No.	272601
Contig ID	38912_1.R1011
5'-most EST	LIB3180-039-P2-M2-F1

Seq. No.	272602
Contig ID	38914_1.R1011
5'-most EST	LIB3180-039-P2-M2-F11
Method	BLASTX
NCBI GI	g728827
BLAST score	381
E value	1.0e-36
Match length	177
% identity	49
NCBI Description	ALLANTOINASE PRECURSOR >gi_458126 (U03471) allantoinase [Rana catesbeiana]

Seq. No.	272603
Contig ID	38949_1.R1011
5'-most EST	LIB3180-040-P2-M2-B10
Method	BLASTX
NCBI GI	g1213629
BLAST score	556
E value	5.0e-57
Match length	178
% identity	59
NCBI Description	(X95991) pectinesterase [Prunus persica]

Seq. No.	272604
Contig ID	38953_1.R1011
5'-most EST	yyf700350270.h1
Method	BLASTX
NCBI GI	g3342800
BLAST score	807
E value	2.0e-86
Match length	160
% identity	99
NCBI Description	(AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	272605
Contig ID	38976_1.R1011
5'-most EST	LIB3180-040-P2-M2-E12

Seq. No.	272606
Contig ID	38978_1.R1011
5'-most EST	LIB3180-040-P2-M2-E4

Seq. No.	272607
Contig ID	38980_1.R1011
5'-most EST	LIB3180-040-P2-M2-E6

Seq. No.	272608
Contig ID	38982_1.R1011
5'-most EST	LIB3180-040-P2-M2-E9
Method	BLASTX
NCBI GI	g418507
BLAST score	326
E value	1.0e-29
Match length	161
% identity	40
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	272609
Contig ID	38995_1.R1011
5'-most EST	LIB3180-040-P2-M2-G2
Method	BLASTX
NCBI GI	g3176684
BLAST score	650
E value	5.0e-68
Match length	219
% identity	62
NCBI Description	(AC003671) Contains similarity to equilibratiave nucleoside transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317, gb_T20785, gb_AA586285 and gb_AA712578 come from this gene. [Arabidopsis thaliana]

Seq. No.	272610
Contig ID	38997_1.R1011
5'-most EST	LIB3180-040-P2-M2-G4
Method	BLASTX
NCBI GI	g4406372
BLAST score	481
E value	2.0e-48
Match length	115
% identity	75
NCBI Description	(AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No.	272611
Contig ID	38997_2.R1011

5'-most EST	rvt700552639.h1
Seq. No.	272612
Contig ID	38997_3.R1011
5'-most EST	LIB83-012-Q1-E1-A2
Method	BLASTX
NCBI GI	g4406372
BLAST score	207
E value	2.0e-16
Match length	103
% identity	45
NCBI Description	(AF109156) thiosulfate sulfurtransferase [Datisca glomerata]
Seq. No.	272613
Contig ID	39000_1.R1011
5'-most EST	LIB3066-055-Q1-K1-A2
Seq. No.	272614
Contig ID	39008_1.R1011
5'-most EST	LIB3136-008-Q1-K1-F8
Method	BLASTX
NCBI GI	g3935168
BLAST score	619
E value	3.0e-64
Match length	279
% identity	52
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]
Seq. No.	272615
Contig ID	39009_1.R1011
5'-most EST	LIB3180-040-P2-M2-H9
Method	BLASTX
NCBI GI	g2651300
BLAST score	212
E value	5.0e-17
Match length	83
% identity	51
NCBI Description	(AC002336) putative initiator tRNA phosphoribosyl-transferase [Arabidopsis thaliana]
Seq. No.	272616
Contig ID	39012_1.R1011
5'-most EST	LIB3180-041-P2-M2-A11
Method	BLASTX
NCBI GI	g3057120
BLAST score	879
E value	5.0e-95
Match length	162
% identity	100
NCBI Description	(AF023159) starch synthase DULL1 [Zea mays]
Seq. No.	272617
Contig ID	39015_1.R1011
5'-most EST	uC-zmrob73033e12b1
Method	BLASTX
NCBI GI	g3094014

BLAST score	249
E value	5.0e-21
Match length	89
% identity	52
NCBI Description	(AF060862) unknown [Homo sapiens]

Seq. No.	272618
Contig ID	39020_1.R1011
5'-most EST	uC-zmflb73040f04b1

Seq. No.	272619
Contig ID	39032_1.R1011
5'-most EST	clt700042241.f1
Method	BLASTX
NCBI GI	g2827139
BLAST score	180
E value	3.0e-17
Match length	85
% identity	57
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	272620
Contig ID	39041_1.R1011
5'-most EST	uer700580618.h1

Seq. No.	272621
Contig ID	39051_1.R1011
5'-most EST	LIB3137-042-Q1-K1-C9
Method	BLASTX
NCBI GI	g1778093
BLAST score	736
E value	5.0e-78
Match length	230
% identity	65
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	272622
Contig ID	39061_1.R1011
5'-most EST	LIB3180-041-P2-M2-G10

Seq. No.	272623
Contig ID	39068_1.R1011
5'-most EST	LIB3180-041-P2-M2-G9

Seq. No.	272624
Contig ID	39078_2.R1011
5'-most EST	LIB3180-042-P2-M2-A10

Seq. No.	272625
Contig ID	39078_3.R1011
5'-most EST	uC-zmflb73091g04b2

Seq. No.	272626
Contig ID	39081_1.R1011
5'-most EST	vux700158192.h1
Method	BLASTX
NCBI GI	g4538911
BLAST score	274
E value	5.0e-24
Match length	150
% identity	41
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272627
Contig ID	39090_1.R1011
5'-most EST	gwl700612441.h1

Seq. No.	272628
Contig ID	39104_1.R1011
5'-most EST	LIB3180-042-P2-M2-D2

Seq. No.	272629
Contig ID	39105_1.R1011
5'-most EST	LIB3180-054-P2-M1-E1
Method	BLASTN
NCBI GI	g548194
BLAST score	75
E value	4.0e-34
Match length	79
% identity	99
NCBI Description	Zea mays IAA-glu synthetase (iaglu) mRNA, complete cds

Seq. No.	272630
Contig ID	39108_1.R1011
5'-most EST	pmx700088181.h1

Seq. No.	272631
Contig ID	39110_1.R1011
5'-most EST	xmt700260909.h1

Seq. No.	272632
Contig ID	39115_1.R1011
5'-most EST	uC-zmflmo17341g07b1
Method	BLASTX
NCBI GI	g3820648
BLAST score	385
E value	4.0e-37
Match length	154
% identity	48
NCBI Description	(Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	272633
Contig ID	39116_1.R1011
5'-most EST	LIB3180-042-P2-M2-E5

Seq. No.	272634
Contig ID	39117_1.R1011
5'-most EST	uC-zmflb73280c08b2
Method	BLASTN

NCBI GI g167080
BLAST score 36
E value 1.0e-10
Match length 48
% identity 94
NCBI Description Hordeum vulgare peroxidase BP 1 (Prx5) mRNA, complete cds

Seq. No. 272635
Contig ID 39117_2.R1011
5'-most EST uC-zmflmo17341c06b1
Method BLASTX
NCBI GI g2388571
BLAST score 441
E value 2.0e-43
Match length 156
% identity 54
NCBI Description (AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb_X98321). [Arabidopsis thaliana] >gi_2738254 (U97684) peroxidase precursor [Arabidopsis thaliana]

Seq. No. 272636
Contig ID 39117_3.R1011
5'-most EST LIB3137-024-Q1-K1-E10
Method BLASTX
NCBI GI g1546692
BLAST score 167
E value 1.0e-11
Match length 48
% identity 60
NCBI Description (X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No. 272637
Contig ID 39129_1.R1011
5'-most EST LIB3180-042-P2-M2-F9

Seq. No. 272638
Contig ID 39135_1.R1011
5'-most EST LIB3180-042-P2-M2-G7
Method BLASTX
NCBI GI g2558654
BLAST score 558
E value 2.0e-57
Match length 189
% identity 51
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 272639
Contig ID 39140_1.R1011
5'-most EST tzu700205430.h1

Seq. No. 272640
Contig ID 39144_1.R1011
5'-most EST LIB3180-042-P2-M2-H6

Seq. No. 272641
Contig ID 39173_1.R1011
5'-most EST LIB3180-043-P2-M2-C8

Method	BLASTX
NCBI GI	g4102600
BLAST score	337
E value	2.0e-31
Match length	151
% identity	53
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	272642
Contig ID	39182_1.R1011
5'-most EST	ntr700073969.h1
Method	BLASTX
NCBI GI	g4206122
BLAST score	261
E value	2.0e-22
Match length	105
% identity	52
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	272643
Contig ID	39203_1.R1011
5'-most EST	LIB3136-004-Q1-K1-A5

Seq. No.	272644
Contig ID	39212_1.R1011
5'-most EST	tfd700571828.h1
Method	BLASTX
NCBI GI	g3482974
BLAST score	323
E value	9.0e-30
Match length	110
% identity	63
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	272645
Contig ID	39218_1.R1011
5'-most EST	uC-zmflb73061f11b1
Method	BLASTX
NCBI GI	g2342682
BLAST score	184
E value	2.0e-13
Match length	41
% identity	83
NCBI Description	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No.	272646
Contig ID	39218_2.R1011
5'-most EST	wyr700237593.h1
Method	BLASTX
NCBI GI	g2342682
BLAST score	540
E value	5.0e-55
Match length	132
% identity	76

NCBI Description	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No.	272647
Contig ID	39219_1.R1011
5'-most EST	uC-zmflb73280e12a1
Method	BLASTX
NCBI GI	g2245005
BLAST score	218
E value	4.0e-35
Match length	281
% identity	40
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272648
Contig ID	39221_1.R1011
5'-most EST	ymt700219078.h1
Method	BLASTX
NCBI GI	g2244898
BLAST score	1378
E value	1.0e-153
Match length	435
% identity	59
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	272649
Contig ID	39241_1.R1011
5'-most EST	LIB83-005-Q1-E1-C10
Method	BLASTX
NCBI GI	g3080420
BLAST score	795
E value	1.0e-104
Match length	265
% identity	74
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	272650
Contig ID	39256_1.R1011
5'-most EST	LIB3180-044-P2-M2-F7
Method	BLASTX
NCBI GI	g4539660
BLAST score	441
E value	5.0e-44
Match length	99
% identity	81
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	272651
Contig ID	39259_1.R1011
5'-most EST	uC-zmflb73049f10b1
Method	BLASTX
NCBI GI	g4337179
BLAST score	196
E value	6.0e-15
Match length	54

% identity	65
NCBI Description	(AC006416) This gene is continued on the 5' end of BAC T12M14. [Arabidopsis thaliana]

Seq. No.	272652
Contig ID	39259_3.R1011
5'-most EST	LIB3180-044-P2-M2-G1
Method	BLASTX
NCBI GI	g4337179
BLAST score	208
E value	2.0e-16
Match length	85
% identity	52
NCBI Description	(AC006416) This gene is continued on the 5' end of BAC T12M14. [Arabidopsis thaliana]

Seq. No.	272653
Contig ID	39287_1.R1011
5'-most EST	uC-zmroteosinte022e05b1
Method	BLASTX
NCBI GI	g3924594
BLAST score	599
E value	7.0e-62
Match length	230
% identity	59
NCBI Description	(AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi_4262139_gb_AAD14439_ (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	272654
Contig ID	39292_1.R1011
5'-most EST	fC-zmle700425210f2

Seq. No.	272655
Contig ID	39295_1.R1011
5'-most EST	LIB3180-045-P2-M2-C4
Method	BLASTX
NCBI GI	g4587513
BLAST score	245
E value	2.0e-26
Match length	147
% identity	46
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	272656
Contig ID	39302_1.R1011
5'-most EST	LIB3060-019-Q1-K1-H12

Seq. No.	272657
Contig ID	39306_1.R1011
5'-most EST	LIB143-038-Q1-E1-G6

Seq. No.	272658
Contig ID	39317_1.R1011
5'-most EST	LIB3180-045-P2-M2-F8

Seq. No.	272659
Contig ID	39345_1.R1011
5'-most EST	LIB3180-046-P2-M2-A9

Seq. No.	272660
Contig ID	39346_1.R1011
5'-most EST	uwc700151641.h1
Method	BLASTX
NCBI GI	g3142301
BLAST score	464
E value	2.0e-46
Match length	126
% identity	74
NCBI Description	(AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb_M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101, gb_H3630

Seq. No.	272661
Contig ID	39353_1.R1011
5'-most EST	LIB3180-046-P2-M2-C10
Method	BLASTX
NCBI GI	g3024991
BLAST score	171
E value	4.0e-12
Match length	85
% identity	45
NCBI Description	HYPOTHETICAL AMINOTRANSFERASE YBDL >gi_1778518 (U82598) hypothetical protein [Escherichia coli] >gi_1786816 (AE000165) putative aminotransferase [Escherichia coli] >gi_4062217_dbj_BAA35230_ (D90701) Aspartate transaminase (EC 2.6.1.1) [Escherichia coli]

Seq. No.	272662
Contig ID	39353_2.R1011
5'-most EST	ceu700422062.h1

Seq. No.	272663
Contig ID	39383_1.R1011
5'-most EST	LIB3180-046-P2-M2-F6

Seq. No.	272664
Contig ID	39384_1.R1011
5'-most EST	LIB3066-005-Q1-K1-F3
Method	BLASTX
NCBI GI	g2827650
BLAST score	555
E value	1.0e-68
Match length	205
% identity	66
NCBI Description	(AL021637) potassium transporter-like protein [Arabidopsis thaliana]

Seq. No.	272665
Contig ID	39387_1.R1011
5'-most EST	LIB3180-046-P2-M2-G10

Seq. No.	272666
Contig ID	39394_1.R1011
5'-most EST	uC-zmflmo17321f03b1
Method	BLASTX
NCBI GI	g2443881
BLAST score	786
E value	2.0e-83
Match length	281
% identity	56
NCBI Description	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]

Seq. No.	272667
Contig ID	39394_2.R1011
5'-most EST	hvj70l623751.h1

Seq. No.	272668
Contig ID	39407_1.R1011
5'-most EST	fdz70l166875.h1

Seq. No.	272669
Contig ID	39410_1.R1011
5'-most EST	LIB3180-047-P2-B10

Seq. No.	272670
Contig ID	39413_1.R1011
5'-most EST	LIB3180-047-P2-B5

Seq. No.	272671
Contig ID	39425_1.R1011
5'-most EST	uC-zmflb73253f11b1
Method	BLASTX
NCBI GI	g1709129
BLAST score	1772
E value	0.0e+00
Match length	409
% identity	82
NCBI Description	GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3 >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) - alfalfa >gi_313148_emb_CAA48472_ (X68409) protein kinase [Medicago sativa]

Seq. No.	272672
Contig ID	39425_2.R1011
5'-most EST	uC-zmflb73169a01b2
Method	BLASTX
NCBI GI	g2398519
BLAST score	266
E value	3.0e-23
Match length	85
% identity	64
NCBI Description	(AJ000732) shaggy-like kinase alpha [Arabidopsis thaliana]

Seq. No.	272673
Contig ID	39435_1.R1011
5'-most EST	LIB3180-047-P2-D9

Method	BLASTX
NCBI GI	g4432855
BLAST score	1693
E value	0.0e+00
Match length	616
% identity	60
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	272674
Contig ID	39435_2.R1011
5'-most EST	ntr700072938.h1
Method	BLASTX
NCBI GI	g4432855
BLAST score	206
E value	4.0e-16
Match length	54
% identity	74
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	272675
Contig ID	39435_3.R1011
5'-most EST	qmh700030205.f1
Method	BLASTX
NCBI GI	g4432855
BLAST score	213
E value	7.0e-17
Match length	54
% identity	76
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	272676
Contig ID	39435_4.R1011
5'-most EST	LIB3137-018-Q1-K1-H1
Method	BLASTX
NCBI GI	g2864615
BLAST score	508
E value	3.0e-51
Match length	252
% identity	65
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	272677
Contig ID	39435_5.R1011
5'-most EST	gct701178642.h1
Method	BLASTX
NCBI GI	g2864615
BLAST score	176
E value	2.0e-12
Match length	75
% identity	48
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	272678
Contig ID	39435_6.R1011
5'-most EST	LIB3062-037-Q1-K1-A3

Seq. No. 272679

Contig ID	39435_7.R1011
5'-most EST	LIB3069-057-Q1-K1-D4
Method	BLASTX
NCBI GI	g3402722
BLAST score	1393
E value	1.0e-154
Match length	359
% identity	72
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No.	272680
Contig ID	39435_8.R1011
5'-most EST	LIB3067-022-Q1-K1-B11
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	8.0e-11
Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	272681
Contig ID	39435_9.R1011
5'-most EST	wyr700239334.h1

Seq. No.	272682
Contig ID	39435_10.R1011
5'-most EST	wen700332449.h1

Seq. No.	272683
Contig ID	39435_11.R1011
5'-most EST	wty700170043.h1

Seq. No.	272684
Contig ID	39436_1.R1011
5'-most EST	LIB3066-031-Q1-K1-E6
Method	BLASTX
NCBI GI	g3021357
BLAST score	760
E value	6.0e-81
Match length	192
% identity	73
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	272685
Contig ID	39447_1.R1011
5'-most EST	LIB3069-023-Q1-K1-A2

Seq. No.	272686
Contig ID	39451_1.R1011
5'-most EST	LIB3066-012-Q1-K1-E8
Method	BLASTN
NCBI GI	g2062705
BLAST score	33
E value	5.0e-09
Match length	37

% identity	97
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	272687
Contig ID	39454_1.R1011
5'-most EST	uC-zmflmo17070f12a1
Method	BLASTX
NCBI GI	g3757521
BLAST score	210
E value	5.0e-17
Match length	78
% identity	60
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	272688
Contig ID	39462_1.R1011
5'-most EST	uC-zmflmo17248e07b1
Method	BLASTX
NCBI GI	g4539291
BLAST score	699
E value	1.0e-73
Match length	234
% identity	59
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	272689
Contig ID	39475_1.R1011
5'-most EST	LIB3180-048-P2-A3

Seq. No.	272690
Contig ID	39478_1.R1011
5'-most EST	LIB3180-048-P2-A7
Method	BLASTX
NCBI GI	g4585884
BLAST score	278
E value	2.0e-24
Match length	143
% identity	42
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	272691
Contig ID	39485_1.R1011
5'-most EST	uC-zmflb73378g04a2
Method	BLASTX
NCBI GI	g4539452
BLAST score	356
E value	9.0e-34
Match length	78
% identity	81
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	272692
Contig ID	39489_1.R1011
5'-most EST	uC-zmflb73165a02b2
Method	BLASTX
NCBI GI	g2245378

BLAST score	792
E value	2.0e-84
Match length	201
% identity	72
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	272693
Contig ID	39495_1.R1011
5'-most EST	xsy700212129.h1
Method	BLASTX
NCBI GI	g3894168
BLAST score	161
E value	1.0e-10
Match length	77
% identity	43
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	272694
Contig ID	39495_2.R1011
5'-most EST	wyr700237356.h1

Seq. No.	272695
Contig ID	39497_1.R1011
5'-most EST	LIB3180-048-P2-C4
Method	BLASTX
NCBI GI	g3309168
BLAST score	170
E value	7.0e-12
Match length	138
% identity	33
NCBI Description	(AF071313) COP9 complex subunit 3 [Mus musculus]

Seq. No.	272696
Contig ID	39504_1.R1011
5'-most EST	xyt700345882.h1

Seq. No.	272697
Contig ID	39516_1.R1011
5'-most EST	LIB3069-009-Q1-K1-C2

Seq. No.	272698
Contig ID	39519_1.R1011
5'-most EST	LIB3180-048-P2-E8
Method	BLASTX
NCBI GI	g2335096
BLAST score	254
E value	2.0e-21
Match length	207
% identity	31
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272699
Contig ID	39520_1.R1011
5'-most EST	uC-zmflmo17113a09b1

Seq. No.	272700

Contig ID	39526_1.R1011
5'-most EST	LIB3180-048-P2-F4

Seq. No.	272701
Contig ID	39531_1.R1011
5'-most EST	uC-zmflMo17014g05b1
Method	BLASTX
NCBI GI	g3128167
BLAST score	251
E value	4.0e-21
Match length	213
% identity	31
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana] >gi_3212874 (AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272702
Contig ID	39546_1.R1011
5'-most EST	uC-zmflb73275b10b1

Seq. No.	272703
Contig ID	39557_1.R1011
5'-most EST	uC-zmroteosinte105f06b1
Method	BLASTX
NCBI GI	g3914006
BLAST score	1392
E value	1.0e-155
Match length	310
% identity	90
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588 (U85495) LON2 [Zea mays]

Seq. No.	272704
Contig ID	39574_1.R1011
5'-most EST	LIB3180-049-P2-M1-D10
Method	BLASTX
NCBI GI	g1707855
BLAST score	157
E value	2.0e-10
Match length	49
% identity	57
NCBI Description	(Y09292) obtusifoliol 14-alpha-demethylase [Triticum aestivum]

Seq. No.	272705
Contig ID	39586_2.R1011
5'-most EST	hvj700623740.h1

Seq. No.	272706
Contig ID	39591_1.R1011
5'-most EST	LIB3180-049-P2-M1-E7

Seq. No.	272707
Contig ID	39594_1.R1011
5'-most EST	LIB3070-004-Q1-N1-E10
Method	BLASTX
NCBI GI	g4337178

BLAST score	665
E value	2.0e-69
Match length	153
% identity	81
NCBI Description	(AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No.	272708
Contig ID	39596_1.R1011
5'-most EST	LIB3180-049-P2-M1-F3

Seq. No.	272709
Contig ID	39605_1.R1011
5'-most EST	LIB3180-049-P2-M1-G3
Method	BLASTX
NCBI GI	g3122914
BLAST score	1060
E value	1.0e-116
Match length	261
% identity	71
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	272710
Contig ID	39607_1.R1011
5'-most EST	uC-zmflm017084f11b1
Method	BLASTX
NCBI GI	g2708745
BLAST score	684
E value	6.0e-72
Match length	161
% identity	81
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	272711
Contig ID	39610_1.R1011
5'-most EST	uC-zmflb73051h12b1
Method	BLASTX
NCBI GI	g2506788
BLAST score	600
E value	5.0e-62
Match length	162
% identity	64
NCBI Description	GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) >gi_1332508_emb_CAA66638_ (X98001) geranylgeranyl transferase II [Homo sapiens]

Seq. No.	272712
Contig ID	39616_1.R1011
5'-most EST	uC-zmflb73066h01b1
Method	BLASTX
NCBI GI	g4455323
BLAST score	342
E value	4.0e-32

Match length	120
% identity	55
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	272713
Contig ID	39628_1.R1011
5'-most EST	pmx700087719.h1

Seq. No.	272714
Contig ID	39629_1.R1011
5'-most EST	LIB3062-038-Q1-K1-B3

Seq. No.	272715
Contig ID	39629_2.R1011
5'-most EST	nbm700470926.h1

Seq. No.	272716
Contig ID	39649_1.R1011
5'-most EST	LIB3180-050-P2-M1-H3

Seq. No.	272717
Contig ID	39665_1.R1011
5'-most EST	LIB3180-051-P2-M1-B7

Seq. No.	272718
Contig ID	39668_1.R1011
5'-most EST	zuv700352723.h1
Method	BLASTX
NCBI GI	g4584540
BLAST score	246
E value	3.0e-20
Match length	366
% identity	32
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	272719
Contig ID	39668_2.R1011
5'-most EST	uC-zmflmo170114c08b1

Seq. No.	272720
Contig ID	39668_3.R1011
5'-most EST	xmt700258826.h1
Method	BLASTX
NCBI GI	g2275210
BLAST score	288
E value	1.0e-25
Match length	143
% identity	42
NCBI Description	(AC002337) peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No.	272721
Contig ID	39668_4.R1011
5'-most EST	uC-zmflmo17283h08b1

Seq. No. 272722

Contig ID	39670_1.R1011
5'-most EST	dyk700103969.h1
Method	BLASTX
NCBI GI	g4588012
BLAST score	457
E value	2.0e-45
Match length	102
% identity	80
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	272723
Contig ID	39679_1.R1011
5'-most EST	LIB3180-051-P2-M1-E10

Seq. No.	272724
Contig ID	39679_2.R1011
5'-most EST	yne700378864.h1

Seq. No.	272725
Contig ID	39686_1.R1011
5'-most EST	uC-zmflb73120a04b1
Method	BLASTX
NCBI GI	g1076758
BLAST score	245
E value	1.0e-23
Match length	136
% identity	57
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir__S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]

Seq. No.	272726
Contig ID	39690_1.R1011
5'-most EST	LIB3180-051-P2-M1-G1

Seq. No.	272727
Contig ID	39695_1.R1011
5'-most EST	LIB3279-018-P1-K1-F6
Method	BLASTX
NCBI GI	g227686
BLAST score	171
E value	3.0e-12
Match length	43
% identity	79
NCBI Description	phytochrome [Zea mays]

Seq. No.	272728
Contig ID	39696_2.R1011
5'-most EST	LIB3180-051-P2-M1-H10
Method	BLASTX
NCBI GI	g1931645
BLAST score	158
E value	2.0e-10
Match length	65
% identity	55

NCBI Description	(U95973) Fe(II) transporter isolog [Arabidopsis thaliana]

Seq. No.	272729
Contig ID	39696_3.R1011
5'-most EST	wyr700239115.h1

Seq. No.	272730
Contig ID	39697_1.R1011
5'-most EST	LIB3060-024-Q1-K1-B5
Method	BLASTX
NCBI GI	g3176667
BLAST score	337
E value	2.0e-31
Match length	112
% identity	61
NCBI Description	(AC004393) Similar to hypothetical 41.9KD protein gb_1001369 from sequence of Synechocystis sp. gb_D64006. [Arabidopsis thaliana]

Seq. No.	272731
Contig ID	39703_1.R1011
5'-most EST	cyk700050721.f1

Seq. No.	272732
Contig ID	39707_1.R1011
5'-most EST	uC-zmflb73100g06b1

Seq. No.	272733
Contig ID	39711_1.R1011
5'-most EST	LIB3180-052-P2-M1-C10
Method	BLASTX
NCBI GI	g3618320
BLAST score	438
E value	2.0e-43
Match length	129
% identity	69
NCBI Description	(AB001888) zinc finger protein [Oryza sativa]

Seq. No.	272734
Contig ID	39734_1.R1011
5'-most EST	LIB3069-056-Q1-K1-G4

Seq. No.	272735
Contig ID	39736_1.R1011
5'-most EST	xjt700094025.h1

Seq. No.	272736
Contig ID	39738_1.R1011
5'-most EST	uC-zmflmo17342e06b1

Seq. No.	272737
Contig ID	39739_1.R1011
5'-most EST	rvt700553329.h1
Method	BLASTX
NCBI GI	g3641837
BLAST score	977
E value	1.0e-106

Match length	318
% identity	62
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	272738
Contig ID	39739_2.R1011
5'-most EST	kem700612083.h1

Seq. No.	272739
Contig ID	39741_1.R1011
5'-most EST	uC-zmflb73349d12a2
Method	BLASTX
NCBI GI	g2583109
BLAST score	228
E value	3.0e-18
Match length	148
% identity	42
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	272740
Contig ID	39750_1.R1011
5'-most EST	uC-zmflmo17070f09b1

Seq. No.	272741
Contig ID	39760_1.R1011
5'-most EST	uwc700153594.h1

Seq. No.	272742
Contig ID	39767_1.R1011
5'-most EST	uC-zmromo17114f07a1
Method	BLASTN
NCBI GI	g22099
BLAST score	45
E value	4.0e-16
Match length	77
% identity	90
NCBI Description	Z.mays 27kDa zein locus DNA

Seq. No.	272743
Contig ID	39775_1.R1011
5'-most EST	LIB3180-053-P2-M1-C12
Method	BLASTX
NCBI GI	g1841468
BLAST score	193
E value	6.0e-15
Match length	52
% identity	63
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No.	272744
Contig ID	39788_1.R1011
5'-most EST	dyk700103995.h1

Seq. No.	272745
Contig ID	39789_2.R1011
5'-most EST	ceu700433201.h1

Method	BLASTX
NCBI GI	g585550
BLAST score	482
E value	9.0e-49
Match length	107
% identity	82
NCBI Description	NADPH-CYTOCHROME P450 REDUCTASE (CPR) >gi_295448 (L07843) NADPH cytochrome P450 [Vigna radiata]

Seq. No.	272746
Contig ID	39793_1.R1011
5'-most EST	xmt700266779.h1

Seq. No.	272747
Contig ID	39801_1.R1011
5'-most EST	LIB3180-053-P2-M1-F7

Seq. No.	272748
Contig ID	39825_1.R1011
5'-most EST	uC-zmroteosinte024b11b1

Seq. No.	272749
Contig ID	39825_2.R1011
5'-most EST	xsy700211325.h1

Seq. No.	272750
Contig ID	39827_1.R1011
5'-most EST	xjt700096646.h1

Seq. No.	272751
Contig ID	39838_1.R1011
5'-most EST	LIB3180-054-P2-M1-E3
Method	BLASTX
NCBI GI	g3628757
BLAST score	184
E value	3.0e-13
Match length	194
% identity	27
NCBI Description	(AF038007) FIC1 [Homo sapiens]

Seq. No.	272752
Contig ID	39865_1.R1011
5'-most EST	LIB3180-055-P2-M1-B3

Seq. No.	272753
Contig ID	39865_2.R1011
5'-most EST	uC-zmflb73184c11a1

Seq. No.	272754
Contig ID	39867_1.R1011
5'-most EST	pwr700450152.h1
Method	BLASTX
NCBI GI	g2244749
BLAST score	683
E value	8.0e-72
Match length	247
% identity	52

NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.	272755
Contig ID	39869_1.R1011
5'-most EST	uC-zmflb73196c03a2
Seq. No.	272756
Contig ID	39875_1.R1011
5'-most EST	LIB3180-055-P2-M1-C7
Method	BLASTX
NCBI GI	g1169186
BLAST score	194
E value	8.0e-15
Match length	51
% identity	69
NCBI Description	THIOL PROTEASE SEN102 PRECURSOR >gi_1085732_pir__S36421 cysteine proteinase - Hemerocallis sp >gi_1364024_pir__S57777 cysteine protease precursor - Hemerocallis x hybrida >gi_396568_emb_CAA52425_ (X74406) thiol-protease [Hemerocallis sp.]
Seq. No.	272757
Contig ID	39876_1.R1011
5'-most EST	LIB3069-028-Q1-K1-C6
Method	BLASTX
NCBI GI	g1072187
BLAST score	366
E value	2.0e-34
Match length	336
% identity	29
NCBI Description	(U40941) coded for by C. elegans cDNA CEESB82F; coded for by C. elegans cDNA CEESE93F [Caenorhabditis elegans]
Seq. No.	272758
Contig ID	39887_1.R1011
5'-most EST	fwa700097388.h1
Method	BLASTX
NCBI GI	g3420233
BLAST score	207
E value	2.0e-16
Match length	56
% identity	70
NCBI Description	(AF058763) uroporphyrinogen decarboxylase [Zea mays]
Seq. No.	272759
Contig ID	39889_1.R1011
5'-most EST	uC-zmroteosinte118d09b1
Method	BLASTX
NCBI GI	g3859659
BLAST score	375
E value	6.0e-36
Match length	157
% identity	49
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]
Seq. No.	272760

Contig ID	39899_1.R1011
5'-most EST	uC-zmflb73100c09b1

Seq. No.	272761
Contig ID	39918_1.R1011
5'-most EST	LIB3062-012-Q1-K1-C1
Method	BLASTX
NCBI GI	g462195
BLAST score	334
E value	5.0e-31
Match length	90
% identity	73
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	272762
Contig ID	39932_1.R1011
5'-most EST	xjt700096374.h1
Method	BLASTX
NCBI GI	g1946372
BLAST score	249
E value	7.0e-21
Match length	78
% identity	65
NCBI Description	(U93215) yeast hypothetical protein YDB1_SCHPO isolog [Arabidopsis thaliana]

Seq. No.	272763
Contig ID	39933_1.R1011
5'-most EST	ymt700220551.h1

Seq. No.	272764
Contig ID	39938_1.R1011
5'-most EST	uC-zmflmo17220f02b1

Seq. No.	272765
Contig ID	39942_1.R1011
5'-most EST	uC-zmroB73014d03b1
Method	BLASTX
NCBI GI	g486849
BLAST score	338
E value	1.0e-31
Match length	86
% identity	83
NCBI Description	licheninase (EC 3.2.1.73) precursor - wheat >gi_311764_emb_CAA80493_ (Z22874) (1,3;1,4) beta glucanase [Triticum aestivum]

Seq. No.	272766
Contig ID	39951_1.R1011
5'-most EST	LIB3059-019-Q1-K1-D9
Method	BLASTX
NCBI GI	g2655098
BLAST score	187

E value	5.0e-14
Match length	97
% identity	42
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	272767
Contig ID	39966_1.R1011
5'-most EST	ceu700421953.h1

Seq. No.	272768
Contig ID	39972_1.R1011
5'-most EST	uC-zmflb73194h10b2
Method	BLASTN
NCBI GI	g1042264
BLAST score	83
E value	1.0e-38
Match length	102
% identity	97
NCBI Description	{Mu1 element insertion site, clone 14} [maize, Transposon, 200 nt]

Seq. No.	272769
Contig ID	39989_1.R1011
5'-most EST	LIB3180-059-P2-M1-C7
Method	BLASTX
NCBI GI	g2454184
BLAST score	378
E value	3.0e-36
Match length	89
% identity	81
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	272770
Contig ID	39997_1.R1011
5'-most EST	LIB3067-053-Q1-K1-B6
Method	BLASTX
NCBI GI	g4099092
BLAST score	580
E value	1.0e-59
Match length	172
% identity	61
NCBI Description	(U83179) unknown [Arabidopsis thaliana]

Seq. No.	272771
Contig ID	40010_1.R1011
5'-most EST	qmh700029694.f1

Seq. No.	272772
Contig ID	40012_1.R1011
5'-most EST	yyf700351639.h1
Method	BLASTX
NCBI GI	g1351947
BLAST score	160
E value	6.0e-11
Match length	96
% identity	36

NCBI Description	CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG (CLATHRIN COAT ASSOCIATED PROTEIN AP47 HOMOLOG) (GOLGI ADAPTOR AP-1 47 KD PROTEIN HOMOLOG) (HA1 47 KD SUBUNIT HOMOLOG) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MED... >gi_2133801_pir__I50530 clathrin-associated adaptor protein p47 - electric ray (Discopyge ommata) >gi_468275 (L07072) clathrin-associated adaptor protein [Discopyge ommata]

Seq. No.	272773
Contig ID	40021_1.R1011
5'-most EST	uC-zmflmo17154e09b1

Seq. No.	272774
Contig ID	40029_1.R1011
5'-most EST	uC-zmflmo17249b08a1
Method	BLASTX
NCBI GI	g629774
BLAST score	217
E value	2.0e-17
Match length	76
% identity	55
NCBI Description	beta-ketoacyl-ACP synthase - barley >gi_498742_emb_CAA84023_ (Z34269) beta-ketoacyl-ACP synthase [Hordeum vulgare]

Seq. No.	272775
Contig ID	40035_1.R1011
5'-most EST	uC-zmflmo17273d01b1
Method	BLASTX
NCBI GI	g2980789
BLAST score	144
E value	8.0e-09
Match length	32
% identity	69
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272776
Contig ID	40041_1.R1011
5'-most EST	wyr700240681.h1

Seq. No.	272777
Contig ID	40041_2.R1011
5'-most EST	uC-zmflmo17283c09b1
Method	BLASTX
NCBI GI	g4510373
BLAST score	173
E value	2.0e-12
Match length	129
% identity	32
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	272778
Contig ID	40050_1.R1011
5'-most EST	LIB3180-060-P2-M1-G1

Seq. No.	272779

Contig ID	40052_1.R1011
5'-most EST	xsy700212938.h1
Method	BLASTX
NCBI GI	g2498312
BLAST score	233
E value	3.0e-19
Match length	120
% identity	42
NCBI Description	PROBABLE DIHYDROPYRIMIDINE DEHYDROGENASE (NADP+) (DPD) (DIHYDROURACIL DEHYDROGENASE) (DIHYDROTHYMINE DEHYDROGENASE) >gi_1049458 (U39742) coded for by C. elegans cDNA yk28e9.3; coded for by C. elegans cDNA yk28e9.5; coded for by C. elegans cDNA yk28h9.3; coded for by C. elegans cDNA yk28h9.5; coded for by C. elegans cDNA yk40e4.5; coded for by C. elegans cDNA yk5h3.5;

Seq. No.	272780
Contig ID	40068_1.R1011
5'-most EST	LIB3180-061-P2-M1-A4
Method	BLASTX
NCBI GI	g4056480
BLAST score	261
E value	2.0e-22
Match length	113
% identity	46
NCBI Description	(AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	272781
Contig ID	40081_1.R1011
5'-most EST	ypc700798842.h1

Seq. No.	272782
Contig ID	40082_1.R1011
5'-most EST	uC-zmflmo17095g05b3

Seq. No.	272783
Contig ID	40088_1.R1011
5'-most EST	LIB3180-061-P2-M1-D12
Method	BLASTX
NCBI GI	g3738306
BLAST score	535
E value	8.0e-55
Match length	142
% identity	68
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	272784
Contig ID	40092_1.R1011
5'-most EST	LIB3180-061-P2-M1-D7

Seq. No.	272785
Contig ID	40095_1.R1011
5'-most EST	LIB3062-007-Q1-K1-F6
Method	BLASTX
NCBI GI	g80302
BLAST score	189
E value	1.0e-13

Match length	162
% identity	34
NCBI Description	hypothetical protein 1 - Bacillus subtilis (fragment) >gi_809662_emb_CAA29533_ (X06168) ORF 1 (178 AA) (1 is 2nd base in codon) [Bacillus subtilis]

Seq. No.	272786
Contig ID	40095_3.R1011
5'-most EST	LIB3180-061-P2-M1-E10

Seq. No.	272787
Contig ID	40095_4.R1011
5'-most EST	hbs701183277.h1

Seq. No.	272788
Contig ID	40104_1.R1011
5'-most EST	xyt700343362.h1
Method	BLASTX
NCBI GI	g2109293
BLAST score	237
E value	8.0e-20
Match length	99
% identity	53
NCBI Description	(U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	272789
Contig ID	40121_1.R1011
5'-most EST	uC-zmflb73224h10b1
Method	BLASTX
NCBI GI	g1143069
BLAST score	791
E value	2.0e-84
Match length	194
% identity	77
NCBI Description	(U30600) 3-ketoacyl carrier protein synthase III [Allium porrum]

Seq. No.	272790
Contig ID	40121_2.R1011
5'-most EST	LIB3180-061-P2-M1-H10
Method	BLASTX
NCBI GI	g1143069
BLAST score	725
E value	6.0e-77
Match length	179
% identity	76
NCBI Description	(U30600) 3-ketoacyl carrier protein synthase III [Allium porrum]

Seq. No.	272791
Contig ID	40121_3.R1011
5'-most EST	uC-zmflmo17224h10a1
Method	BLASTX
NCBI GI	g1143069
BLAST score	229
E value	1.0e-18

Match length	50
% identity	90
NCBI Description	(U30600) 3-ketoacyl carrier protein synthase III [Allium porrum]

Seq. No.	272792
Contig ID	40130_1.R1011
5'-most EST	uC-zmflb73028g10b1
Method	BLASTX
NCBI GI	g3367520
BLAST score	181
E value	3.0e-16
Match length	86
% identity	55
NCBI Description	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb_D12522 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	272793
Contig ID	40130_2.R1011
5'-most EST	xmt700265464.h1

Seq. No.	272794
Contig ID	40132_1.R1011
5'-most EST	LIB3180-062-P2-M1-A12
Method	BLASTX
NCBI GI	g3510253
BLAST score	314
E value	4.0e-29
Match length	108
% identity	56
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272795
Contig ID	40138_1.R1011
5'-most EST	LIB3180-062-P2-M1-B6

Seq. No.	272796
Contig ID	40144_1.R1011
5'-most EST	LIB189-018-Q1-E1-C6
Method	BLASTX
NCBI GI	g4099921
BLAST score	199
E value	3.0e-15
Match length	69
% identity	57
NCBI Description	(U91982) EREBP-3 homolog [Stylosanthes hamata]

Seq. No.	272797
Contig ID	40144_2.R1011
5'-most EST	LIB3066-025-Q1-K1-D10
Method	BLASTN
NCBI GI	g4099913
BLAST score	40
E value	4.0e-13
Match length	96
% identity	85

NCBI Description	Stylosanthes hamata ethylene-responsive element binding protein homolog gene, complete cds
Seq. No.	272798
Contig ID	40145_1.R1011
5'-most EST	wyr700239784.h1
Seq. No.	272799
Contig ID	40147_1.R1011
5'-most EST	LIB3137-014-Q1-K1-E7
Method	BLASTX
NCBI GI	g2341042
BLAST score	196
E value	2.0e-14
Match length	235
% identity	34
NCBI Description	(AC000104) F19P19.26 [Arabidopsis thaliana]
Seq. No.	272800
Contig ID	40152_1.R1011
5'-most EST	uC-zmflm017082e05b1
Method	BLASTX
NCBI GI	g3334150
BLAST score	1271
E value	1.0e-140
Match length	319
% identity	80
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase subunit (46 kD) [Glycine max]
Seq. No.	272801
Contig ID	40153_1.R1011
5'-most EST	LIB3180-062-P2-M1-D12
Seq. No.	272802
Contig ID	40164_1.R1011
5'-most EST	uC-zmflb73039c01b1
Method	BLASTX
NCBI GI	g3522943
BLAST score	263
E value	9.0e-23
Match length	107
% identity	49
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
Seq. No.	272803
Contig ID	40164_2.R1011
5'-most EST	LIB3180-062-P2-M1-E4
Method	BLASTX
NCBI GI	g3522943
BLAST score	1140
E value	1.0e-125
Match length	277
% identity	40

NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	272804
Contig ID	40171_1.R1011
5'-most EST	LIB3180-062-P2-M1-F2

Seq. No.	272805
Contig ID	40172_1.R1011
5'-most EST	LIB3068-042-Q1-K1-E4
Method	BLASTX
NCBI GI	g4567275
BLAST score	259
E value	2.0e-22
Match length	92
% identity	54
NCBI Description	(AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272806
Contig ID	40185_1.R1011
5'-most EST	LIB3180-062-P2-M1-G8
Method	BLASTX
NCBI GI	g4336436
BLAST score	862
E value	1.0e-92
Match length	271
% identity	61
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	272807
Contig ID	40187_1.R1011
5'-most EST	uC-zmroB73015e09b1

Seq. No.	272808
Contig ID	40202_1.R1011
5'-most EST	LIB3067-049-Q1-K1-H11
Method	BLASTX
NCBI GI	g2342685
BLAST score	183
E value	7.0e-16
Match length	121
% identity	47
NCBI Description	(AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No.	272809
Contig ID	40203_1.R1011
5'-most EST	LIB3181-001-P1-M1-B7

Seq. No.	272810
Contig ID	40217_2.R1011
5'-most EST	ntr700074938.h1

Seq. No.	272811
Contig ID	40226_1.R1011
5'-most EST	uC-zmflm017018d03b1
Method	BLASTX

NCBI GI	g3426043
BLAST score	1177
E value	1.0e-129
Match length	341
% identity	64
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	272812
Contig ID	40226_3.R1011
5'-most EST	uC-zmflb73126e06a1
Method	BLASTX
NCBI GI	g3426043
BLAST score	204
E value	6.0e-16
Match length	52
% identity	67
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	272813
Contig ID	40226_4.R1011
5'-most EST	uC-zmflb73083d04b2
Method	BLASTX
NCBI GI	g3426043
BLAST score	162
E value	5.0e-11
Match length	65
% identity	52
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	272814
Contig ID	40230_1.R1011
5'-most EST	LIB3069-005-Q1-K1-D12

Seq. No.	272815
Contig ID	40250_1.R1011
5'-most EST	uC-zmflMo17019g09b1

Seq. No.	272816
Contig ID	40250_2.R1011
5'-most EST	LIB3060-049-Q1-K1-H11
Method	BLASTX
NCBI GI	g3757527
BLAST score	466
E value	2.0e-46
Match length	104
% identity	78
NCBI Description	(AC005167) putative ribosomal protein L27 [Arabidopsis thaliana]

Seq. No.	272817
Contig ID	40250_3.R1011
5'-most EST	LIB36-008-Q1-E1-C3
Method	BLASTX
NCBI GI	g3757527
BLAST score	281
E value	8.0e-25
Match length	60

% identity	85
NCBI Description	(AC005167) putative ribosomal protein L27 [Arabidopsis thaliana]
Seq. No.	272818
Contig ID	40253_1.R1011
5'-most EST	uC-zmflmo17022a04b1
Method	BLASTX
NCBI GI	g4204294
BLAST score	704
E value	3.0e-74
Match length	192
% identity	74
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	272819
Contig ID	40256_1.R1011
5'-most EST	xjt700096042.h1
Seq. No.	272820
Contig ID	40258_1.R1011
5'-most EST	uC-zmflmo17011a02b1
Seq. No.	272821
Contig ID	40273_1.R1011
5'-most EST	LIB3181-003-P1-K2-D12
Method	BLASTX
NCBI GI	g2894572
BLAST score	296
E value	7.0e-53
Match length	138
% identity	76
NCBI Description	(AL021890) calcium-dependent protein kinase - like protein [Arabidopsis thaliana] >gi_2961339_emb_CAA18097.1_ (AL022140) calcium-dependent protein kinase - like protein [Arabidopsis thaliana]
Seq. No.	272822
Contig ID	40277_2.R1011
5'-most EST	LIB3067-009-Q1-K1-A4
Seq. No.	272823
Contig ID	40285_1.R1011
5'-most EST	LIB3181-003-P1-M1-H2
Method	BLASTN
NCBI GI	g507844
BLAST score	75
E value	6.0e-34
Match length	167
% identity	87
NCBI Description	Zea mays A188 retrotransposon gag gene, complete cds
Seq. No.	272824
Contig ID	40348_1.R1011
5'-most EST	LIB3181-004-P1-M1-C2
Method	BLASTX

NCBI GI	g4539422
BLAST score	489
E value	3.0e-49
Match length	147
% identity	64
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	272825
Contig ID	40351_1.R1011
5'-most EST	cat700016851.r1
Method	BLASTX
NCBI GI	g3702321
BLAST score	162
E value	4.0e-11
Match length	31
% identity	90
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No.	272826
Contig ID	40360_1.R1011
5'-most EST	uC-zmflmo17158g07a1
Method	BLASTX
NCBI GI	g4455754
BLAST score	152
E value	1.0e-09
Match length	108
% identity	35
NCBI Description	(AL035478) hypothetical protein SC2G5.30 [Streptomyces coelicolor]

Seq. No.	272827
Contig ID	40363_1.R1011
5'-most EST	mwy700440028.h1

Seq. No.	272828
Contig ID	40371_1.R1011
5'-most EST	ntr700072746.h1
Method	BLASTX
NCBI GI	g1871526
BLAST score	506
E value	2.0e-67
Match length	273
% identity	54
NCBI Description	(X81997) leucine-rich-repeat protein [Helianthus annuus]

Seq. No.	272829
Contig ID	40377_1.R1011
5'-most EST	LIB3181-006-P1-K2-F8

Seq. No.	272830
Contig ID	40382_1.R1011
5'-most EST	cyk700048344.f1

Seq. No.	272831
Contig ID	40384_1.R1011
5'-most EST	uC-zmflmo17219c04b1

Method	BLASTX
NCBI GI	g4454458
BLAST score	348
E value	1.0e-32
Match length	127
% identity	58
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	272832
Contig ID	40392_1.R1011
5'-most EST	LIB3181-007-P1-M1-E10
Method	BLASTX
NCBI GI	g2244831
BLAST score	251
E value	2.0e-30
Match length	148
% identity	54
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272833
Contig ID	40394_1.R1011
5'-most EST	LIB3181-007-P1-M1-D12

Seq. No.	272834
Contig ID	40397_1.R1011
5'-most EST	LIB3181-007-P1-K2-F6
Method	BLASTX
NCBI GI	g2618693
BLAST score	191
E value	2.0e-14
Match length	133
% identity	35
NCBI Description	(AC002510) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	272835
Contig ID	40399_1.R1011
5'-most EST	LIB3181-007-P1-M1-G1

Seq. No.	272836
Contig ID	40401_1.R1011
5'-most EST	xmt700256906.h1

Seq. No.	272837
Contig ID	40417_1.R1011
5'-most EST	LIB3181-007-P1-M1-B9

Seq. No.	272838
Contig ID	40445_1.R1011
5'-most EST	LIB3181-008-P1-K2-A10
Method	BLASTX
NCBI GI	g2245006
BLAST score	163
E value	4.0e-11
Match length	85
% identity	40
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272839
Contig ID	40450_1.R1011
5'-most EST	LIB3181-008-P1-K2-A6
Method	BLASTX
NCBI GI	g3600049
BLAST score	350
E value	4.0e-33
Match length	149
% identity	54
NCBI Description	(AF080120) similar to initiation factor IF2-beta (Pfam: GTP_EFTU.hmm, score: 226.67) [Arabidopsis thaliana]

Seq. No.	272840
Contig ID	40455_1.R1011
5'-most EST	xmt700266753.h1
Method	BLASTN
NCBI GI	g3046856
BLAST score	42
E value	9.0e-14
Match length	90
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	272841
Contig ID	40455_2.R1011
5'-most EST	LIB3136-010-Q1-K1-C3
Method	BLASTN
NCBI GI	g3046856
BLAST score	43
E value	1.0e-14
Match length	95
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	272842
Contig ID	40458_1.R1011
5'-most EST	LIB3067-028-Q1-K1-F9

Seq. No.	272843
Contig ID	40464_1.R1011
5'-most EST	LIB3069-044-Q1-K1-C2

Seq. No.	272844
Contig ID	40465_1.R1011
5'-most EST	LIB3181-008-P1-K2-D2

Seq. No.	272845
Contig ID	40468_1.R1011
5'-most EST	LIB3181-008-P1-K2-E4

Seq. No.	272846
Contig ID	40469_1.R1011
5'-most EST	uC-zmflmo17134c06a1

Seq. No.	272847
Contig ID	40471_1.R1011
5'-most EST	nbm700465509.h1
Method	BLASTX
NCBI GI	g166410
BLAST score	566
E value	3.0e-58
Match length	123
% identity	81
NCBI Description	(L07291) Alfin-1 [Medicago sativa]

Seq. No.	272848
Contig ID	40472_1.R1011
5'-most EST	LIB3181-008-P1-K2-F4
Method	BLASTX
NCBI GI	g4505829
BLAST score	156
E value	3.0e-10
Match length	130
% identity	33
NCBI Description	gene from NF2/meningioma region of 22q12 >gi_2135172_pir__I39463 gene anonymous protein - human >gi_388012 (L18972) anonymous [Homo sapiens]

Seq. No.	272849
Contig ID	40507_1.R1011
5'-most EST	uC-zmflb73018f10a1

Seq. No.	272850
Contig ID	40516_1.R1011
5'-most EST	xsy700211611.h1
Method	BLASTX
NCBI GI	g3687239
BLAST score	666
E value	8.0e-70
Match length	141
% identity	89
NCBI Description	(AC005169) putative clathrin coat assembly protein [Arabidopsis thaliana]

Seq. No.	272851
Contig ID	40522_1.R1011
5'-most EST	uC-zmflb73193d01b1
Method	BLASTX
NCBI GI	g2245131
BLAST score	425
E value	1.0e-41
Match length	138
% identity	67
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272852
Contig ID	40532_1.R1011
5'-most EST	uC-zmroteosinte120b07b2
Method	BLASTX
NCBI GI	g913227
BLAST score	316

E value	1.0e-28
Match length	148
% identity	49
NCBI Description	transcription factor XlDP-1 [Xenopus laevis, embryos, Peptide, 409 aa]

Seq. No.	272853
Contig ID	40533_1.R1011
5'-most EST	uC-zmflmo17334c02b1

Seq. No.	272854
Contig ID	40537_1.R1011
5'-most EST	LIB3181-010-P1-K2-B1

Seq. No.	272855
Contig ID	40543_1.R1011
5'-most EST	LIB3181-010-P1-M1-B9

Seq. No.	272856
Contig ID	40549_1.R1011
5'-most EST	LIB3181-010-P1-K2-D2
Method	BLASTX
NCBI GI	g1087073
BLAST score	549
E value	2.0e-56
Match length	144
% identity	70
NCBI Description	(S79243) calmodulin-binding heat-shock protein, CaMBP [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa] [Nicotiana tabacum]

Seq. No.	272857
Contig ID	40592_1.R1011
5'-most EST	uC-zmflmo17037e11a1

Seq. No.	272858
Contig ID	40618_1.R1011
5'-most EST	hvj7000620344.h1
Method	BLASTX
NCBI GI	g4567246
BLAST score	440
E value	2.0e-43
Match length	160
% identity	57
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	272859
Contig ID	40618_2.R1011
5'-most EST	uC-zmflb73017d04b1
Method	BLASTX
NCBI GI	g4567246
BLAST score	342
E value	4.0e-32
Match length	104
% identity	66
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	272860
Contig ID	40618_3.R1011
5'-most EST	xyt700345525.h1
Method	BLASTX
NCBI GI	g4567246
BLAST score	162
E value	2.0e-11
Match length	37
% identity	78
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	272861
Contig ID	40619_1.R1011
5'-most EST	pmx700083816.h1
Method	BLASTX
NCBI GI	g2651316
BLAST score	504
E value	7.0e-51
Match length	132
% identity	73
NCBI Description	(AC002336) unknown protein [Arabidopsis thaliana]

Seq. No.	272862
Contig ID	40619_2.R1011
5'-most EST	uC-zmflmo17054c06a1
Method	BLASTX
NCBI GI	g2651316
BLAST score	182
E value	2.0e-13
Match length	56
% identity	61
NCBI Description	(AC002336) unknown protein [Arabidopsis thaliana]

Seq. No.	272863
Contig ID	40623_1.R1011
5'-most EST	uC-zmflmo17097d05b1

Seq. No.	272864
Contig ID	40626_1.R1011
5'-most EST	LIB3067-055-Q1-K1-D12

Seq. No.	272865
Contig ID	40630_1.R1011
5'-most EST	LIB3181-013-P1-K2-C8

Seq. No.	272866
Contig ID	40635_1.R1011
5'-most EST	qmh700028205.f1
Method	BLASTX
NCBI GI	g2832623
BLAST score	453
E value	4.0e-45
Match length	166
% identity	55
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	272867
Contig ID	40652_1.R1011
5'-most EST	uC-zmflb73274h06b1

Seq. No.	272868
Contig ID	40657_1.R1011
5'-most EST	LIB3181-014-P1-K2-B5
Method	BLASTX
NCBI GI	g542176
BLAST score	289
E value	1.0e-25
Match length	114
% identity	56
NCBI Description	probable finger protein WZF1 - wheat >gi_485814_dbj_BAA03901_ (D16415) WZF1 [Triticum aestivum] >gi_485816_dbj_BAA03902_ (D16416) WZF1 [Triticum aestivum]

Seq. No.	272869
Contig ID	40668_1.R1011
5'-most EST	LIB3181-014-P1-M1-E1
Method	BLASTX
NCBI GI	g2673917
BLAST score	262
E value	7.0e-23
Match length	82
% identity	65
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	272870
Contig ID	40674_1.R1011
5'-most EST	LIB3181-014-P1-K2-E8
Method	BLASTX
NCBI GI	g121472
BLAST score	220
E value	6.0e-18
Match length	102
% identity	48
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No.	272871
Contig ID	40675_1.R1011
5'-most EST	LIB3181-014-P1-M1-E9

Seq. No.	272872
Contig ID	40681_1.R1011
5'-most EST	tfd700574177.h1
Method	BLASTX
NCBI GI	g416657
BLAST score	484
E value	2.0e-48
Match length	151

% identity	58
NCBI Description	ANTI-SILENCING PROTEIN 1 >gi_320638_pir__S30766 ASF1 protein - yeast (Saccharomyces cerevisiae) >gi_171091 (L07593) ASF1 [Saccharomyces cerevisiae] >gi_1008304_emb_CAA89410_ (Z49390) ORF YJL115w [Saccharomyces cerevisiae]
Seq. No.	272873
Contig ID	40682_1.R1011
5'-most EST	LIB3181-014-P1-M1-G10
Method	BLASTX
NCBI GI	g1175611
BLAST score	298
E value	5.0e-27
Match length	136
% identity	49
NCBI Description	HYPOTHETICAL PROTEIN HI1590 >gi_1074851_pir__F64172 hypothetical protein HI1590 - Haemophilus influenzae (strain Rd KW20) >gi_1574435 (U32833) conserved hypothetical protein [Haemophilus influenzae Rd]
Seq. No.	272874
Contig ID	40749_1.R1011
5'-most EST	xdb700341642.h1
Seq. No.	272875
Contig ID	40755_1.R1011
5'-most EST	uC-zmflmo17180h08b1
Method	BLASTX
NCBI GI	g2772516
BLAST score	168
E value	1.0e-11
Match length	63
% identity	52
NCBI Description	(U44979) kinesin-related protein 2 [Rattus norvegicus]
Seq. No.	272876
Contig ID	40756_1.R1011
5'-most EST	LIB3060-047-Q1-K1-D1
Seq. No.	272877
Contig ID	40782_1.R1011
5'-most EST	LIB84-010-Q1-E1-G3
Seq. No.	272878
Contig ID	40789_1.R1011
5'-most EST	uC-zmflmo17293e09b1
Seq. No.	272879
Contig ID	40796_1.R1011
5'-most EST	xsy700217044.h1
Method	BLASTX
NCBI GI	g2801538
BLAST score	538
E value	1.0e-54
Match length	206
% identity	54

NCBI Description	(AF039532) harpin induced gene 1 homolog [Oryza sativa]

Seq. No.	272880
Contig ID	40804_1.R1011
5'-most EST	ypc700799256.h1

Seq. No.	272881
Contig ID	40808_1.R1011
5'-most EST	xjt700094652.h1
Method	BLASTX
NCBI GI	g3894197
BLAST score	812
E value	7.0e-87
Match length	184
% identity	79
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272882
Contig ID	40812_1.R1011
5'-most EST	uC-zmflmo17030f02b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	272883
Contig ID	40812_2.R1011
5'-most EST	wty700169575.h1
Method	BLASTX
NCBI GI	g2117624
BLAST score	156
E value	3.0e-10
Match length	56
% identity	55
NCBI Description	peroxidase (EC 1.11.1.7) 2 - alfalfa >gi_971564_emb_CAA62228_ (X90695) peroxidase2 [Medicago sativa]

Seq. No.	272884
Contig ID	40824_1.R1011
5'-most EST	LIB83-002-Q1-E1-B3

Seq. No.	272885
Contig ID	40831_1.R1011
5'-most EST	jfc700968601.h1
Method	BLASTX
NCBI GI	g3182886
BLAST score	273
E value	1.0e-23
Match length	135
% identity	44
NCBI Description	ACTIN 1 >gi_2653412_emb_CAA74015_ (Y13664) actin [Saccoglossus kowalevskii]

Seq. No.	272886
Contig ID	40831_2.R1011
5'-most EST	LIB3137-013-Q1-K1-E12

Seq. No.	272887
Contig ID	40847_1.R1011
5'-most EST	nwy700445930.h1

Seq. No.	272888
Contig ID	40848_1.R1011
5'-most EST	uC-zmflmo17015f10b1
Method	BLASTX
NCBI GI	g2462822
BLAST score	668
E value	1.0e-69
Match length	394
% identity	37
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272889
Contig ID	40866_1.R1011
5'-most EST	LIB3182-005-P2-M1-G10
Method	BLASTX
NCBI GI	g1055162
BLAST score	357
E value	2.0e-33
Match length	313
% identity	32
NCBI Description	(U40029) coded for by C. elegans cDNA yk16b1.3; coded for by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA yk8g6.3; coded for by C. elegans cDNA yk6d3.5; coded for by C. elegans cDNA yk6d3.3; coded for by C. elegans cDNA yk7e12.5; co

Seq. No.	272890
Contig ID	40871_1.R1011
5'-most EST	tfd700570708.h1

Seq. No.	272891
Contig ID	40904_1.R1011
5'-most EST	LIB143-006-Q1-E1-H11

Seq. No.	272892
Contig ID	40925_1.R1011
5'-most EST	LIB3060-023-Q1-K1-B6
Method	BLASTX
NCBI GI	g2105137
BLAST score	706
E value	8.0e-75
Match length	155
% identity	85
NCBI Description	(U66876) ADP-glucose pyrophosphorylase large subunit [Hordeum vulgare]

Seq. No.	272893
Contig ID	40943_1.R1011
5'-most EST	xsy700217696.h1

Seq. No.	272894
Contig ID	40945_1.R1011
5'-most EST	pmx700089534.h1

Seq. No.	272895
Contig ID	40954_1.R1011
5'-most EST	uC-zmflb73175h06a2

Seq. No.	272896
Contig ID	40955_1.R1011
5'-most EST	LIB3117-012-Q1-K1-C12

Seq. No.	272897
Contig ID	40960_1.R1011
5'-most EST	xmt700267490.h1

Seq. No.	272898
Contig ID	40961_1.R1011
5'-most EST	nbm700464633.h1
Method	BLASTX
NCBI GI	g4512667
BLAST score	617
E value	1.0e-63
Match length	299
% identity	49
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	272899
Contig ID	40969_1.R1011
5'-most EST	nbm700474251.h1
Method	BLASTX
NCBI GI	g3702338
BLAST score	451
E value	1.0e-44
Match length	147
% identity	56
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	272900
Contig ID	40981_1.R1011
5'-most EST	LIB3182-012-P2-M1-A6

Seq. No.	272901
Contig ID	40995_1.R1011
5'-most EST	LIB189-022-Q1-E1-G8
Method	BLASTX
NCBI GI	g1076758
BLAST score	469
E value	5.0e-47
Match length	101
% identity	84
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir__S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]

Seq. No.	272902
Contig ID	41015_1.R1011
5'-most EST	zuv700356860.h1
Method	BLASTX
NCBI GI	g2245064
BLAST score	234
E value	2.0e-19
Match length	67
% identity	57
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272903
Contig ID	41028_1.R1011
5'-most EST	pmx700091290.h1

Seq. No.	272904
Contig ID	41047_1.R1011
5'-most EST	gct701172175.h1
Method	BLASTX
NCBI GI	g3451078
BLAST score	170
E value	5.0e-12
Match length	99
% identity	33
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	272905
Contig ID	41048_1.R1011
5'-most EST	LIB3136-007-Q1-K1-C4

Seq. No.	272906
Contig ID	41062_1.R1011
5'-most EST	uC-zmflb73193g03b1
Method	BLASTX
NCBI GI	g4432841
BLAST score	487
E value	6.0e-49
Match length	167
% identity	57
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272907
Contig ID	41062_3.R1011
5'-most EST	fwa700099553.h1
Method	BLASTX
NCBI GI	g4432841
BLAST score	169
E value	3.0e-12
Match length	82
% identity	48
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272908
Contig ID	41074_1.R1011
5'-most EST	LIB3182-016-P2-M1-B4
Method	BLASTX
NCBI GI	g1350680

BLAST score	490
E value	1.0e-49
Match length	114
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	272909
Contig ID	41077_1.R1011
5'-most EST	LIB3117-004-Q1-K1-E1

Seq. No.	272910
Contig ID	41078_1.R1011
5'-most EST	fC-zmle700446705a3
Method	BLASTX
NCBI GI	g439434
BLAST score	531
E value	1.0e-53
Match length	337
% identity	37
NCBI Description	(L25941) integral nuclear envelope inner membrane protein [Homo sapiens]

Seq. No.	272911
Contig ID	41097_1.R1011
5'-most EST	LIB3059-007-Q1-K1-A12

Seq. No.	272912
Contig ID	41100_1.R1011
5'-most EST	uC-zmflmo17185c06b1

Seq. No.	272913
Contig ID	41103_1.R1011
5'-most EST	uC-zmflmo17303d11b1
Method	BLASTX
NCBI GI	g4469019
BLAST score	287
E value	2.0e-25
Match length	105
% identity	58
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	272914
Contig ID	41121_1.R1011
5'-most EST	LIB3279-003-P1-K1-A7

Seq. No.	272915
Contig ID	41123_1.R1011
5'-most EST	LIB3279-003-P1-K1-B1

Seq. No.	272916
Contig ID	41123_2.R1011
5'-most EST	xyt700344285.h1
Method	BLASTX
NCBI GI	g2827699
BLAST score	240
E value	3.0e-20
Match length	130

% identity	44
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	272917
Contig ID	41129_1.R1011
5'-most EST	LIB3069-035-Q1-K1-F5
Seq. No.	272918
Contig ID	41140_1.R1011
5'-most EST	LIB3279-004-P1-K1-D6
Method	BLASTX
NCBI GI	g1050918
BLAST score	212
E value	1.0e-16
Match length	94
% identity	45
NCBI Description	(X92648) lipid transfer protein [Helianthus annuus]
Seq. No.	272919
Contig ID	41149_1.R1011
5'-most EST	ntr700072937.h1
Seq. No.	272920
Contig ID	41150_1.R1011
5'-most EST	yyf700350740.h1
Method	BLASTX
NCBI GI	g1053045
BLAST score	149
E value	2.0e-09
Match length	93
% identity	45
NCBI Description	(U38424) histone H3 [Glycine max]
Seq. No.	272921
Contig ID	41151_1.R1011
5'-most EST	LIB3061-011-Q1-K1-E11
Method	BLASTX
NCBI GI	g470340
BLAST score	364
E value	4.0e-39
Match length	196
% identity	45
NCBI Description	(U00043) similar to beta-mannosyltransferase [Caenorhabditis elegans]
Seq. No.	272922
Contig ID	41154_1.R1011
5'-most EST	uC-zmflmo17052h06a1
Seq. No.	272923
Contig ID	41156_1.R1011
5'-most EST	LIB3279-003-P1-K1-D8
Seq. No.	272924
Contig ID	41158_1.R1011
5'-most EST	wyr700239831.h1
Method	BLASTX

NCBI GI	g4314358
BLAST score	473
E value	7.0e-48
Match length	314
% identity	41
NCBI Description	(AC006340) putative kinesin heavy chain protein [Arabidopsis thaliana]

Seq. No.	272925
Contig ID	41167_1.R1011
5'-most EST	LIB3279-003-P1-K1-E7

Seq. No.	272926
Contig ID	41171_1.R1011
5'-most EST	LIB36-016-Q2-E2-E2
Method	BLASTX
NCBI GI	g2245001
BLAST score	443
E value	6.0e-44
Match length	101
% identity	82
NCBI Description	(Z97341) similarity to NADH dehydrogenase (ubiquinone) [Arabidopsis thaliana]

Seq. No.	272927
Contig ID	41177_1.R1011
5'-most EST	ypc700800789.h1

Seq. No.	272928
Contig ID	41179_1.R1011
5'-most EST	yyf700351522.h1
Method	BLASTX
NCBI GI	g1652609
BLAST score	163
E value	1.0e-11
Match length	180
% identity	32
NCBI Description	(D90906) 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase [Synechocystis sp.]

Seq. No.	272929
Contig ID	41182_1.R1011
5'-most EST	LIB3279-003-P1-K1-G11
Method	BLASTN
NCBI GI	g2944039
BLAST score	328
E value	0.0e+00
Match length	496
% identity	99
NCBI Description	Zea mays indeterminate spikelet 1 (ids1) mRNA, complete cds

Seq. No.	272930
Contig ID	41184_1.R1011
5'-most EST	LIB3279-003-P1-K1-G3

Seq. No.	272931
Contig ID	41191_1.R1011

5'-most EST	LIB3067-032-Q1-K1-F4
Seq. No.	272932
Contig ID	41223_1.R1011
5'-most EST	vux700157224.h1
Method	BLASTX
NCBI GI	g3355474
BLAST score	959
E value	1.0e-104
Match length	217
% identity	82
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.	272933
Contig ID	41244_1.R1011
5'-most EST	LIB143-039-Q1-E1-B6
Method	BLASTX
NCBI GI	g2909583
BLAST score	447
E value	3.0e-44
Match length	200
% identity	48
NCBI Description	(AL021926) oxcA [Mycobacterium tuberculosis]
Seq. No.	272934
Contig ID	41248_1.R1011
5'-most EST	uC-zmflmo17310b07a1
Method	BLASTX
NCBI GI	g2344889
BLAST score	355
E value	3.0e-33
Match length	124
% identity	50
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.	272935
Contig ID	41251_1.R1011
5'-most EST	uC-zmflb73169a07b2
Seq. No.	272936
Contig ID	41252_1.R1011
5'-most EST	ymt700220579.h1
Method	BLASTX
NCBI GI	g1346763
BLAST score	1428
E value	1.0e-159
Match length	316
% identity	80
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 >gi_1084363_pir__S46282 phosphoprotein phosphatase 1 - Alfalfa >gi_575672_emb_CAA56766_ (X80788) potentially catalitic subunit of the ser /thr protein phosphatase 1 [Medicago sativa subsp. X varia]
Seq. No.	272937
Contig ID	41256_1.R1011
5'-most EST	LIB3279-017-P1-K1-F7

Seq. No.	272938
Contig ID	41256_2.R1011
5'-most EST	fdz701161306.h1

Seq. No.	272939
Contig ID	41260_1.R1011
5'-most EST	pmx700081812.h1
Method	BLASTX
NCBI GI	g2959781
BLAST score	441
E value	3.0e-48
Match length	131
% identity	73
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	272940
Contig ID	41264_1.R1011
5'-most EST	uC-zmflb73265g06b4
Method	BLASTX
NCBI GI	g130582
BLAST score	358
E value	8.0e-40
Match length	144
% identity	55
NCBI Description	RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94 [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] >gi_100342_pir__S04273 hypothetical protein - common tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana tabacum]

Seq. No.	272941
Contig ID	41270_1.R1011
5'-most EST	LIB3279-004-P1-K1-H10
Method	BLASTN
NCBI GI	g22212
BLAST score	98
E value	1.0e-47
Match length	257
% identity	64
NCBI Description	Z.mays DNA for c1 locus

Seq. No.	272942
Contig ID	41282_1.R1011
5'-most EST	tfd700574050.h1

Seq. No.	272943
Contig ID	41286_1.R1011
5'-most EST	xjt700093776.h1
Method	BLASTX
NCBI GI	g3618214
BLAST score	216
E value	6.0e-17
Match length	189
% identity	34
NCBI Description	(AL031579) dihydrofolate reductase [Schizosaccharomyces pombe]

Seq. No.	272944
Contig ID	41286_3.R1011
5'-most EST	LIB3062-034-Q1-K1-F8
Seq. No.	272945
Contig ID	41290_1.R1011
5'-most EST	uC-zmflb73076h12b2
Method	BLASTX
NCBI GI	g4218002
BLAST score	451
E value	4.0e-44
Match length	456
% identity	32
NCBI Description	(AC006135) putative UTP-glucose glucosyltransferase [Arabidopsis thaliana]
Seq. No.	272946
Contig ID	41290_2.R1011
5'-most EST	uC-zmflb73274b06b1
Seq. No.	272947
Contig ID	41290_3.R1011
5'-most EST	uC-zmflmo17129b01a1
Seq. No.	272948
Contig ID	41291_1.R1011
5'-most EST	LIB3279-054-P1-K1-E10
Seq. No.	272949
Contig ID	41292_1.R1011
5'-most EST	LIB3279-006-P1-K1-A8
Seq. No.	272950
Contig ID	41293_1.R1011
5'-most EST	LIB3066-017-Q1-K1-H3
Seq. No.	272951
Contig ID	41299_1.R1011
5'-most EST	xmt700260384.h1
Method	BLASTX
NCBI GI	g4503293
BLAST score	341
E value	2.0e-31
Match length	233
% identity	33
NCBI Description	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 >gi_3913445_sp_O60231_DDXX_HUMAN PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (ATP-DEPENDENT RNA HELICASE #3) (KIAA0577) >gi_3107913_dbj_BAA25908_ (AB001601) ATP-dependent RNA helicase #3 [Homo sapiens]
Seq. No.	272952
Contig ID	41301_1.R1011
5'-most EST	uC-zmflb73003d08a1
Seq. No.	272953

Contig ID	41308_1.R1011
5'-most EST	vux700157343.h1
Method	BLASTX
NCBI GI	g2443329
BLAST score	368
E value	7.0e-35
Match length	104
% identity	65
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	272954
Contig ID	41309_1.R1011
5'-most EST	LIB3279-005-P1-K1-D1
Method	BLASTX
NCBI GI	g3264611
BLAST score	450
E value	2.0e-44
Match length	96
% identity	85
NCBI Description	(AF061511) seven in absentia homolog [Zea mays]

Seq. No.	272955
Contig ID	41310_1.R1011
5'-most EST	pwf700321707.h1
Method	BLASTX
NCBI GI	g2104446
BLAST score	263
E value	3.0e-22
Match length	300
% identity	24
NCBI Description	(Z95396) WD-repeat protein [Schizosaccharomyces pombe]

Seq. No.	272956
Contig ID	41322_1.R1011
5'-most EST	LIB3279-005-P1-K1-E10

Seq. No.	272957
Contig ID	41325_1.R1011
5'-most EST	LIB3279-005-P1-K1-E2
Method	BLASTX
NCBI GI	g2253010
BLAST score	744
E value	3.0e-79
Match length	167
% identity	81
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	272958
Contig ID	41326_1.R1011
5'-most EST	xsy700213009.h1
Method	BLASTX
NCBI GI	g3212863
BLAST score	902
E value	2.0e-97
Match length	235
% identity	75

NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	272959
Contig ID	41327_1.R1011
5'-most EST	LIB3279-005-P1-K1-E4

Seq. No.	272960
Contig ID	41329_2.R1011
5'-most EST	LIB3059-015-Q1-K1-C5

Seq. No.	272961
Contig ID	41332_1.R1011
5'-most EST	hbs701181442.h1

Seq. No.	272962
Contig ID	41335_1.R1011
5'-most EST	wty700172749.h1
Method	BLASTX
NCBI GI	g2160167
BLAST score	647
E value	1.0e-67
Match length	219
% identity	67
NCBI Description	(AC000132) Identical to A. thaliana Myb-like protein (gb_D58424). [Arabidopsis thaliana]

Seq. No.	272963
Contig ID	41355_1.R1011
5'-most EST	LIB3279-005-P1-K1-H11
Method	BLASTX
NCBI GI	g3953458
BLAST score	391
E value	1.0e-37
Match length	171
% identity	50
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	272964
Contig ID	41355_2.R1011
5'-most EST	xjt700092371.h1
Method	BLASTX
NCBI GI	g3953458
BLAST score	232
E value	4.0e-19
Match length	69
% identity	64
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	272965
Contig ID	41356_1.R1011
5'-most EST	LIB3279-005-P1-K1-H2

Seq. No.	272966
Contig ID	41363_1.R1011
5'-most EST	vqh700053184.r1
Method	BLASTX

NCBI GI	g1351989
BLAST score	1537
E value	0.0e+00
Match length	558
% identity	75
NCBI Description	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_984262_emb_CAA58052_ (X82849) asparragine synthetase [Zea mays]

Seq. No.	272967
Contig ID	41363_3.R1011
5'-most EST	ntr700077337.h1
Method	BLASTX
NCBI GI	g1351983
BLAST score	198
E value	8.0e-25
Match length	78
% identity	74
NCBI Description	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) 1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 1) >gi_2147131_pir__S57931 asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - Lotus japonicus >gi_2147133_pir__S69182 asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) 1 - Lotus japonicus >gi_897771_emb_CAA61589_ (X89409) asparagine synthase (glutamine-hydrolysing) [Lotus japonicus]

Seq. No.	272968
Contig ID	41363_4.R1011
5'-most EST	tzu700204290.h1
Method	BLASTX
NCBI GI	g1351989
BLAST score	200
E value	5.0e-26
Match length	69
% identity	93
NCBI Description	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_984262_emb_CAA58052_ (X82849) asparragine synthetase [Zea mays]

Seq. No.	272969
Contig ID	41366_1.R1011
5'-most EST	uC-zmflb73299c10b1
Method	BLASTX
NCBI GI	g3128169
BLAST score	194
E value	1.0e-14
Match length	72
% identity	51
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272970
Contig ID	41375_1.R1011
5'-most EST	LIB3279-006-P1-K1-B4

Seq. No.	272971
Contig ID	41385_1.R1011
5'-most EST	yyf700352039.h1
Method	BLASTX
NCBI GI	g1742883
BLAST score	154
E value	4.0e-10
Match length	115
% identity	34
NCBI Description	(D90820) 2-dehydro-3-deoxygluconokinase (EC 2.7.1.45) (2-keto-3- Deoxygluconokinase) (3-deoxy-2-oxo-d-gluconate kinase) (Kdg kinase). [Escherichia coli] >gi_1742891_dbj_BAA15570_ (D90821) 2-dehydro-3-deoxygluconokinase (EC 2.7.1.45) (2-keto-3-Deoxygluconokinase) (3-deoxy-2-oxo-d-gluconate kinase) (Kdg kinase). [Escherichia coli] >gi_1788071 (AE000272) putative kinase [Escherichia coli]

Seq. No.	272972
Contig ID	41390_1.R1011
5'-most EST	xjt700096085.h1

Seq. No.	272973
Contig ID	41391_1.R1011
5'-most EST	rvl700456337.h1

Seq. No.	272974
Contig ID	41396_1.R1011
5'-most EST	pmx700089058.h1
Method	BLASTX
NCBI GI	g4220489
BLAST score	511
E value	1.0e-51
Match length	238
% identity	35
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272975
Contig ID	41401_1.R1011
5'-most EST	LIB3279-006-P1-K1-D9

Seq. No.	272976
Contig ID	41404_1.R1011
5'-most EST	LIB3279-006-P1-K1-E12

Seq. No.	272977
Contig ID	41412_1.R1011
5'-most EST	wen700332682.h1
Method	BLASTX
NCBI GI	g586021
BLAST score	155
E value	3.0e-10
Match length	64
% identity	44
NCBI Description	PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION PROTEIN C) >gi_2127242_pir__S66083 stage V sporulation protein - Bacillus subtilis >gi_467442_dbj_BAA05288_

(D26185) stage V sporulation [Bacillus subtilis] >gi_2632320_emb_CAB11829_ (Z99104) thermosensitive mutant blocks spore coat formation (stage V sporulation) [Bacillus subtilis]

Seq. No.	272978
Contig ID	41415_1.R1011
5'-most EST	LIB3279-006-P1-K1-F11

Seq. No.	272979
Contig ID	41420_1.R1011
5'-most EST	LIB3279-006-P1-K1-F6
Method	BLASTX
NCBI GI	g2108252
BLAST score	1017
E value	1.0e-111
Match length	297
% identity	35
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	272980
Contig ID	41424_1.R1011
5'-most EST	LIB3279-006-P1-K1-G1
Method	BLASTX
NCBI GI	g3738327
BLAST score	214
E value	2.0e-17
Match length	85
% identity	47
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	272981
Contig ID	41429_1.R1011
5'-most EST	LIB3279-006-P1-K1-H10

Seq. No.	272982
Contig ID	41432_1.R1011
5'-most EST	zuv700353248.h1

Seq. No.	272983
Contig ID	41432_2.R1011
5'-most EST	clt700043639.f1

Seq. No.	272984
Contig ID	41436_1.R1011
5'-most EST	LIB3279-006-P1-K1-H6

Seq. No.	272985
Contig ID	41436_2.R1011
5'-most EST	uC-zmflb73222b08a1

Seq. No.	272986
Contig ID	41447_1.R1011

5'-most EST	uC-zmroteosinte008d10b1
Method	BLASTX
NCBI GI	g4506043
BLAST score	1126
E value	1.0e-123
Match length	326
% identity	62
NCBI Description	prolyl endopeptidase >gi_1346769_sp_P48147_PPCE_HUMAN PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase [Homo sapiens]

Seq. No.	272987
Contig ID	41453_1.R1011
5'-most EST	LIB3136-005-Q1-K1-A6
Method	BLASTX
NCBI GI	g2980778
BLAST score	145
E value	5.0e-09
Match length	69
% identity	41
NCBI Description	(AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No.	272988
Contig ID	41458_1.R1011
5'-most EST	uC-zmroteosinte008f12b1
Method	BLASTX
NCBI GI	g3201477
BLAST score	618
E value	7.0e-64
Match length	352
% identity	43
NCBI Description	(AJ006021) putative PRL1 associated protein [Arabidopsis thaliana]

Seq. No.	272989
Contig ID	41459_1.R1011
5'-most EST	ymt700224048.h1
Method	BLASTX
NCBI GI	g4503527
BLAST score	163
E value	5.0e-11
Match length	116
% identity	40
NCBI Description	UNKNOWN >gi_1778051 (U62583) Prt1 homolog [Homo sapiens]

Seq. No.	272990
Contig ID	41461_1.R1011
5'-most EST	LIB3279-007-P1-K1-C3
Method	BLASTX
NCBI GI	g4314378
BLAST score	210
E value	1.0e-16
Match length	84
% identity	52
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	272991
Contig ID	41462_1.R1011
5'-most EST	LIB3279-054-P1-K1-A11

Seq. No.	272992
Contig ID	41463_1.R1011
5'-most EST	uer700581684.h1

Seq. No.	272993
Contig ID	41463_2.R1011
5'-most EST	pmx700083062.h1

Seq. No.	272994
Contig ID	41465_1.R1011
5'-most EST	uC-zmflmo17070b03a1

Seq. No.	272995
Contig ID	41470_1.R1011
5'-most EST	LIB3279-007-P1-K1-D12
Method	BLASTX
NCBI GI	g3297819
BLAST score	554
E value	1.0e-56
Match length	165
% identity	66
NCBI Description	(AL031032) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	272996
Contig ID	41479_1.R1011
5'-most EST	uC-zmroteosinte063f04b1
Method	BLASTX
NCBI GI	g3193330
BLAST score	465
E value	4.0e-46
Match length	218
% identity	51
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	272997
Contig ID	41481_1.R1011
5'-most EST	LIB3062-028-Q1-K1-F1

Seq. No.	272998
Contig ID	41486_1.R1011
5'-most EST	uC-zmflb73116d10b2
Method	BLASTX
NCBI GI	g1076486
BLAST score	394
E value	2.0e-60
Match length	229
% identity	55
NCBI Description	cim1 protein - soybean >gi_555616 (U03860) cytokinin induced message [Glycine max]

Seq. No.	272999
Contig ID	41487_1.R1011
5'-most EST	uC-zmflmo17268a04b1

Seq. No.	273000
Contig ID	41488_1.R1011
5'-most EST	uC-zmflb73160g06b2
Method	BLASTX
NCBI GI	g4100433
BLAST score	318
E value	3.0e-29
Match length	151
% identity	46
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	273001
Contig ID	41498_1.R1011
5'-most EST	uC-zmflmo17117e12b1
Method	BLASTX
NCBI GI	g3935148
BLAST score	923
E value	1.0e-100
Match length	208
% identity	80
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	273002
Contig ID	41498_2.R1011
5'-most EST	uC-zmflmo17316a08a1
Method	BLASTN
NCBI GI	g22176
BLAST score	53
E value	6.0e-21
Match length	85
% identity	45
NCBI Description	Z.mays P gene

Seq. No.	273003
Contig ID	41500_1.R1011
5'-most EST	LIB3279-007-P1-K1-G10

Seq. No.	273004
Contig ID	41505_1.R1011
5'-most EST	LIB3279-007-P1-K1-G5

Seq. No.	273005
Contig ID	41506_1.R1011
5'-most EST	LIB3279-007-P1-K1-G6
Method	BLASTX
NCBI GI	g3059131
BLAST score	259
E value	3.0e-22
Match length	98
% identity	48
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No. 273006

Contig ID	41510_1.R1011
5'-most EST	uC-zmflb73303b02b1
Seq. No.	273007
Contig ID	41511_1.R1011
5'-most EST	LIB3279-007-P1-K1-H10
Method	BLASTX
NCBI GI	g3201477
BLAST score	202
E value	2.0e-15
Match length	134
% identity	32
NCBI Description	(AJ006021) putative PRL1 associated protein [Arabidopsis thaliana]
Seq. No.	273008
Contig ID	41524_1.R1011
5'-most EST	LIB3279-008-P1-K1-A3
Seq. No.	273009
Contig ID	41526_1.R1011
5'-most EST	LIB3279-053-P1-K1-A8
Seq. No.	273010
Contig ID	41532_1.R1011
5'-most EST	cjh700194691.h1
Method	BLASTX
NCBI GI	g3880399
BLAST score	170
E value	6.0e-12
Match length	76
% identity	43
NCBI Description	(Z71267) predicted using Genefinder; cDNA EST yk275h2.3 comes from this gene; cDNA EST yk309g11.3 comes from this gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST yk275h2.5 comes from this gene [Caenorhabditis elegans]
Seq. No.	273011
Contig ID	41535_1.R1011
5'-most EST	LIB143-044-Q1-E1-C6
Method	BLASTX
NCBI GI	g3170570
BLAST score	174
E value	4.0e-12
Match length	148
% identity	30
NCBI Description	(AF058302) FrnE [Streptomyces roseofulvus]
Seq. No.	273012
Contig ID	41535_2.R1011
5'-most EST	rvt700551055.h1
Seq. No.	273013
Contig ID	41535_3.R1011
5'-most EST	uC-zmflmo17259f09b1
Seq. No.	273014

Contig ID	41536_1.R1011
5'-most EST	LIB3279-010-P1-K1-D7
Method	BLASTX
NCBI GI	g3695379
BLAST score	370
E value	3.0e-35
Match length	107
% identity	67
NCBI Description	(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana]

Seq. No.	273015
Contig ID	41536_2.R1011
5'-most EST	xyt700344516.h1
Method	BLASTX
NCBI GI	g3695379
BLAST score	198
E value	1.0e-23
Match length	69
% identity	79
NCBI Description	(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana]

Seq. No.	273016
Contig ID	41542_1.R1011
5'-most EST	LIB3279-008-P1-K1-C10
Method	BLASTX
NCBI GI	g2911072
BLAST score	197
E value	4.0e-15
Match length	88
% identity	45
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	273017
Contig ID	41550_1.R1011
5'-most EST	LIB3279-008-P1-K1-C9

Seq. No.	273018
Contig ID	41551_1.R1011
5'-most EST	LIB3279-008-P1-K1-D1
Method	BLASTX
NCBI GI	g4538911
BLAST score	348
E value	1.0e-32
Match length	126
% identity	55
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273019
Contig ID	41579_1.R1011
5'-most EST	LIB3279-008-P1-K1-F4
Method	BLASTX

NCBI GI	g4510400
BLAST score	580
E value	7.0e-60
Match length	127
% identity	81
NCBI Description	(AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis thaliana]

Seq. No.	273020
Contig ID	41583_1.R1011
5'-most EST	LIB3136-035-Q1-K1-C10
Method	BLASTX
NCBI GI	g2262143
BLAST score	478
E value	1.0e-47
Match length	160
% identity	59
NCBI Description	(AC002330) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	273021
Contig ID	41591_1.R1011
5'-most EST	LIB3279-008-P1-K1-G4
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	273022
Contig ID	41600_1.R1011
5'-most EST	uC-zmflb73200e07b1

Seq. No.	273023
Contig ID	41602_1.R1011
5'-most EST	uC-zmflmo17035f06b1
Method	BLASTX
NCBI GI	g3264767
BLAST score	250
E value	9.0e-21
Match length	66
% identity	70
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	273024
Contig ID	41606_1.R1011
5'-most EST	uC-zmflb73162a10b2

Seq. No.	273025
Contig ID	41610_1.R1011
5'-most EST	uC-zmroteosinte047a11b1
Method	BLASTX
NCBI GI	g4006866
BLAST score	218
E value	1.0e-17

Match length 78
% identity 58
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 273026
Contig ID 41628_1.R1011
5'-most EST LIB3060-002-Q1-K2-H10
Method BLASTX
NCBI GI g3298538
BLAST score 422
E value 2.0e-41
Match length 129
% identity 58
NCBI Description (AC004681) hypothetical protein [Arabidopsis thaliana]

Seq. No. 273027
Contig ID 41628_2.R1011
5'-most EST xsy700211293.h1

Seq. No. 273028
Contig ID 41629_1.R1011
5'-most EST hbs701180856.h1
Method BLASTX
NCBI GI g3249071
BLAST score 371
E value 1.0e-35
Match length 140
% identity 50
NCBI Description (AC004473) Contains similarity to protein-tyrosine phosphatase gb_L15420 from Dictyostelium discoideum. EST gb_N38718 comes from this g [Arabidopsis thaliana]

Seq. No. 273029
Contig ID 41630_1.R1011
5'-most EST uC-zmflb73161g03b2
Method BLASTX
NCBI GI g642134
BLAST score 1431
E value 1.0e-159
Match length 352
% identity 74
NCBI Description (D45355) protein kinase [Arabidopsis thaliana] >gi_3063704_emb_CAA18595.1_ (AL022537) protein kinase AME3 [Arabidopsis thaliana]

Seq. No. 273030
Contig ID 41636_1.R1011
5'-most EST LIB3279-009-P1-K1-H11

Seq. No. 273031
Contig ID 41638_1.R1011
5'-most EST LIB3060-049-Q1-K1-G7
Method BLASTX
NCBI GI g1699023
BLAST score 223
E value 6.0e-18
Match length 167

% identity	34
NCBI Description	(U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi_1699051 (U78867) putative aspartate-arginine-rich mRNA binding protein [Arabidopsis thaliana]

Seq. No.	273032
Contig ID	41638_2.R1011
5'-most EST	uC-zmflb73100e03b1
Method	BLASTX
NCBI GI	g1699023
BLAST score	188
E value	5.0e-14
Match length	99
% identity	43
NCBI Description	(U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi_1699051 (U78867) putative aspartate-arginine-rich mRNA binding protein [Arabidopsis thaliana]

Seq. No.	273033
Contig ID	41654_1.R1011
5'-most EST	xsy700208165.h1
Method	BLASTX
NCBI GI	g3928519
BLAST score	574
E value	3.0e-59
Match length	137
% identity	80
NCBI Description	(AB011670) wpk4 protein kinase [Triticum aestivum]

Seq. No.	273034
Contig ID	41657_1.R1011
5'-most EST	wty700165172.h1
Method	BLASTX
NCBI GI	g2244749
BLAST score	1436
E value	1.0e-160
Match length	345
% identity	78
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	273035
Contig ID	41658_1.R1011
5'-most EST	uwc700155449.h1
Method	BLASTX
NCBI GI	g4249385
BLAST score	676
E value	6.0e-71
Match length	207
% identity	63
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	273036
Contig ID	41669_1.R1011
5'-most EST	cyk700047484.f1

Seq. No.	273037
Contig ID	41687_1.R1011
5'-most EST	LIB3279-010-P1-K1-A2
Method	BLASTX
NCBI GI	g2224699
BLAST score	148
E value	3.0e-09
Match length	81
% identity	42
NCBI Description	(AB002377) KIAA0379 [Homo sapiens]

Seq. No.	273038
Contig ID	41689_1.R1011
5'-most EST	LIB3279-010-P1-K1-A6
Method	BLASTX
NCBI GI	g3334659
BLAST score	263
E value	1.0e-22
Match length	106
% identity	56
NCBI Description	(Y10489) putative cytochrome P450 [Glycine max]

Seq. No.	273039
Contig ID	41699_1.R1011
5'-most EST	fdz701165634.h1
Method	BLASTX
NCBI GI	g3695392
BLAST score	427
E value	1.0e-41
Match length	198
% identity	45
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	273040
Contig ID	41700_1.R1011
5'-most EST	ymt700220284.h1

Seq. No.	273041
Contig ID	41727_2.R1011
5'-most EST	LIB3060-008-Q1-K1-G2

Seq. No.	273042
Contig ID	41729_1.R1011
5'-most EST	LIB3279-010-P1-K1-E2

Seq. No.	273043
Contig ID	41730_1.R1011
5'-most EST	LIB3069-035-Q1-K1-B8
Method	BLASTX
NCBI GI	g1766046
BLAST score	527
E value	7.0e-54
Match length	106
% identity	95
NCBI Description	(U81993) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	273044
Contig ID	41739_1.R1011
5'-most EST	LIB3279-010-P1-K1-G12
Method	BLASTX
NCBI GI	g1136432
BLAST score	167
E value	1.0e-11
Match length	81
% identity	47
NCBI Description	(D80008) KIAA0186 [Homo sapiens]

Seq. No.	273045
Contig ID	41745_1.R1011
5'-most EST	uC-zmroteosinte032h03b1
Method	BLASTX
NCBI GI	g2384758
BLAST score	856
E value	5.0e-92
Match length	182
% identity	88
NCBI Description	(AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No.	273046
Contig ID	41754_1.R1011
5'-most EST	LIB3279-010-P1-K1-G6

Seq. No.	273047
Contig ID	41761_1.R1011
5'-most EST	uC-zmflmo17046a09b1
Method	BLASTX
NCBI GI	g2213626
BLAST score	306
E value	9.0e-28
Match length	123
% identity	51
NCBI Description	(AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No.	273048
Contig ID	41761_2.R1011
5'-most EST	xjt700092377.h1

Seq. No.	273049
Contig ID	41763_1.R1011
5'-most EST	LIB3279-010-P1-K1-H4
Method	BLASTX
NCBI GI	g4038035
BLAST score	285
E value	2.0e-25
Match length	91
% identity	62
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	273050
Contig ID	41765_1.R1011
5'-most EST	LIB3279-010-P1-K1-H6

Seq. No.	273051
Contig ID	41766_1.R1011
5'-most EST	uC-zmflb73030g07b1

Seq. No.	273052
Contig ID	41767_1.R1011
5'-most EST	LIB3279-010-P1-K1-H8
Method	BLASTN
NCBI GI	g4416300
BLAST score	35
E value	4.0e-10
Match length	59
% identity	90
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	273053
Contig ID	41769_1.R1011
5'-most EST	xsy700207458.h1

Seq. No.	273054
Contig ID	41769_2.R1011
5'-most EST	uC-zmflmo17078d05b1

Seq. No.	273055
Contig ID	41786_1.R1011
5'-most EST	bdu700382748.h1

Seq. No.	273056
Contig ID	41792_1.R1011
5'-most EST	LIB3279-011-P1-K1-C10
Method	BLASTX
NCBI GI	g3023527
BLAST score	188
E value	3.0e-14
Match length	68
% identity	50
NCBI Description	PUTATIVE UBIQUINONE BIOSYNTHESIS MONOOXGENASE COQ6 >gi_2088820 (AF003384) strong similarity to the E. coli VISC protein (SP:P25535) [Caenorhabditis elegans]

Seq. No.	273057
Contig ID	41793_1.R1011
5'-most EST	LIB83-002-Q1-E1-B6
Method	BLASTX
NCBI GI	g320130
BLAST score	922
E value	1.0e-100
Match length	179
% identity	98
NCBI Description	acetolactate synthase (EC 4.1.3.18) (clone pSOG109) - maize >gi_22141_emb_CAA45117_ (X63554) acetohydroxyacid synthase [Zea mays]

Seq. No.	273058
Contig ID	41793_2.R1011

5'-most EST	uC-zmflmo17009f11a1
Method	BLASTX
NCBI GI	g100849
BLAST score	226
E value	1.0e-18
Match length	42
% identity	100
NCBI Description	acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize >gi_22139_emb_CAA45116_ (X63553) acetohydroxyacid synthase [Zea mays]

Seq. No.	273059
Contig ID	41799_1.R1011
5'-most EST	cyk700048560.f1
Method	BLASTX
NCBI GI	g3152558
BLAST score	428
E value	4.0e-42
Match length	120
% identity	66
NCBI Description	(AC002986) Similar to M. tuberculosis gene gb_Z96072 and M. leprae gene gb_400019. [Arabidopsis thaliana]

Seq. No.	273060
Contig ID	41807_1.R1011
5'-most EST	LIB3279-011-P1-K1-D5

Seq. No.	273061
Contig ID	41819_1.R1011
5'-most EST	uC-zmflb73275g06b1
Method	BLASTX
NCBI GI	g4455201
BLAST score	453
E value	3.0e-55
Match length	161
% identity	76
NCBI Description	(AL035440) grpE like protein [Arabidopsis thaliana]

Seq. No.	273062
Contig ID	41827_1.R1011
5'-most EST	uC-zmflb73136c07b1
Method	BLASTX
NCBI GI	g3885342
BLAST score	564
E value	7.0e-58
Match length	254
% identity	45
NCBI Description	(AC005623) putative DNA polymerase [Arabidopsis thaliana]

Seq. No.	273063
Contig ID	41834_1.R1011
5'-most EST	hvj700618732.h1

Seq. No.	273064
Contig ID	41835_1.R1011
5'-most EST	zla700380722.h1

Seq. No.	273065
Contig ID	41843_1.R1011
5'-most EST	uC-zmflmo17290g05a1

Seq. No.	273066
Contig ID	41845_1.R1011
5'-most EST	uC-zmroteosinte115a11b1
Method	BLASTX
NCBI GI	g4263795
BLAST score	600
E value	5.0e-62
Match length	245
% identity	46
NCBI Description	(AC006068) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	273067
Contig ID	41858_1.R1011
5'-most EST	LIB3279-012-P1-K1-A11

Seq. No.	273068
Contig ID	41861_1.R1011
5'-most EST	LIB3279-012-P1-K1-A3

Seq. No.	273069
Contig ID	41862_1.R1011
5'-most EST	LIB3136-033-Q1-K1-A11
Method	BLASTX
NCBI GI	g3461835
BLAST score	807
E value	1.0e-86
Match length	178
% identity	82
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No.	273070
Contig ID	41864_1.R1011
5'-most EST	uC-zmflmo17153f09a1
Method	BLASTX
NCBI GI	g3183454
BLAST score	403
E value	7.0e-39
Match length	165
% identity	50
NCBI Description	HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION >gi_2632217_emb_CAA10859_ (AJ222587) YkwC protein [Bacillus subtilis] >gi_2633767_emb_CAB13269_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No.	273071
Contig ID	41868_1.R1011
5'-most EST	yyf700351502.h1
Method	BLASTX
NCBI GI	g3522961
BLAST score	1403

E value	1.0e-156
Match length	359
% identity	76
NCBI Description	(AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No.	273072
Contig ID	41868_2.R1011
5'-most EST	fC-zmf1700552649f3
Method	BLASTX
NCBI GI	g3522961
BLAST score	286
E value	1.0e-25
Match length	71
% identity	77
NCBI Description	(AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No.	273073
Contig ID	41868_3.R1011
5'-most EST	xsy700207945.h1

Seq. No.	273074
Contig ID	41868_4.R1011
5'-most EST	wyr700240526.h1

Seq. No.	273075
Contig ID	41868_5.R1011
5'-most EST	wyr700236605.h1
Method	BLASTX
NCBI GI	g1586940
BLAST score	199
E value	4.0e-27
Match length	91
% identity	71
NCBI Description	Ser/Thr kinase [Lycopersicon esculentum]

Seq. No.	273076
Contig ID	41872_1.R1011
5'-most EST	xjt700096095.h1

Seq. No.	273077
Contig ID	41886_1.R1011
5'-most EST	LIB3279-012-P1-K1-C5
Method	BLASTX
NCBI GI	g2149640
BLAST score	488
E value	4.0e-49
Match length	174
% identity	57
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	273078
Contig ID	41889_1.R1011
5'-most EST	uwc700152672.h1
Method	BLASTX
NCBI GI	g3860797
BLAST score	219
E value	2.0e-17

Match length	100
% identity	42
NCBI Description	(AJ235271) 30S RIBOSOMAL PROTEIN S9 (rpsI) [Rickettsia prowazekii]

Seq. No.	273079
Contig ID	41896_1.R1011
5'-most EST	wyr700240179.h1
Method	BLASTX
NCBI GI	g3757520
BLAST score	170
E value	5.0e-12
Match length	57
% identity	58
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	273080
Contig ID	41905_1.R1011
5'-most EST	LIB3279-012-P1-K1-E2
Method	BLASTX
NCBI GI	g4455338
BLAST score	671
E value	1.0e-70
Match length	189
% identity	65
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	273081
Contig ID	41911_1.R1011
5'-most EST	LIB3279-012-P1-K1-F1
Method	BLASTX
NCBI GI	g2832625
BLAST score	263
E value	5.0e-23
Match length	88
% identity	50
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	273082
Contig ID	41936_1.R1011
5'-most EST	LIB3279-012-P1-K1-H3

Seq. No.	273083
Contig ID	41941_1.R1011
5'-most EST	LIB3279-012-P1-K1-H8

Seq. No.	273084
Contig ID	41943_1.R1011
5'-most EST	dhd700198085.h1
Method	BLASTX
NCBI GI	g4204315
BLAST score	167
E value	3.0e-12
Match length	70
% identity	49
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	273085
Contig ID	41961_1.R1011
5'-most EST	uC-zmflmo17097b11b1
Method	BLASTX
NCBI GI	g3449282
BLAST score	765
E value	2.0e-81
Match length	190
% identity	77
NCBI Description	(AB006139) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Arabidopsis thaliana] >gi_3449284_dbj_BAA32457_ (AB008929) N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase [Arabidopsis thaliana] >gi_4510353_gb_AAD21442.1_ (AC006921) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Arabidopsis thaliana]

Seq. No.	273086
Contig ID	41961_2.R1011
5'-most EST	LIB3136-022-Q1-K1-A4
Method	BLASTX
NCBI GI	g3449282
BLAST score	298
E value	6.0e-27
Match length	70
% identity	81
NCBI Description	(AB006139) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Arabidopsis thaliana] >gi_3449284_dbj_BAA32457_ (AB008929) N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase [Arabidopsis thaliana] >gi_4510353_gb_AAD21442.1_ (AC006921) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Arabidopsis thaliana]

Seq. No.	273087
Contig ID	41961_3.R1011
5'-most EST	uC-zmflb73163f11b2

Seq. No.	273088
Contig ID	41968_1.R1011
5'-most EST	xjt700094159.h1
Method	BLASTX
NCBI GI	g2961384
BLAST score	314
E value	1.0e-47
Match length	154
% identity	62
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	273089
Contig ID	41969_1.R1011
5'-most EST	LIB3137-012-Q1-K1-G11
Method	BLASTX
NCBI GI	g4585976

BLAST score	875
E value	6.0e-94
Match length	316
% identity	55
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	273090
Contig ID	41976_1.R1011
5'-most EST	LIB3060-018-Q1-K1-C4
Method	BLASTX
NCBI GI	g4455358
BLAST score	233
E value	4.0e-19
Match length	72
% identity	61
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	273091
Contig ID	41984_1.R1011
5'-most EST	LIB3279-013-P1-K1-E12
Method	BLASTX
NCBI GI	g3859597
BLAST score	227
E value	2.0e-18
Match length	93
% identity	48
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana]

Seq. No.	273092
Contig ID	41985_1.R1011
5'-most EST	cyk700049574.f1
Method	BLASTX
NCBI GI	g4193320
BLAST score	859
E value	1.0e-92
Match length	161
% identity	99
NCBI Description	(AF045473) histone deacetylase [Zea mays]

Seq. No.	273093
Contig ID	41990_1.R1011
5'-most EST	uC-zmroteosinte093b01b2
Method	BLASTX
NCBI GI	g1079393
BLAST score	341
E value	1.0e-31
Match length	237
% identity	32
NCBI Description	chromokinesin - chicken >gi_603761 (U18309) chromokinesin [Gallus gallus]

Seq. No.	273094
Contig ID	41995_1.R1011
5'-most EST	LIB3279-013-P1-K1-F2

Seq. No.	273095
Contig ID	42000_1.R1011

5'-most EST	LIB3279-013-P1-K1-F9
Method	BLASTX
NCBI GI	g3970652
BLAST score	578
E value	7.0e-62
Match length	186
% identity	65
NCBI Description	(X77499) amino acid permease [Arabidopsis thaliana]

Seq. No.	273096
Contig ID	42004_1.R1011
5'-most EST	xyt700346374.h1
Method	BLASTX
NCBI GI	g469801
BLAST score	336
E value	6.0e-31
Match length	260
% identity	37
NCBI Description	(Z31725) predicted trithorax protein [Drosophila melanogaster] >gi_1052594_emb_CAA90514_ (Z50152) trithorax protein trxI [Drosophila melanogaster]

Seq. No.	273097
Contig ID	42008_1.R1011
5'-most EST	LIB3279-013-P1-K1-G5

Seq. No.	273098
Contig ID	42009_1.R1011
5'-most EST	LIB3279-013-P1-K1-G6

Seq. No.	273099
Contig ID	42013_1.R1011
5'-most EST	nbm700473367.h1
Method	BLASTX
NCBI GI	g2982458
BLAST score	926
E value	1.0e-100
Match length	263
% identity	71
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	273100
Contig ID	42013_2.R1011
5'-most EST	uC-zmflmo17286d08b1
Method	BLASTX
NCBI GI	g2982458
BLAST score	193
E value	1.0e-14
Match length	98
% identity	62
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	273101
Contig ID	42022_1.R1011
5'-most EST	vvh700281914.h2

Seq. No.	273102

Contig ID	42023_1.R1011
5'-most EST	uC-zmf1B73002b04b1
Method	BLASTX
NCBI GI	g3738334
BLAST score	259
E value	3.0e-22
Match length	119
% identity	45
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	273103
Contig ID	42037_1.R1011
5'-most EST	LIB3279-014-P1-K1-B8

Seq. No.	273104
Contig ID	42039_1.R1011
5'-most EST	pmx700091970.h1

Seq. No.	273105
Contig ID	42052_1.R1011
5'-most EST	xsy700209582.h1

Seq. No.	273106
Contig ID	42052_2.R1011
5'-most EST	wyr700237532.h1

Seq. No.	273107
Contig ID	42052_3.R1011
5'-most EST	dyk700105738.h1

Seq. No.	273108
Contig ID	42052_5.R1011
5'-most EST	nbm700465065.h1

Seq. No.	273109
Contig ID	42055_1.R1011
5'-most EST	LIB3279-014-P1-K1-E1
Method	BLASTX
NCBI GI	g4235228
BLAST score	266
E value	2.0e-41
Match length	248
% identity	43
NCBI Description	(AF061026) leucine zipper-EF-hand containing transmembrane protein 1 [Mus musculus]

Seq. No.	273110
Contig ID	42057_1.R1011
5'-most EST	uC-zmf1b73239g02a1

Seq. No.	273111
Contig ID	42058_1.R1011
5'-most EST	uC-zmroteosinte094b11b2
Method	BLASTX
NCBI GI	g1723515
BLAST score	190
E value	4.0e-14

Match length	149
% identity	28
NCBI Description	HYPOTHETICAL PROTEIN C22E12.01 IN CHROMOSOME I >gi_1220276_emb_CAA93888_ (Z70043) unknown [Schizosaccharomyces pombe]

Seq. No.	273112
Contig ID	42059_1.R1011
5'-most EST	xmt700262237.h1
Method	BLASTX
NCBI GI	g4103635
BLAST score	295
E value	4.0e-26
Match length	131
% identity	44
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	273113
Contig ID	42060_1.R1011
5'-most EST	rvt700551930.h1
Method	BLASTX
NCBI GI	g2586157
BLAST score	458
E value	9.0e-46
Match length	124
% identity	76
NCBI Description	(AF002220) kinesin-like calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	273114
Contig ID	42063_1.R1011
5'-most EST	uC-zmflmo17055e06b1

Seq. No.	273115
Contig ID	42077_1.R1011
5'-most EST	LIB84-006-Q1-E1-F11
Method	BLASTX
NCBI GI	g2565436
BLAST score	671
E value	1.0e-70
Match length	146
% identity	88
NCBI Description	(AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No.	273116
Contig ID	42078_1.R1011
5'-most EST	cyk700051079.f1
Method	BLASTX
NCBI GI	g2146739
BLAST score	520
E value	6.0e-53
Match length	156
% identity	65
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No. 273117

Contig ID	42082_1.R1011
5'-most EST	uC-zmflmo17262e06b1
Seq. No.	273118
Contig ID	42082_2.R1011
5'-most EST	fwa700099353.h1
Seq. No.	273119
Contig ID	42084_1.R1011
5'-most EST	LIB3279-015-P1-K1-A11
Method	BLASTX
NCBI GI	g2190419
BLAST score	548
E value	3.0e-56
Match length	146
% identity	74
NCBI Description	(Y13632) dem [Lycopersicon esculentum]
Seq. No.	273120
Contig ID	42107_1.R1011
5'-most EST	LIB3279-015-P1-K1-C2
Seq. No.	273121
Contig ID	42112_1.R1011
5'-most EST	hbs701180907.h1
Method	BLASTX
NCBI GI	g4432846
BLAST score	394
E value	9.0e-38
Match length	225
% identity	48
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.	273122
Contig ID	42113_1.R1011
5'-most EST	nbm700477925.h1
Method	BLASTX
NCBI GI	g4006861
BLAST score	374
E value	1.0e-35
Match length	210
% identity	40
NCBI Description	(Z99707) tubulin-like protein [Arabidopsis thaliana]
Seq. No.	273123
Contig ID	42116_1.R1011
5'-most EST	LIB3137-004-Q1-K1-G7
Method	BLASTX
NCBI GI	g4416302
BLAST score	1265
E value	1.0e-140
Match length	253
% identity	96
NCBI Description	(AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.	273124
Contig ID	42121_1.R1011

5'-most EST	pmx700085850.h1
Seq. No.	273125
Contig ID	42122_1.R1011
5'-most EST	nbm700476884.h1
Method	BLASTX
NCBI GI	g3805842
BLAST score	294
E value	2.0e-26
Match length	158
% identity	46
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	273126
Contig ID	42132_1.R1011
5'-most EST	gct701176539.h1
Seq. No.	273127
Contig ID	42132_2.R1011
5'-most EST	LIB3067-054-Q1-K1-H6
Method	BLASTX
NCBI GI	g4469023
BLAST score	1201
E value	1.0e-132
Match length	312
% identity	74
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	273128
Contig ID	42140_1.R1011
5'-most EST	LIB3066-016-Q1-K1-E3
Seq. No.	273129
Contig ID	42140_2.R1011
5'-most EST	uC-zmflb73057h07b1
Method	BLASTX
NCBI GI	g2760324
BLAST score	348
E value	2.0e-32
Match length	144
% identity	51
NCBI Description	(AC002130) F1N21.9 [Arabidopsis thaliana]
Seq. No.	273130
Contig ID	42142_1.R1011
5'-most EST	LIB3279-015-P1-K1-F2
Method	BLASTX
NCBI GI	g3021512
BLAST score	170
E value	8.0e-12
Match length	62
% identity	56
NCBI Description	(X96728) isocitrate dehydrogenase (NADP+) [Nicotiana tabacum]
Seq. No.	273131
Contig ID	42142_2.R1011

5'-most EST	LIB3070-014-Q1-N1-G7
Seq. No.	273132
Contig ID	42143_1.R1011
5'-most EST	LIB3279-015-P1-K1-F3
Method	BLASTX
NCBI GI	g4589686
BLAST score	261
E value	2.0e-22
Match length	146
% identity	40
NCBI Description	(AB023235) KIAA1018 protein [Homo sapiens]
Seq. No.	273133
Contig ID	42155_1.R1011
5'-most EST	LIB3279-015-P1-K1-G4
Seq. No.	273134
Contig ID	42155_3.R1011
5'-most EST	LIB3137-021-Q1-K1-B8
Seq. No.	273135
Contig ID	42169_1.R1011
5'-most EST	LIB36-014-Q1-E1-C1
Seq. No.	273136
Contig ID	42179_1.R1011
5'-most EST	LIB3060-043-Q1-K1-D10
Method	BLASTX
NCBI GI	g629561
BLAST score	561
E value	2.0e-57
Match length	265
% identity	45
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]
Seq. No.	273137
Contig ID	42181_1.R1011
5'-most EST	xmt700258941.h1
Method	BLASTX
NCBI GI	g1931640
BLAST score	231
E value	4.0e-19
Match length	97
% identity	46
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]
Seq. No.	273138
Contig ID	42184_1.R1011
5'-most EST	pmx700090780.h1
Method	BLASTX
NCBI GI	g1931641
BLAST score	364
E value	4.0e-34

Match length	163
% identity	52
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]

Seq. No.	273139
Contig ID	42184_2.R1011
5'-most EST	wty700167067.h1
Method	BLASTX
NCBI GI	g1931641
BLAST score	198
E value	1.0e-15
Match length	65
% identity	63
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]

Seq. No.	273140
Contig ID	42191_1.R1011
5'-most EST	LIB3279-016-P1-K1-B6

Seq. No.	273141
Contig ID	42192_1.R1011
5'-most EST	LIB3279-016-P1-K1-B7
Method	BLASTX
NCBI GI	g4038592
BLAST score	186
E value	2.0e-13
Match length	149
% identity	35
NCBI Description	(Y10403) RNA-directed RNA polymerase [Lycopersicon esculentum]

Seq. No.	273142
Contig ID	42193_1.R1011
5'-most EST	LIB3137-020-Q1-K1-H2

Seq. No.	273143
Contig ID	42196_1.R1011
5'-most EST	LIB3279-016-P1-K1-C10

Seq. No.	273144
Contig ID	42204_1.R1011
5'-most EST	LIB3279-016-P1-K1-C7

Seq. No.	273145
Contig ID	42210_1.R1011
5'-most EST	LIB3066-055-Q1-K1-G10
Method	BLASTX
NCBI GI	g2864608
BLAST score	504
E value	7.0e-51
Match length	181
% identity	60
NCBI Description	(AL021811) ferredoxin--NADP+ reductase - like protein [Arabidopsis thaliana] >gi_4049338_emb_CAA22563_ (AL034567) ferredoxin-NADP+ reductase-like protein [Arabidopsis thaliana]

Seq. No.	273146
Contig ID	42210_2.R1011
5'-most EST	uC-zmflb73039b07b1
Method	BLASTX
NCBI GI	g2864608
BLAST score	484
E value	2.0e-63
Match length	235
% identity	58
NCBI Description	(AL021811) ferredoxin--NADP+ reductase - like protein [Arabidopsis thaliana] >gi_4049338_emb_CAA22563_ (AL034567) ferredoxin-NADP+ reductase-like protein [Arabidopsis thaliana]

Seq. No.	273147
Contig ID	42212_1.R1011
5'-most EST	uC-zmflb73097g08b1

Seq. No.	273148
Contig ID	42214_1.R1011
5'-most EST	LIB3067-043-Q1-K1-G9

Seq. No.	273149
Contig ID	42214_3.R1011
5'-most EST	pmx700090585.h1
Method	BLASTX
NCBI GI	g3659692
BLAST score	212
E value	1.0e-16
Match length	199
% identity	31
NCBI Description	(AF068748) sphingosine kinase [Mus musculus]

Seq. No.	273150
Contig ID	42214_4.R1011
5'-most EST	fwa700098331.h1
Method	BLASTN
NCBI GI	g3702728
BLAST score	35
E value	5.0e-10
Match length	83
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	273151
Contig ID	42216_1.R1011
5'-most EST	uwc700155301.h1
Method	BLASTX
NCBI GI	g2829889
BLAST score	164
E value	2.0e-11
Match length	48
% identity	58
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	273152

Contig ID	42222_1.R1011
5'-most EST	LIB3279-016-P1-K1-E3

Seq. No.	273153
Contig ID	42225_1.R1011
5'-most EST	LIB3279-016-P1-K1-G6
Method	BLASTX
NCBI GI	g4539394
BLAST score	209
E value	3.0e-16
Match length	168
% identity	11
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	273154
Contig ID	42240_1.R1011
5'-most EST	LIB3069-042-Q1-K1-D4
Method	BLASTX
NCBI GI	g2501491
BLAST score	194
E value	1.0e-14
Match length	192
% identity	34
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 1) >gi_542014_pir__S41950 UTP-glucose glucosyltransferase - cassava >gi_453246_emb_CAA54609_ (X77459) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No.	273155
Contig ID	42243_1.R1011
5'-most EST	nbm700471464.h1
Method	BLASTX
NCBI GI	g4097587
BLAST score	412
E value	7.0e-40
Match length	115
% identity	67
NCBI Description	(U64926) NTGP5 [Nicotiana tabacum]

Seq. No.	273156
Contig ID	42243_2.R1011
5'-most EST	LIB3279-016-P1-K1-G11
Method	BLASTX
NCBI GI	g4097587
BLAST score	152
E value	7.0e-10
Match length	43
% identity	63
NCBI Description	(U64926) NTGP5 [Nicotiana tabacum]

Seq. No.	273157
Contig ID	42244_1.R1011
5'-most EST	mwy700438190.h1
Method	BLASTX
NCBI GI	g2191151
BLAST score	522

E value	6.0e-53
Match length	194
% identity	58
NCBI Description	(AF007269) contains similarity to membrane associated salt-inducible protein [Arabidopsis thaliana]

Seq. No.	273158
Contig ID	42257_1.R1011
5'-most EST	LIB3279-016-P1-K1-H3
Method	BLASTX
NCBI GI	g2367431
BLAST score	370
E value	2.0e-35
Match length	130
% identity	52
NCBI Description	(AF000403) putative cytochrome P450 [Lotus japonicus]

Seq. No.	273159
Contig ID	42272_1.R1011
5'-most EST	uer700583346.h1
Method	BLASTX
NCBI GI	g2864616
BLAST score	273
E value	8.0e-24
Match length	68
% identity	74
NCBI Description	(AL021811) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273160
Contig ID	42272_2.R1011
5'-most EST	uC-zmrob73039g06a1

Seq. No.	273161
Contig ID	42281_1.R1011
5'-most EST	LIB3279-017-P1-K1-B7

Seq. No.	273162
Contig ID	42287_1.R1011
5'-most EST	LIB3279-017-P1-K1-C11

Seq. No.	273163
Contig ID	42290_1.R1011
5'-most EST	LIB3279-017-P1-K1-C3

Seq. No.	273164
Contig ID	42292_1.R1011
5'-most EST	LIB3279-017-P1-K1-C5

Seq. No.	273165
Contig ID	42302_1.R1011
5'-most EST	uC-zmflm017214c11b1
Method	BLASTX
NCBI GI	g3080398
BLAST score	288
E value	1.0e-25
Match length	164
% identity	33

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 273166
Contig ID 42314_1.R1011
5'-most EST LIB36-004-Q1-E1-D3
Method BLASTX
NCBI GI g3885340
BLAST score 737
E value 6.0e-78
Match length 277
% identity 56
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 273167
Contig ID 42322_1.R1011
5'-most EST uC-zmflb73195h03b1
Method BLASTX
NCBI GI g2425111
BLAST score 152
E value 2.0e-09
Match length 322
% identity 22
NCBI Description (AF019980) ZipA [Dictyostelium discoideum]

Seq. No. 273168
Contig ID 42332_1.R1011
5'-most EST xyt700346717.h1

Seq. No. 273169
Contig ID 42338_1.R1011
5'-most EST nbm700471889.h1

Seq. No. 273170
Contig ID 42340_1.R1011
5'-most EST uC-zmflb73356b08a2
Method BLASTX
NCBI GI g3832528
BLAST score 226
E value 6.0e-18
Match length 398
% identity 25
NCBI Description (AF100167) unknown [Glycine max]

Seq. No. 273171
Contig ID 42342_1.R1011
5'-most EST ymt700218990.h1
Method BLASTX
NCBI GI g3004565
BLAST score 438
E value 3.0e-43
Match length 131
% identity 63
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 273172
Contig ID 42346_1.R1011
5'-most EST uC-zmroteosinte045g06b2

Seq. No.	273173
Contig ID	42350_1.R1011
5'-most EST	LIB3279-018-P1-K1-A11

Seq. No.	273174
Contig ID	42353_1.R1011
5'-most EST	xsy700217259.h1
Method	BLASTX
NCBI GI	g4586049
BLAST score	610
E value	3.0e-63
Match length	251
% identity	44
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273175
Contig ID	42354_1.R1011
5'-most EST	uC-zmflmo17294g11b1
Method	BLASTX
NCBI GI	g1076316
BLAST score	189
E value	5.0e-14
Match length	80
% identity	44
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	273176
Contig ID	42356_1.R1011
5'-most EST	nbm700466916.h1

Seq. No.	273177
Contig ID	42365_1.R1011
5'-most EST	pmx700084089.h1
Method	BLASTX
NCBI GI	g4539383
BLAST score	591
E value	1.0e-60
Match length	368
% identity	36
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	273178
Contig ID	42373_1.R1011
5'-most EST	LIB3279-018-P1-K1-C12
Method	BLASTX
NCBI GI	g4455210
BLAST score	339
E value	7.0e-32
Match length	75
% identity	85
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	273179
Contig ID	42375_1.R1011
5'-most EST	LIB3279-018-P1-K1-C3
Method	BLASTX
NCBI GI	g2827080
BLAST score	363
E value	9.0e-35
Match length	103
% identity	75
NCBI Description	(AF020271) malate dehydrogenase precursor [Medicago sativa]

Seq. No.	273180
Contig ID	42376_1.R1011
5'-most EST	LIB3279-018-P1-K1-C4
Method	BLASTN
NCBI GI	g3046856
BLAST score	47
E value	6.0e-17
Match length	165
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	273181
Contig ID	42382_1.R1011
5'-most EST	LIB3279-018-P1-K1-D1
Method	BLASTX
NCBI GI	g4185499
BLAST score	194
E value	4.0e-15
Match length	85
% identity	41
NCBI Description	(AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.	273182
Contig ID	42384_1.R1011
5'-most EST	LIB143-030-Q1-E1-A6
Method	BLASTN
NCBI GI	g2274989
BLAST score	64
E value	2.0e-27
Match length	139
% identity	87
NCBI Description	Hordeum vulgare mRNA for expressed sequence tag

Seq. No.	273183
Contig ID	42385_1.R1011
5'-most EST	LIB3279-018-P1-K1-D12

Seq. No.	273184
Contig ID	42402_1.R1011
5'-most EST	gwl700615467.h1
Method	BLASTX
NCBI GI	g3335337

BLAST score	360
E value	5.0e-34
Match length	91
% identity	78
NCBI Description	(AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330 come from this gene

Seq. No.	273185
Contig ID	42413_1.R1011
5'-most EST	uC-zmflb73064f05a2

Seq. No.	273186
Contig ID	42415_1.R1011
5'-most EST	hvj700622168.h1
Method	BLASTX
NCBI GI	g3805851
BLAST score	338
E value	1.0e-36
Match length	119
% identity	64
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	273187
Contig ID	42416_1.R1011
5'-most EST	LIB3279-018-P1-K1-H1

Seq. No.	273188
Contig ID	42417_1.R1011
5'-most EST	uC-zmflmo17019g02a1
Method	BLASTX
NCBI GI	g2702281
BLAST score	1606
E value	1.0e-179
Match length	419
% identity	71
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	273189
Contig ID	42424_1.R1011
5'-most EST	uC-zmflb73099e02b1
Method	BLASTX
NCBI GI	g4191791
BLAST score	576
E value	8.0e-90
Match length	261
% identity	57
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	273190
Contig ID	42442_1.R1011
5'-most EST	mwy700440689.h1

Seq. No.	273191
Contig ID	42442_2.R1011
5'-most EST	LIB3279-049-P1-K1-B10

Seq. No.	273192
Contig ID	42447_1.R1011
5'-most EST	LIB3279-049-P1-K1-B4

Seq. No.	273193
Contig ID	42453_1.R1011
5'-most EST	LIB3279-049-P1-K1-C7
Method	BLASTX
NCBI GI	g4455259
BLAST score	257
E value	5.0e-22
Match length	171
% identity	38
NCBI Description	(AL035523) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	273194
Contig ID	42457_1.R1011
5'-most EST	LIB3279-060-P1-K1-H3
Method	BLASTX
NCBI GI	g4335749
BLAST score	683
E value	1.0e-126
Match length	301
% identity	75
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	273195
Contig ID	42464_1.R1011
5'-most EST	uC-zmroteosinte100d02b2
Method	BLASTX
NCBI GI	g2335108
BLAST score	790
E value	4.0e-84
Match length	297
% identity	50
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No.	273196
Contig ID	42464_2.R1011
5'-most EST	uC-zmflb73325c03a1
Method	BLASTX
NCBI GI	g2335108
BLAST score	163
E value	4.0e-11
Match length	73
% identity	41
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No.	273197
Contig ID	42471_1.R1011
5'-most EST	LIB3279-049-P1-K1-D5

Seq. No.	273198
Contig ID	42490_1.R1011
5'-most EST	LIB3279-049-P1-K1-F11

Seq. No.	273199
Contig ID	42494_1.R1011
5'-most EST	xsy700210711.h1
Method	BLASTX
NCBI GI	g1752734
BLAST score	834
E value	2.0e-89
Match length	228
% identity	69
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	273200
Contig ID	42495_1.R1011
5'-most EST	LIB3279-049-P1-K1-F5

Seq. No.	273201
Contig ID	42508_1.R1011
5'-most EST	uer700580620.h1

Seq. No.	273202
Contig ID	42508_2.R1011
5'-most EST	LIB3279-049-P1-K1-H1

Seq. No.	273203
Contig ID	42526_1.R1011
5'-most EST	dyk700106343.h1
Method	BLASTX
NCBI GI	g3979937
BLAST score	146
E value	7.0e-09
Match length	74
% identity	39
NCBI Description	(AL034393) predicted using Genefinder; cDNA EST EMBL:D65716 comes from this gene; cDNA EST yk263b1.3 comes from this gene; cDNA EST yk263b1.5 comes from this gene; cDNA EST EMBL:D69251 comes from this gene [Caenorhabditis elegans]

Seq. No.	273204
Contig ID	42541_1.R1011
5'-most EST	xjt700095233.h1
Method	BLASTX
NCBI GI	g3928084
BLAST score	276
E value	7.0e-26
Match length	206
% identity	34
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No.	273205
Contig ID	42547_1.R1011
5'-most EST	LIB3061-009-Q1-K1-C3
Method	BLASTX

NCBI GI	g1657619
BLAST score	401
E value	6.0e-39
Match length	158
% identity	51
NCBI Description	(U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No.	273206
Contig ID	42550_1.R1011
5'-most EST	wty700170403.h1
Method	BLASTX
NCBI GI	g2145356
BLAST score	359
E value	2.0e-34
Match length	106
% identity	66
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	273207
Contig ID	42560_1.R1011
5'-most EST	uC-zmroteosinte084b10b1
Method	BLASTX
NCBI GI	g1173225
BLAST score	231
E value	1.0e-18
Match length	162
% identity	39
NCBI Description	30S RIBOSOMAL PROTEIN S1 >gi_1075612_pir__S51485 rps1 homolog protein 307 - Synechococcus sp >gi_666973_dbj_BAA05946_ (D28752) ribosomal protein S1 [Synechococcus sp.]

Seq. No.	273208
Contig ID	42564_1.R1011
5'-most EST	zuv700356187.h1

Seq. No.	273209
Contig ID	42567_1.R1011
5'-most EST	LIB3137-032-Q1-K1-F11

Seq. No.	273210
Contig ID	42570_1.R1011
5'-most EST	gct701178537.h1
Method	BLASTX
NCBI GI	g2245094
BLAST score	161
E value	4.0e-11
Match length	86
% identity	48
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273211
Contig ID	42578_1.R1011
5'-most EST	uer700583977.h1
Method	BLASTX

NCBI GI g2661676
BLAST score 148
E value 4.0e-09
Match length 70
% identity 41
NCBI Description (AL009199) hypothetical ATP/GTP binding protein [Streptomyces coelicolor]

Seq. No. 273212
Contig ID 42584_1.R1011
5'-most EST uC-zmflb73130g04b2
Method BLASTX
NCBI GI g2980793
BLAST score 624
E value 6.0e-65
Match length 196
% identity 60
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 273213
Contig ID 42591_1.R1011
5'-most EST pwr700449524.h1

Seq. No. 273214
Contig ID 42600_1.R1011
5'-most EST uC-zmflMo17003a12b1
Method BLASTX
NCBI GI g3668089
BLAST score 574
E value 2.0e-98
Match length 242
% identity 76
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 273215
Contig ID 42603_1.R1011
5'-most EST uC-zmflmo17270c10b1

Seq. No. 273216
Contig ID 42615_1.R1011
5'-most EST xyt700345626.h1
Method BLASTX
NCBI GI g4432817
BLAST score 278
E value 2.0e-24
Match length 117
% identity 48
NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]

Seq. No. 273217
Contig ID 42617_1.R1011
5'-most EST uC-zmflb73298b10b1

Seq. No. 273218
Contig ID 42629_1.R1011
5'-most EST LIB3279-051-P1-K1-C5
Method BLASTX

NCBI GI	g4115938
BLAST score	580
E value	6.0e-64
Match length	201
% identity	66
NCBI Description	(AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana]

Seq. No.	273219
Contig ID	42630_1.R1011
5'-most EST	LIB3279-057-P1-K1-A12
Method	BLASTX
NCBI GI	g2673868
BLAST score	169
E value	6.0e-12
Match length	90
% identity	48
NCBI Description	(Y14856) fimbriata-associated protein [Antirrhinum majus]

Seq. No.	273220
Contig ID	42632_1.R1011
5'-most EST	pmx700091654.h1
Method	BLASTX
NCBI GI	g401238
BLAST score	576
E value	4.0e-68
Match length	158
% identity	84
NCBI Description	UBIQUITIN-ACTIVATING ENZYME E1 3 >gi_170686 (M90664) ubiquitin activating enzyme [Triticum aestivum]

Seq. No.	273221
Contig ID	42634_1.R1011
5'-most EST	uC-zmflb73148g09b1
Method	BLASTX
NCBI GI	g4263704
BLAST score	389
E value	5.0e-57
Match length	230
% identity	52
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	273222
Contig ID	42634_3.R1011
5'-most EST	dyk700104368.h1
Method	BLASTN
NCBI GI	g575425
BLAST score	194
E value	1.0e-105
Match length	205
% identity	99
NCBI Description	Z.mays mRNA for sugar-starvation induced protein

Seq. No.	273223
Contig ID	42634_5.R1011

5'-most EST	wyr700237113.h1
Seq. No.	273224
Contig ID	42653_1.R1011
5'-most EST	xmt700263319.h1
Method	BLASTX
NCBI GI	g4455250
BLAST score	406
E value	5.0e-76
Match length	299
% identity	53
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]
Seq. No.	273225
Contig ID	42656_1.R1011
5'-most EST	xsy700217442.h1
Method	BLASTX
NCBI GI	g1313926
BLAST score	190
E value	2.0e-14
Match length	73
% identity	60
NCBI Description	(X97677) non intermediate filament IFA binding protein [Brassica oleracea]
Seq. No.	273226
Contig ID	42662_1.R1011
5'-most EST	uC-zmrob73012f09b1
Seq. No.	273227
Contig ID	42672_1.R1011
5'-most EST	LIB3279-051-P1-K1-G2
Method	BLASTX
NCBI GI	g2500510
BLAST score	178
E value	5.0e-13
Match length	69
% identity	55
NCBI Description	DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (18S RRNA DIMETHYLASE)
Seq. No.	273228
Contig ID	42682_2.R1011
5'-most EST	dyk700106165.h1
Method	BLASTX
NCBI GI	g1418125
BLAST score	541
E value	3.0e-55
Match length	116
% identity	82
NCBI Description	(D58404) CTP:phosphocholine cytidylyltransferase [Brassica napus]
Seq. No.	273229
Contig ID	42687_1.R1011
5'-most EST	LIB3279-051-P1-K1-H7

Method	BLASTX
NCBI GI	g2245131
BLAST score	217
E value	1.0e-17
Match length	50
% identity	86
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273230
Contig ID	42696_1.R1011
5'-most EST	LIB3067-010-Q1-K1-H8
Method	BLASTX
NCBI GI	g2443329
BLAST score	474
E value	3.0e-47
Match length	106
% identity	79
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	273231
Contig ID	42704_1.R1011
5'-most EST	uC-zmflmo17068f12b2

Seq. No.	273232
Contig ID	42710_1.R1011
5'-most EST	LIB3279-052-P1-K1-B6

Seq. No.	273233
Contig ID	42711_1.R1011
5'-most EST	LIB3279-052-P1-K1-B7

Seq. No.	273234
Contig ID	42712_1.R1011
5'-most EST	LIB3279-052-P1-K1-B9
Method	BLASTX
NCBI GI	g2894612
BLAST score	284
E value	3.0e-35
Match length	105
% identity	72
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	273235
Contig ID	42719_1.R1011
5'-most EST	ymt70O224002.h1
Method	BLASTN
NCBI GI	g4220645
BLAST score	79
E value	5.0e-36
Match length	255
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	273236
Contig ID	42727_1.R1011
5'-most EST	uC-zmflm017205e10b1

Seq. No.	273237
Contig ID	42733_1.R1011
5'-most EST	LIB3279-052-P1-K1-D9
Seq. No.	273238
Contig ID	42734_1.R1011
5'-most EST	uC-zmflmo17130f05b1
Seq. No.	273239
Contig ID	42735_1.R1011
5'-most EST	LIB3137-035-Q1-K1-D7
Seq. No.	273240
Contig ID	42745_1.R1011
5'-most EST	LIB3060-018-Q1-K1-H8
Method	BLASTX
NCBI GI	g3859548
BLAST score	1613
E value	1.0e-180
Match length	306
% identity	95
NCBI Description	(AF097182) protein phosphatase 2A catalytic subunit [Oryza sativa]
Seq. No.	273241
Contig ID	42745_3.R1011
5'-most EST	LIB3279-052-P1-K1-E9
Method	BLASTX
NCBI GI	g3859548
BLAST score	523
E value	3.0e-53
Match length	109
% identity	90
NCBI Description	(AF097182) protein phosphatase 2A catalytic subunit [Oryza sativa]
Seq. No.	273242
Contig ID	42745_6.R1011
5'-most EST	hbs7011180958.h1
Method	BLASTX
NCBI GI	g3859548
BLAST score	261
E value	9.0e-23
Match length	48
% identity	98
NCBI Description	(AF097182) protein phosphatase 2A catalytic subunit [Oryza sativa]
Seq. No.	273243
Contig ID	42746_1.R1011
5'-most EST	uC-zmflmo17072d11b1
Seq. No.	273244
Contig ID	42752_1.R1011
5'-most EST	uwc700151534.h1

Seq. No.	273245
Contig ID	42758_1.R1011
5'-most EST	LIB3070-003-Q1-N1-B4
Method	BLASTX
NCBI GI	g2398681
BLAST score	257
E value	3.0e-22
Match length	84
% identity	58
NCBI Description	(Y14798) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	273246
Contig ID	42769_1.R1011
5'-most EST	uC-zmflb73175d10b1
Method	BLASTX
NCBI GI	g4220485
BLAST score	1256
E value	1.0e-139
Match length	332
% identity	70
NCBI Description	(AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	273247
Contig ID	42775_1.R1011
5'-most EST	LIB3279-052-P1-K1-H7

Seq. No.	273248
Contig ID	42787_1.R1011
5'-most EST	LIB3279-053-P1-K1-A9
Method	BLASTX
NCBI GI	g3776071
BLAST score	227
E value	1.0e-18
Match length	107
% identity	41
NCBI Description	(AJ011972) histone deacetylase-like protein [Homo sapiens]

Seq. No.	273249
Contig ID	42794_1.R1011
5'-most EST	uC-zmflb73175h01b1

Seq. No.	273250
Contig ID	42797_1.R1011
5'-most EST	LIB3279-053-P1-K1-B8
Method	BLASTX
NCBI GI	g2832652
BLAST score	467
E value	9.0e-47
Match length	114
% identity	82
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	273251
Contig ID	42801_1.R1011
5'-most EST	uC-zmflb73151e04b1

Method	BLASTX
NCBI GI	g2956717
BLAST score	785
E value	8.0e-84
Match length	194
% identity	75
NCBI Description	(Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]

Seq. No.	273252
Contig ID	42802_1.R1011
5'-most EST	hvj700622417.h1
Method	BLASTX
NCBI GI	g4008372
BLAST score	252
E value	2.0e-21
Match length	183
% identity	33
NCBI Description	(Z27079) cDNA EST CEMSF67FB comes from this gene; cDNA EST CEMSF67R comes from this gene; cDNA EST yk195e10.3 comes from this gene; cDNA EST yk195e10.5 comes from this gene; cDNA EST yk397a5.3 comes from this gene; cDNA EST yk3

Seq. No.	273253
Contig ID	42816_1.R1011
5'-most EST	LIB143-019-Q1-E1-A10
Method	BLASTX
NCBI GI	g2982459
BLAST score	745
E value	7.0e-79
Match length	225
% identity	66
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	273254
Contig ID	42826_1.R1011
5'-most EST	uC-zmflmo17011b05b1
Method	BLASTN
NCBI GI	g22371
BLAST score	68
E value	9.0e-30
Match length	68
% identity	100
NCBI Description	Maize Mu4 transposable element DNA

Seq. No.	273255
Contig ID	42831_1.R1011
5'-most EST	uC-zmflmo17263h05b1
Method	BLASTX
NCBI GI	g4469019
BLAST score	1045
E value	1.0e-114
Match length	265
% identity	78
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	273256
Contig ID	42831_2.R1011

5'-most EST	uC-zmflb73177h09b1
Method	BLASTX
NCBI GI	g4469019
BLAST score	498
E value	2.0e-50
Match length	125
% identity	78
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	273257
Contig ID	42836_1.R1011
5'-most EST	LIB3279-053-P1-K1-F8

Seq. No.	273258
Contig ID	42842_1.R1011
5'-most EST	qmh700027957.f1
Method	BLASTX
NCBI GI	g2190547
BLAST score	1154
E value	1.0e-127
Match length	350
% identity	61
NCBI Description	(AC001229) ESTs gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come from this gene. [Arabidopsis thaliana]

Seq. No.	273259
Contig ID	42842_2.R1011
5'-most EST	uC-zmflb73070a07b1

Seq. No.	273260
Contig ID	42844_1.R1011
5'-most EST	LIB3279-053-P1-K1-G8

Seq. No.	273261
Contig ID	42847_1.R1011
5'-most EST	LIB3279-053-P1-K1-H2

Seq. No.	273262
Contig ID	42854_1.R1011
5'-most EST	LIB3279-054-P1-K1-A10

Seq. No.	273263
Contig ID	42865_1.R1011
5'-most EST	LIB3279-054-P1-K1-B10

Seq. No.	273264
Contig ID	42869_1.R1011
5'-most EST	LIB3279-054-P1-K1-B3

Seq. No.	273265
Contig ID	42882_1.R1011
5'-most EST	uC-zmflmo17240d09b1

Seq. No.	273266
Contig ID	42900_1.R1011
5'-most EST	LIB3068-028-Q1-K1-E9

Method	BLASTX
NCBI GI	g2829889
BLAST score	226
E value	2.0e-18
Match length	98
% identity	46
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	273267
Contig ID	42911_1.R1011
5'-most EST	ntr700077279.h1

Seq. No.	273268
Contig ID	42913_1.R1011
5'-most EST	LIB3279-054-P1-K1-F8

Seq. No.	273269
Contig ID	42915_1.R1011
5'-most EST	ydl700405320.h1
Method	BLASTX
NCBI GI	g280401
BLAST score	2353
E value	0.0e+00
Match length	544
% identity	82
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - curled-leaved tobacco >gi_170206 (M27888) H+-translocating ATPase [Nicotiana plumbaginifolia]

Seq. No.	273270
Contig ID	42918_1.R1011
5'-most EST	LIB3279-054-P1-K1-G2

Seq. No.	273271
Contig ID	42918_2.R1011
5'-most EST	cyk700048992.f1

Seq. No.	273272
Contig ID	42929_1.R1011
5'-most EST	uC-zmf1b73219g02b2
Method	BLASTX
NCBI GI	g421843
BLAST score	1868
E value	0.0e+00
Match length	504
% identity	73
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	273273
Contig ID	42929_2.R1011
5'-most EST	tzu700202331.h1

Seq. No.	273274
Contig ID	42933_1.R1011
5'-most EST	LIB3279-054-P1-K1-H8

Seq. No.	273275
Contig ID	42935_2.R1011
5'-most EST	wty700170539.h1

Seq. No.	273276
Contig ID	42935_3.R1011
5'-most EST	kem700611547.h1
Method	BLASTX
NCBI GI	g2245394
BLAST score	330
E value	7.0e-31
Match length	104
% identity	59
NCBI Description	(U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No.	273277
Contig ID	42939_1.R1011
5'-most EST	LIB143-002-Q1-E1-E5
Method	BLASTX
NCBI GI	g4091008
BLAST score	670
E value	2.0e-70
Match length	137
% identity	92
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	273278
Contig ID	42939_2.R1011
5'-most EST	LIB3279-055-P1-K1-A3
Method	BLASTX
NCBI GI	g4091008
BLAST score	679
E value	8.0e-72
Match length	123
% identity	97
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	273279
Contig ID	42946_1.R1011
5'-most EST	wyr700237365.h1
Method	BLASTX
NCBI GI	g4263703
BLAST score	1028
E value	1.0e-112
Match length	251
% identity	74
NCBI Description	(AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273280
Contig ID	42955_1.R1011
5'-most EST	LIB3279-055-P1-K1-B8

Seq. No.	273281
Contig ID	42963_1.R1011
5'-most EST	LIB3060-008-Q1-K1-F10

Seq. No.	273282
Contig ID	42968_1.R1011
5'-most EST	LIB3279-055-P1-K1-C9
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	273283
Contig ID	42974_1.R1011
5'-most EST	LIB3279-055-P1-K1-D3

Seq. No.	273284
Contig ID	42989_1.R1011
5'-most EST	LIB3066-002-Q1-K1-C2
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	273285
Contig ID	43001_1.R1011
5'-most EST	LIB3279-055-P1-K1-F8
Method	BLASTX
NCBI GI	g3047083
BLAST score	592
E value	3.0e-61
Match length	180
% identity	72
NCBI Description	(AF058914) similar to FLAP endonuclease-1 (SW:P39748) [Arabidopsis thaliana]

Seq. No.	273286
Contig ID	43004_1.R1011
5'-most EST	LIB3279-055-P1-K1-G11
Method	BLASTX
NCBI GI	g3252827
BLAST score	287
E value	1.0e-25
Match length	129
% identity	40
NCBI Description	(AC004382) Unknown gene product [Homo sapiens]

Seq. No.	273287
Contig ID	43011_1.R1011
5'-most EST	LIB3066-025-Q1-K1-D3

Seq. No.	273288
Contig ID	43011_2.R1011
5'-most EST	LIB3279-055-P1-K1-G7

Seq. No.	273289
Contig ID	43019_1.R1011
5'-most EST	LIB3279-055-P1-K1-H3

Seq. No.	273290
Contig ID	43034_1.R1011
5'-most EST	wty700168412.h1
Method	BLASTX
NCBI GI	g3776574
BLAST score	592
E value	3.0e-61
Match length	176
% identity	65
NCBI Description	(AC005388) Similar to T11J7.13 gi_2880051 putative protein kinase from Arabidopsis thaliana BAC gb_AC002340. [Arabidopsis thaliana]

Seq. No.	273291
Contig ID	43036_1.R1011
5'-most EST	LIB3136-034-Q1-K1-E9
Method	BLASTX
NCBI GI	g3785989
BLAST score	267
E value	2.0e-23
Match length	149
% identity	44
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	273292
Contig ID	43049_1.R1011
5'-most EST	uer700581407.h1

Seq. No.	273293
Contig ID	43049_2.R1011
5'-most EST	LIB3279-057-P1-K1-C12
Method	BLASTX
NCBI GI	g3288648
BLAST score	192
E value	3.0e-14
Match length	121
% identity	44
NCBI Description	(Y16385) origin recognition complex subunit 4 [Xenopus laevis]

Seq. No.	273294
Contig ID	43049_3.R1011
5'-most EST	yyf700349704.h1

Seq. No.	273295
Contig ID	43055_1.R1011
5'-most EST	pmx700089103.h1
Method	BLASTX
NCBI GI	g4455325
BLAST score	507
E value	3.0e-51
Match length	158
% identity	59

NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	273296
Contig ID	43066_1.R1011
5'-most EST	LIB3279-057-P1-K1-D6
Method	BLASTX
NCBI GI	g1177320
BLAST score	565
E value	6.0e-58
Match length	205
% identity	53
NCBI Description	(X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza sativa]

Seq. No.	273297
Contig ID	43067_1.R1011
5'-most EST	xyt700345528.h1

Seq. No.	273298
Contig ID	43069_1.R1011
5'-most EST	LIB3279-057-P1-K1-D9
Method	BLASTX
NCBI GI	g3941468
BLAST score	414
E value	2.0e-40
Match length	109
% identity	67
NCBI Description	(AF062888) putative transcription factor [Arabidopsis thaliana]

Seq. No.	273299
Contig ID	43072_1.R1011
5'-most EST	ntr700074729.h1
Method	BLASTX
NCBI GI	g2244952
BLAST score	661
E value	4.0e-69
Match length	176
% identity	73
NCBI Description	(Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]

Seq. No.	273300
Contig ID	43072_2.R1011
5'-most EST	LIB84-013-Q1-E1-H1
Method	BLASTX
NCBI GI	g3785983
BLAST score	324
E value	5.0e-30
Match length	121
% identity	55
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273301
Contig ID	43072_3.R1011
5'-most EST	uer700577069.h1

Seq. No.	273302
Contig ID	43072_4.R1011
5'-most EST	uC-zmflmo17335h07a1

Seq. No.	273303
Contig ID	43072_5.R1011
5'-most EST	uer700579510.h1
Method	BLASTX
NCBI GI	g2244952
BLAST score	178
E value	5.0e-13
Match length	57
% identity	60
NCBI Description	(Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]

Seq. No.	273304
Contig ID	43082_1.R1011
5'-most EST	LIB3137-028-Q1-K1-D3
Method	BLASTX
NCBI GI	g2094888
BLAST score	343
E value	6.0e-32
Match length	95
% identity	60
NCBI Description	Cucumber Basic Protein, A Blue Copper Protein

Seq. No.	273305
Contig ID	43082_2.R1011
5'-most EST	uC-zmflm017092e10b1
Method	BLASTX
NCBI GI	g3860333
BLAST score	355
E value	1.0e-33
Match length	100
% identity	59
NCBI Description	(AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No.	273306
Contig ID	43089_1.R1011
5'-most EST	wty700171527.h1

Seq. No.	273307
Contig ID	43091_1.R1011
5'-most EST	uC-zmflb73367h04a1
Method	BLASTX
NCBI GI	g3822225
BLAST score	200
E value	2.0e-15
Match length	62
% identity	50
NCBI Description	(AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]

Seq. No.	273308
Contig ID	43094_1.R1011
5'-most EST	uC-zmflb73224h11b2

Seq. No.	273309
Contig ID	43097_1.R1011
5'-most EST	fC-zmf1700339851a5
Method	BLASTX
NCBI GI	g3297819
BLAST score	235
E value	2.0e-19
Match length	115
% identity	53
NCBI Description	(AL031032) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	273310
Contig ID	43104_1.R1011
5'-most EST	ceu700422240.h1

Seq. No.	273311
Contig ID	43110_1.R1011
5'-most EST	LIB3279-057-P1-K1-H9

Seq. No.	273312
Contig ID	43147_1.R1011
5'-most EST	tzu700202324.h1
Method	BLASTX
NCBI GI	g2443886
BLAST score	909
E value	4.0e-98
Match length	238
% identity	76
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	273313
Contig ID	43150_1.R1011
5'-most EST	uC-zmflm017093b08b1

Seq. No.	273314
Contig ID	43190_1.R1011
5'-most EST	uC-zmroteosinte096g06b2
Method	BLASTX
NCBI GI	g3193292
BLAST score	1005
E value	1.0e-109
Match length	244
% identity	82
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	273315
Contig ID	43191_1.R1011
5'-most EST	LIB3136-012-Q1-K1-B6
Method	BLASTX
NCBI GI	g2565010
BLAST score	309
E value	3.0e-28
Match length	67

% identity	84
NCBI Description	(AC002983) putative microfibril-associated protein [Arabidopsis thaliana] >gi_3377811 (AF076275) contains similarity to ATP synthase B/B' (Pfam: ATP-synt_B.hmm, score: 11.71) [Arabidopsis thaliana]

Seq. No.	273316
Contig ID	43205_1.R1011
5'-most EST	LIB3279-060-P1-K1-A7
Method	BLASTX
NCBI GI	g2244792
BLAST score	227
E value	4.0e-18
Match length	101
% identity	44
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	273317
Contig ID	43205_2.R1011
5'-most EST	LIB3117-003-Q1-K1-C4

Seq. No.	273318
Contig ID	43208_1.R1011
5'-most EST	LIB189-020-Q1-E1-A10
Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	3.0e-10
Match length	36
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	273319
Contig ID	43220_1.R1011
5'-most EST	LIB3279-060-P1-K1-C10
Method	BLASTX
NCBI GI	g3894189
BLAST score	379
E value	3.0e-36
Match length	127
% identity	58
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273320
Contig ID	43222_1.R1011
5'-most EST	uC-zmflm017205e11b1

Seq. No.	273321
Contig ID	43222_3.R1011
5'-most EST	uC-zmflb73257b09b3

Seq. No.	273322
Contig ID	43226_1.R1011
5'-most EST	LIB3279-060-P1-K1-C7
Method	BLASTX
NCBI GI	g1651907
BLAST score	217

E value	1.0e-17
Match length	71
% identity	56
NCBI Description	(D90901) spore germination protein c2 [Synechocystis sp.]

Seq. No.	273323
Contig ID	43236_1.R1011
5'-most EST	LIB3279-060-P1-K1-D7
Method	BLASTX
NCBI GI	g1171579
BLAST score	563
E value	8.0e-58
Match length	152
% identity	71
NCBI Description	(X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No.	273324
Contig ID	43242_1.R1011
5'-most EST	uC-zmflmo17058g09a1
Method	BLASTX
NCBI GI	g4415942
BLAST score	320
E value	3.0e-29
Match length	149
% identity	48
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273325
Contig ID	43246_1.R1011
5'-most EST	uC-zmroteosinte101b06b2
Method	BLASTX
NCBI GI	g2435511
BLAST score	286
E value	1.0e-42
Match length	127
% identity	67
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	273326
Contig ID	43249_1.R1011
5'-most EST	LIB3279-060-P1-K1-F1
Method	BLASTX
NCBI GI	g3747044
BLAST score	451
E value	6.0e-45
Match length	84
% identity	100
NCBI Description	(AF093537) blue copper protein [Zea mays]

Seq. No.	273327
Contig ID	43256_1.R1011
5'-most EST	LIB3279-060-P1-K1-F6
Method	BLASTX
NCBI GI	g3334349
BLAST score	271
E value	2.0e-47

Match length	172
% identity	60
NCBI Description	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS) >gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	273328
Contig ID	43260_1.R1011
5'-most EST	hvj700620782.h1

Seq. No.	273329
Contig ID	43270_1.R1011
5'-most EST	LIB3066-031-Q1-K1-H6

Seq. No.	273330
Contig ID	43283_1.R1011
5'-most EST	LIB143-001-Q1-E1-A4

Seq. No.	273331
Contig ID	43285_1.R1011
5'-most EST	ydl700405437.h1
Method	BLASTX
NCBI GI	g4567312
BLAST score	764
E value	3.0e-81
Match length	219
% identity	66
NCBI Description	(AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273332
Contig ID	43291_1.R1011
5'-most EST	LIB143-041-Q1-E1-C6
Method	BLASTN
NCBI GI	g1915959
BLAST score	43
E value	6.0e-15
Match length	83
% identity	89
NCBI Description	T.aestivum mRNA for peptidylprolyl isomerase

Seq. No.	273333
Contig ID	43299_1.R1011
5'-most EST	qmh700029831.f1
Method	BLASTX
NCBI GI	g1352469
BLAST score	872
E value	1.0e-102
Match length	224
% identity	83
NCBI Description	BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) >gi_736359 (U17695) invertase [Zea mays] >gi_1582380_prf__2118364A cell wall invertase [Zea mays]

Seq. No.	273334
Contig ID	43302_1.R1011
5'-most EST	LIB143-001-Q1-E1-C9

Seq. No.	273335
Contig ID	43306_1.R1011
5'-most EST	LIB143-001-Q1-E1-D2

Seq. No.	273336
Contig ID	43307_1.R1011
5'-most EST	LIB143-001-Q1-E1-D3
Method	BLASTX
NCBI GI	g4455251
BLAST score	411
E value	4.0e-40
Match length	108
% identity	67
NCBI Description	(AL035523) magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	273337
Contig ID	43314_1.R1011
5'-most EST	uC-zmflb73146e12b1
Method	BLASTX
NCBI GI	g4455367
BLAST score	639
E value	1.0e-86
Match length	256
% identity	68
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	273338
Contig ID	43315_1.R1011
5'-most EST	uC-zmflmo17329c07a1

Seq. No.	273339
Contig ID	43321_1.R1011
5'-most EST	uC-zmflb73084c09b2

Seq. No.	273340
Contig ID	43326_1.R1011
5'-most EST	LIB143-035-Q1-E1-B2
Method	BLASTX
NCBI GI	g1122317
BLAST score	327
E value	2.0e-30
Match length	111
% identity	60
NCBI Description	(X94193) heat shock protein 17.9 [Pennisetum glaucum]

Seq. No.	273341
Contig ID	43327_1.R1011
5'-most EST	uC-zmflb73183b10b1
Method	BLASTX
NCBI GI	g995714
BLAST score	149
E value	1.0e-09
Match length	68
% identity	38
NCBI Description	(X91258) L3177 [Saccharomyces cerevisiae]

Seq. No.	273342
Contig ID	43328_1.R1011
5'-most EST	LIB3136-010-Q1-K1-G5
Method	BLASTX
NCBI GI	g4587579
BLAST score	384
E value	9.0e-37
Match length	209
% identity	38
NCBI Description	(AC006550) F10O3.1 [Arabidopsis thaliana]

Seq. No.	273343
Contig ID	43342_1.R1011
5'-most EST	LIB143-016-Q1-E1-A11

Seq. No.	273344
Contig ID	43345_1.R1011
5'-most EST	nwy700444076.h1
Method	BLASTX
NCBI GI	g3402678
BLAST score	727
E value	7.0e-77
Match length	201
% identity	71
NCBI Description	(AC004697) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	273345
Contig ID	43345_2.R1011
5'-most EST	LIB143-001-Q1-E1-H4

Seq. No.	273346
Contig ID	43348_1.R1011
5'-most EST	LIB143-001-Q1-E1-H8
Method	BLASTX
NCBI GI	g3776559
BLAST score	622
E value	6.0e-65
Match length	154
% identity	71
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	273347
Contig ID	43349_1.R1011
5'-most EST	LIB143-002-Q1-E1-A1
Method	BLASTX
NCBI GI	g2760325
BLAST score	519
E value	2.0e-52
Match length	130
% identity	76
NCBI Description	(AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No.	273348

Contig ID	43355_1.R1011
5'-most EST	LIB143-013-Q1-E1-A2
Method	BLASTX
NCBI GI	g1169369
BLAST score	227
E value	2.0e-18
Match length	153
% identity	38
NCBI Description	DNAJ PROTEIN >gi_541427_pir__S41758 heat shock protein dnaJ - Clostridium acetobutylicum >gi_433079_emb_CAA48792_ (X69050) DnaJ [Clostridium acetobutylicum]

Seq. No.	273349
Contig ID	43356_1.R1011
5'-most EST	LIB3137-021-Q1-K1-F6

Seq. No.	273350
Contig ID	43368_1.R1011
5'-most EST	qmh700027864.f1
Method	BLASTX
NCBI GI	g3805962
BLAST score	324
E value	4.0e-30
Match length	64
% identity	89
NCBI Description	(Y13772) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	273351
Contig ID	43370_1.R1011
5'-most EST	LIB143-002-Q1-E1-C6
Method	BLASTX
NCBI GI	g4406815
BLAST score	295
E value	2.0e-26
Match length	81
% identity	67
NCBI Description	(AC006201) putative peptide methionine sulfoxide reductase [Arabidopsis thaliana]

Seq. No.	273352
Contig ID	43375_1.R1011
5'-most EST	LIB3067-019-Q1-K1-B6

Seq. No.	273353
Contig ID	43376_1.R1011
5'-most EST	LIB143-050-Q1-E1-E7
Method	BLASTX
NCBI GI	g426482
BLAST score	2279
E value	0.0e+00
Match length	439
% identity	95
NCBI Description	(L25805) alpha-amylase [Zea mays]

Seq. No.	273354
Contig ID	43376_2.R1011
5'-most EST	hvj700621517.h1

Method	BLASTX
NCBI GI	g113766
BLAST score	539
E value	5.0e-55
Match length	106
% identity	90
NCBI Description	ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (ISOZYME 1B) >gi_100660_pir__S10013 alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-OSg2) - rice >gi_20167_emb_CAA34516_ (X16509) alpha-amylase [Oryza sativa]

Seq. No.	273355
Contig ID	43376_3.R1011
5'-most EST	fC-zmle700440623a3
Method	BLASTX
NCBI GI	g113678
BLAST score	731
E value	1.0e-147
Match length	298
% identity	82
NCBI Description	ALPHA-AMYLASE ISOZYME 2A PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) >gi_82456_pir__JQ1527 alpha-amylase (EC 3.2.1.1) 2A - rice >gi_169769 (M74177) alpha-amylase [Oryza sativa]

Seq. No.	273356
Contig ID	43376_4.R1011
5'-most EST	LIB143-064-Q1-E1-G3
Method	BLASTX
NCBI GI	g113766
BLAST score	569
E value	8.0e-59
Match length	128
% identity	80
NCBI Description	ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (ISOZYME 1B) >gi_100660_pir__S10013 alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-OSg2) - rice >gi_20167_emb_CAA34516_ (X16509) alpha-amylase [Oryza sativa]

Seq. No.	273357
Contig ID	43376_5.R1011
5'-most EST	LIB143-019-Q1-E1-G10
Method	BLASTX
NCBI GI	g426482
BLAST score	222
E value	1.0e-28
Match length	76
% identity	87
NCBI Description	(L25805) alpha-amylase [Zea mays]

Seq. No.	273358
Contig ID	43376_6.R1011
5'-most EST	vux700158360.h1
Method	BLASTX
NCBI GI	g3549648

BLAST score	265
E value	3.0e-36
Match length	95
% identity	80
NCBI Description	(AJ010728) alpha amylase [Avena fatua]

Seq. No.	273359
Contig ID	43376_8.R1011
5'-most EST	vux700156515.h1
Method	BLASTX
NCBI GI	g3549648
BLAST score	352
E value	2.0e-33
Match length	71
% identity	89
NCBI Description	(AJ010728) alpha amylase [Avena fatua]

Seq. No.	273360
Contig ID	43382_1.R1011
5'-most EST	LIB143-014-Q1-E1-B11
Method	BLASTX
NCBI GI	g3786008
BLAST score	234
E value	2.0e-19
Match length	85
% identity	54
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	273361
Contig ID	43382_2.R1011
5'-most EST	LIB143-045-Q1-E1-F7
Method	BLASTX
NCBI GI	g3786008
BLAST score	224
E value	3.0e-18
Match length	94
% identity	50
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	273362
Contig ID	43383_1.R1011
5'-most EST	LIB143-002-Q1-E1-E1
Method	BLASTX
NCBI GI	g1389768
BLAST score	305
E value	7.0e-28
Match length	96
% identity	66
NCBI Description	(U58942) phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	273363
Contig ID	43385_1.R1011
5'-most EST	LIB143-002-Q1-E1-E2

Seq. No.	273364
Contig ID	43385_2.R1011

5'-most EST	LIB3069-034-Q1-K1-E3
Seq. No.	273365
Contig ID	43393_1.R1011
5'-most EST	LIB143-035-Q1-E1-F1
Method	BLASTX
NCBI GI	g2801536
BLAST score	502
E value	1.0e-50
Match length	175
% identity	55
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]
Seq. No.	273366
Contig ID	43396_1.R1011
5'-most EST	LIB143-002-Q1-E1-F5
Seq. No.	273367
Contig ID	43397_1.R1011
5'-most EST	uC-zmflmo17041b04b1
Method	BLASTX
NCBI GI	g2894598
BLAST score	576
E value	3.0e-59
Match length	199
% identity	58
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	273368
Contig ID	43397_2.R1011
5'-most EST	uC-zmflb73041b10b1
Method	BLASTX
NCBI GI	g2894598
BLAST score	368
E value	3.0e-35
Match length	81
% identity	78
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	273369
Contig ID	43407_1.R1011
5'-most EST	uC-zmflb73372g03a1
Method	BLASTX
NCBI GI	g4490702
BLAST score	417
E value	9.0e-41
Match length	206
% identity	46
NCBI Description	(AL035680) hypothetical protein [Arabidopsis thaliana]
Seq. No.	273370
Contig ID	43417_1.R1011
5'-most EST	dyk700102930.h1
Method	BLASTN
NCBI GI	g3747043
BLAST score	42
E value	5.0e-14

Match length	42
% identity	100
NCBI Description	Zea mays blue copper protein mRNA, partial cds

Seq. No.	273371
Contig ID	43419_1.R1011
5'-most EST	LIB143-003-Q1-E1-A12
Method	BLASTX
NCBI GI	g3482933
BLAST score	338
E value	1.0e-31
Match length	92
% identity	68
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	273372
Contig ID	43420_1.R1011
5'-most EST	uC-zmflmo17041e11b1
Method	BLASTX
NCBI GI	g3798740
BLAST score	172
E value	4.0e-12
Match length	152
% identity	31
NCBI Description	(AB011261) supercoiling factor [Drosophila melanogaster]

Seq. No.	273373
Contig ID	43438_1.R1011
5'-most EST	vux700161562.h1
Method	BLASTX
NCBI GI	g2190992
BLAST score	410
E value	5.0e-40
Match length	113
% identity	67
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No.	273374
Contig ID	43439_1.R1011
5'-most EST	LIB143-003-Q1-E1-C5

Seq. No.	273375
Contig ID	43447_1.R1011
5'-most EST	LIB3136-014-Q1-K2-E9
Method	BLASTX
NCBI GI	g4490333
BLAST score	469
E value	1.0e-46
Match length	134
% identity	69
NCBI Description	(AL035656) EF-Hand containing protein-like [Arabidopsis thaliana]

Seq. No.	273376
Contig ID	43453_1.R1011

5'-most EST	uC-zmflb73152g03b1
Seq. No.	273377
Contig ID	43459_1.R1011
5'-most EST	uC-zmflmo17044d02b1
Method	BLASTX
NCBI GI	g2633727
BLAST score	645
E value	6.0e-67
Match length	392
% identity	36
NCBI Description	(Z99111) ykrT [Bacillus subtilis]
Seq. No.	273378
Contig ID	43460_1.R1011
5'-most EST	LIB3061-001-Q1-K2-H7
Method	BLASTX
NCBI GI	g3850581
BLAST score	353
E value	3.0e-33
Match length	120
% identity	56
NCBI Description	(AC005278) EST gb_N96383 comes from this gene. [Arabidopsis thaliana]
Seq. No.	273379
Contig ID	43465_1.R1011
5'-most EST	LIB143-003-Q1-E1-F5
Method	BLASTX
NCBI GI	g2662099
BLAST score	316
E value	7.0e-29
Match length	135
% identity	51
NCBI Description	(AB007869) KIAA0409 [Homo sapiens]
Seq. No.	273380
Contig ID	43467_1.R1011
5'-most EST	LIB143-020-Q1-E1-B6
Method	BLASTX
NCBI GI	g3236253
BLAST score	386
E value	4.0e-37
Match length	146
% identity	52
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	273381
Contig ID	43470_1.R1011
5'-most EST	LIB143-003-Q1-E1-G1
Method	BLASTX
NCBI GI	g4512685
BLAST score	163
E value	9.0e-11
Match length	73
% identity	49

NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273382
Contig ID	43470_2.R1011
5'-most EST	LIB84-014-Q1-E1-H2

Seq. No.	273383
Contig ID	43472_1.R1011
5'-most EST	gct701178805.h1
Method	BLASTX
NCBI GI	g4572671
BLAST score	721
E value	3.0e-76
Match length	205
% identity	73
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	273384
Contig ID	43487_1.R1011
5'-most EST	sem700930219.h1
Method	BLASTX
NCBI GI	g3386604
BLAST score	204
E value	3.0e-16
Match length	92
% identity	53
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	273385
Contig ID	43494_1.R1011
5'-most EST	LIB143-004-Q1-E1-A5

Seq. No.	273386
Contig ID	43494_2.R1011
5'-most EST	LIB189-013-Q1-E1-D4

Seq. No.	273387
Contig ID	43511_1.R1011
5'-most EST	ntr700072217.h1
Method	BLASTX
NCBI GI	g398966
BLAST score	357
E value	8.0e-34
Match length	169
% identity	45
NCBI Description	4-COUMARATE--COA LIGASE 2 (4CL) (CLONE 4CL16) >gi_541937_pir__PQ0772 4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL1B) - soybean (fragment) >gi_18520_emb_CAA49576_ (X69955) 4-coumarate--CoA ligase [Glycine max]

Seq. No.	273388
Contig ID	43514_1.R1011
5'-most EST	LIB143-038-Q1-E1-D4

Method	BLASTX
NCBI GI	g1514953
BLAST score	1282
E value	1.0e-141
Match length	349
% identity	72
NCBI Description	(D76415) cysteine proteinase [Oryza sativa]

Seq. No.	273389
Contig ID	43514_2.R1011
5'-most EST	LIB143-004-Q1-E1-C4
Method	BLASTX
NCBI GI	g1514953
BLAST score	342
E value	4.0e-32
Match length	89
% identity	73
NCBI Description	(D76415) cysteine proteinase [Oryza sativa]

Seq. No.	273390
Contig ID	43514_3.R1011
5'-most EST	LIB143-041-Q1-E1-B9
Method	BLASTX
NCBI GI	g4426617
BLAST score	304
E value	2.0e-27
Match length	75
% identity	77
NCBI Description	(AF099203) cysteine endopeptidase precursor [Oryza sativa]

Seq. No.	273391
Contig ID	43514_5.R1011
5'-most EST	hvj700618989.h1
Method	BLASTX
NCBI GI	g629792
BLAST score	169
E value	4.0e-12
Match length	50
% identity	62
NCBI Description	cysteine proteinase - rice >gi_530335_emb_CAA56844_ (X80876) cysteine protease [Oryza sativa]

Seq. No.	273392
Contig ID	43518_1.R1011
5'-most EST	fC-zmf1700465406a2
Method	BLASTX
NCBI GI	g2660664
BLAST score	417
E value	1.0e-40
Match length	183
% identity	49
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	273393
Contig ID	43521_2.R1011
5'-most EST	cat700018356.r1

Seq. No.	273394
Contig ID	43526_1.R1011
5'-most EST	LIB143-004-Q1-E1-D5

Seq. No.	273395
Contig ID	43530_1.R1011
5'-most EST	afb700381540.h1

Seq. No.	273396
Contig ID	43541_1.R1011
5'-most EST	LIB143-019-Q1-E1-A2
Method	BLASTX
NCBI GI	g400094
BLAST score	291
E value	1.0e-25
Match length	143
% identity	43
NCBI Description	23 KD JASMONATE-INDUCED PROTEIN >gi_282989_pir__S22514 jasmonate-induced protein 1 - barley

Seq. No.	273397
Contig ID	43559_1.R1011
5'-most EST	tfd700574448.h1
Method	BLASTX
NCBI GI	g2832629
BLAST score	423
E value	2.0e-41
Match length	134
% identity	57
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	273398
Contig ID	43564_1.R1011
5'-most EST	xjt700096940.h1
Method	BLASTX
NCBI GI	g4098238
BLAST score	303
E value	3.0e-27
Match length	256
% identity	31
NCBI Description	(U76384) o-methyltransferase [Triticum aestivum]

Seq. No.	273399
Contig ID	43574_1.R1011
5'-most EST	LIB3059-012-Q1-K1-G8
Method	BLASTX
NCBI GI	g3885343
BLAST score	173
E value	3.0e-12
Match length	63
% identity	52
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273400
Contig ID	43577_1.R1011
5'-most EST	uC-zmflmo17301g08b1

Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	273401
Contig ID	43577_2.R1011
5'-most EST	ymt700222504.h1

Seq. No.	273402
Contig ID	43588_1.R1011
5'-most EST	LIB143-005-Q1-E1-B4

Seq. No.	273403
Contig ID	43591_1.R1011
5'-most EST	uC-zmf1b73050h07b1
Method	BLASTX
NCBI GI	g3135611
BLAST score	535
E value	2.0e-54
Match length	204
% identity	52
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	273404
Contig ID	43599_1.R1011
5'-most EST	qmh700028615.f1

Seq. No.	273405
Contig ID	43599_2.R1011
5'-most EST	uC-zmf1b73080g02b2

Seq. No.	273406
Contig ID	43602_1.R1011
5'-most EST	LIB143-005-Q1-E1-D9
Method	BLASTX
NCBI GI	g1362007
BLAST score	598
E value	1.0e-67
Match length	139
% identity	81
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	273407
Contig ID	43603_1.R1011
5'-most EST	LIB189-010-Q1-E1-G9
Method	BLASTX
NCBI GI	g4467147
BLAST score	933
E value	1.0e-101
Match length	304
% identity	64

NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]
Seq. No.	273408
Contig ID	43605_1.R1011
5'-most EST	uwc700152827.h1
Method	BLASTX
NCBI GI	g1666171
BLAST score	1192
E value	1.0e-131
Match length	254
% identity	85
NCBI Description	(Y09105) unknown [Nicotiana plumbaginifolia]
Seq. No.	273409
Contig ID	43607_1.R1011
5'-most EST	LIB143-005-Q1-E1-D5
Seq. No.	273410
Contig ID	43612_1.R1011
5'-most EST	wyr700235692.h1
Method	BLASTX
NCBI GI	g1077569
BLAST score	409
E value	1.0e-39
Match length	196
% identity	41
NCBI Description	probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) >gi_747884_emb_CAA88663_ (Z48758) unknown [Saccharomyces cerevisiae]
Seq. No.	273411
Contig ID	43613_1.R1011
5'-most EST	LIB143-057-Q1-E1-F7
Method	BLASTX
NCBI GI	g4138647
BLAST score	363
E value	1.0e-34
Match length	140
% identity	51
NCBI Description	(AJ011939) peroxidase [Trifolium repens]
Seq. No.	273412
Contig ID	43613_2.R1011
5'-most EST	xsy700210737.h1
Method	BLASTX
NCBI GI	g1402906
BLAST score	279
E value	6.0e-25
Match length	97
% identity	54
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]
Seq. No.	273413
Contig ID	43615_1.R1011
5'-most EST	LIB143-005-Q1-E1-E4

Seq. No.	273414
Contig ID	43619_1.R1011
5'-most EST	fdz701163458.h1
Method	BLASTX
NCBI GI	g4008006
BLAST score	765
E value	2.0e-81
Match length	217
% identity	70
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	273415
Contig ID	43624_1.R1011
5'-most EST	LIB143-005-Q1-E1-F4

Seq. No.	273416
Contig ID	43625_1.R1011
5'-most EST	LIB143-065-Q1-E1-F4

Seq. No.	273417
Contig ID	43634_1.R1011
5'-most EST	LIB143-005-Q1-E1-G2
Method	BLASTX
NCBI GI	g4510389
BLAST score	758
E value	1.0e-80
Match length	202
% identity	73
NCBI Description	(AC007017) putative solute carrier protein [Arabidopsis thaliana]

Seq. No.	273418
Contig ID	43635_1.R1011
5'-most EST	LIB143-005-Q1-E1-G6

Seq. No.	273419
Contig ID	43636_1.R1011
5'-most EST	xjt700096970.h1
Method	BLASTX
NCBI GI	g3600032
BLAST score	727
E value	7.0e-77
Match length	279
% identity	52
NCBI Description	(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	273420
Contig ID	43649_1.R1011
5'-most EST	uC-zmflmo17238a06b1

Seq. No.	273421
Contig ID	43652_2.R1011
5'-most EST	ypc700805878.h1

Seq. No.	273422
Contig ID	43669_1.R1011
5'-most EST	hvj700620908.h1
Method	BLASTX
NCBI GI	g2507455
BLAST score	1880
E value	0.0e+00
Match length	429
% identity	83
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	273423
Contig ID	43669_2.R1011
5'-most EST	LIB143-006-Q1-E1-C2
Method	BLASTX
NCBI GI	g2507455
BLAST score	467
E value	1.0e-46
Match length	117
% identity	76
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	273424
Contig ID	43674_1.R1011
5'-most EST	LIB3117-012-Q1-K1-H3
Method	BLASTX
NCBI GI	g4566505
BLAST score	858
E value	2.0e-92
Match length	205
% identity	82
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	273425
Contig ID	43679_1.R1011
5'-most EST	uC-zmflmo17309b12b1

Seq. No.	273426
Contig ID	43682_1.R1011
5'-most EST	uC-zmroB73020e06b1
Method	BLASTX
NCBI GI	g1076414
BLAST score	822
E value	1.0e-104
Match length	301
% identity	65
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis

thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	273427
Contig ID	43683_1.R1011
5'-most EST	mwy700439775.h1
Method	BLASTX
NCBI GI	g3044212
BLAST score	1384
E value	1.0e-154
Match length	305
% identity	84
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	273428
Contig ID	43684_1.R1011
5'-most EST	LIB189-011-Q1-E1-G4
Method	BLASTX
NCBI GI	g4432839
BLAST score	150
E value	5.0e-09
Match length	76
% identity	42
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	273429
Contig ID	43684_3.R1011
5'-most EST	hbs701182456.h1

Seq. No.	273430
Contig ID	43688_1.R1011
5'-most EST	uC-zmflmo17294g03b1
Method	BLASTX
NCBI GI	g2828279
BLAST score	440
E value	2.0e-43
Match length	109
% identity	73
NCBI Description	(AL021687) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273431
Contig ID	43690_1.R1011
5'-most EST	LIB3068-023-Q1-K1-E6
Method	BLASTX
NCBI GI	g3252813
BLAST score	823
E value	7.0e-90
Match length	202
% identity	73
NCBI Description	(AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi_3810586 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No.	273432
Contig ID	43702_1.R1011
5'-most EST	uC-zmflmo17292e09b1
Method	BLASTX

NCBI GI	g3445416
BLAST score	599
E value	5.0e-67
Match length	181
% identity	74
NCBI Description	(Y11154) DEAD box-like RNA helicase [Arabidopsis thaliana]

Seq. No.	273433
Contig ID	43702_2.R1011
5'-most EST	pmx700088184.h1
Method	BLASTX
NCBI GI	g3445416
BLAST score	203
E value	9.0e-16
Match length	75
% identity	57
NCBI Description	(Y11154) DEAD box-like RNA helicase [Arabidopsis thaliana]

Seq. No.	273434
Contig ID	43711_1.R1011
5'-most EST	yyf700351914.h1
Method	BLASTX
NCBI GI	g2959781
BLAST score	1576
E value	1.0e-176
Match length	337
% identity	88
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	273435
Contig ID	43727_1.R1011
5'-most EST	LIB143-044-Q1-E1-G7
Method	BLASTX
NCBI GI	g232282
BLAST score	165
E value	5.0e-17
Match length	84
% identity	54
NCBI Description	22.0 KD CLASS IV HEAT SHOCK PROTEIN PRECURSOR >gi_477760_pir__B48113 heat shock protein HSP22.0 - soybean >gi_18661_emb_CAA44882_ (X63198) heat shock protein [Glycine max]

Seq. No.	273436
Contig ID	43727_2.R1011
5'-most EST	LIB3061-052-Q1-K1-C11
Method	BLASTX
NCBI GI	g232282
BLAST score	247
E value	5.0e-21
Match length	66
% identity	64
NCBI Description	22.0 KD CLASS IV HEAT SHOCK PROTEIN PRECURSOR >gi_477760_pir__B48113 heat shock protein HSP22.0 - soybean >gi_18661_emb_CAA44882_ (X63198) heat shock protein [Glycine max]

Seq. No.	273437
Contig ID	43735_1.R1011
5'-most EST	LIB143-026-Q1-E1-H12
Method	BLASTN
NCBI GI	g4416300
BLAST score	298
E value	1.0e-167
Match length	358
% identity	43
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	273438
Contig ID	43740_1.R1011
5'-most EST	LIB143-011-Q1-E1-B7
Method	BLASTX
NCBI GI	g3941528
BLAST score	539
E value	3.0e-55
Match length	106
% identity	86
NCBI Description	(AF062918) putative transcription factor [Arabidopsis thaliana]

Seq. No.	273439
Contig ID	43740_2.R1011
5'-most EST	uC-zmflb73001f02b1
Method	BLASTX
NCBI GI	g3941482
BLAST score	250
E value	2.0e-21
Match length	46
% identity	85
NCBI Description	(AF062895) putative transcription factor [Arabidopsis thaliana]

Seq. No.	273440
Contig ID	43745_1.R1011
5'-most EST	nbm700477369.h1

Seq. No.	273441
Contig ID	43764_1.R1011
5'-most EST	uC-zmflb73003e12b1
Method	BLASTX
NCBI GI	g4581150
BLAST score	523
E value	1.0e-110
Match length	395
% identity	42
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273442
Contig ID	43775_1.R1011
5'-most EST	tzu700203684.h1
Method	BLASTX
NCBI GI	g1352057
BLAST score	153

E value	1.0e-09
Match length	56
% identity	59
NCBI Description	AUXIN-INDUCED PROTEIN IAA4 >gi_629633_pir__S39075 auxin-induced protein - garden pea >gi_414181_emb_CAA48297_ (X68215) auxin-induced protein [Pisum sativum]

Seq. No.	273443
Contig ID	43775_2.R1011
5'-most EST	LIB3068-035-Q1-K1-C11
Method	BLASTX
NCBI GI	g452777
BLAST score	215
E value	5.0e-17
Match length	160
% identity	35
NCBI Description	(X68216) auxin-induced protein [Pisum sativum]

Seq. No.	273444
Contig ID	43777_1.R1011
5'-most EST	fdz701161434.h1
Method	BLASTX
NCBI GI	g548702
BLAST score	320
E value	2.0e-29
Match length	123
% identity	45
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9) (RPB14.5) >gi_543001_pir__S41621 DNA-directed RNA polymerase (EC 2.7.7.6) II 14.5K chain - human >gi_397150_emb_CAA80649_ (Z23102) RNA Polymerase II subunit 14.5 kD [Homo sapiens] >gi_1905901 (AD001527) HUMAN DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo sapiens]

Seq. No.	273445
Contig ID	43778_1.R1011
5'-most EST	LIB3136-019-Q1-K1-F5

Seq. No.	273446
Contig ID	43780_1.R1011
5'-most EST	LIB143-011-Q1-E1-F3

Seq. No.	273447
Contig ID	43780_2.R1011
5'-most EST	LIB3068-019-Q1-K1-H6

Seq. No.	273448
Contig ID	43781_1.R1011
5'-most EST	uC-zmflb73051d12b1
Method	BLASTX
NCBI GI	g3004565
BLAST score	907
E value	8.0e-98
Match length	336
% identity	54
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	273449
Contig ID	43786_1.R1011
5'-most EST	mwy700438577.h1
Method	BLASTX
NCBI GI	g3522946
BLAST score	264
E value	5.0e-23
Match length	93
% identity	51
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	273450
Contig ID	43805_1.R1011
5'-most EST	LIB143-012-Q1-E1-A11
Method	BLASTX
NCBI GI	g3024541
BLAST score	195
E value	2.0e-14
Match length	297
% identity	10
NCBI Description	RESTIN >gi_2338714 (AF014012) restin [Gallus gallus]

Seq. No.	273451
Contig ID	43807_1.R1011
5'-most EST	LIB143-012-Q1-E1-A2

Seq. No.	273452
Contig ID	43814_1.R1011
5'-most EST	LIB143-012-Q1-E1-B11

Seq. No.	273453
Contig ID	43814_2.R1011
5'-most EST	LIB3136-051-Q1-K1-G9

Seq. No.	273454
Contig ID	43814_3.R1011
5'-most EST	tfd700569694.h1

Seq. No.	273455
Contig ID	43820_1.R1011
5'-most EST	LIB143-064-Q1-E1-E11

Seq. No.	273456
Contig ID	43820_2.R1011
5'-most EST	LIB143-034-Q1-E1-D6

Seq. No.	273457
Contig ID	43823_1.R1011
5'-most EST	LIB143-012-Q1-E1-C1
Method	BLASTX
NCBI GI	g1084461
BLAST score	347
E value	2.0e-32
Match length	80
% identity	81
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	273458
Contig ID	43824_1.R1011
5'-most EST	LIB143-012-Q1-E1-C10

Seq. No.	273459
Contig ID	43830_1.R1011
5'-most EST	LIB143-060-Q1-E1-D9
Method	BLASTX
NCBI GI	g2132293
BLAST score	177
E value	4.0e-12
Match length	313
% identity	22
NCBI Description	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae) >gi_1066487 (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae]

Seq. No.	273460
Contig ID	43830_2.R1011
5'-most EST	LIB3117-008-Q1-K1-C6

Seq. No.	273461
Contig ID	43835_1.R1011
5'-most EST	LIB143-012-Q1-E1-D4
Method	BLASTX
NCBI GI	g2586083
BLAST score	210
E value	1.0e-16
Match length	80
% identity	56
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	273462
Contig ID	43838_1.R1011
5'-most EST	LIB143-012-Q1-E1-D8
Method	BLASTX
NCBI GI	g3157951
BLAST score	671
E value	1.0e-96
Match length	218
% identity	86
NCBI Description	(AC002131) Contains similarity to vesicle trafficking protein gb_U91538 from Mus musculus. ESTs gb_F15494 and gb_F14097 come from this gene. [Arabidopsis thaliana]

Seq. No.	273463
Contig ID	43840_1.R1011
5'-most EST	uC-zmflmo170112e06b1
Method	BLASTX
NCBI GI	g2914710
BLAST score	963
E value	1.0e-104
Match length	216

% identity	75
NCBI Description	(AC003974) putative beta-D-galactosidase [Arabidopsis thaliana]

Seq. No.	273464
Contig ID	43844_1.R1011
5'-most EST	LIB189-012-Q1-E1-G8
Method	BLASTX
NCBI GI	g632148
BLAST score	205
E value	8.0e-16
Match length	189
% identity	33
NCBI Description	narbonin - Vicia narbonensis >gi_1364114_pir__S56697 narbonin (clone pNaF6) - Vicia narbonensis >gi_396823_emb_CAA80983_ (Z25536) narbonin [Vicia narbonensis]

Seq. No.	273465
Contig ID	43850_1.R1011
5'-most EST	LIB3060-024-Q1-K1-B7

Seq. No.	273466
Contig ID	43861_1.R1011
5'-most EST	xjt700096308.h1
Method	BLASTX
NCBI GI	g4539470
BLAST score	283
E value	5.0e-25
Match length	89
% identity	61
NCBI Description	(AL049500) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273467
Contig ID	43869_1.R1011
5'-most EST	nbm700471023.h1
Method	BLASTX
NCBI GI	g4567283
BLAST score	484
E value	3.0e-48
Match length	180
% identity	53
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	273468
Contig ID	43880_1.R1011
5'-most EST	LIB3069-039-Q1-K1-F8
Method	BLASTX
NCBI GI	g2344901
BLAST score	1030
E value	1.0e-112
Match length	244
% identity	84
NCBI Description	(AC002388) serine/threonine protein kinase isolog [Arabidopsis thaliana]

Seq. No.	273469

Contig ID	43885_1.R1011
5'-most EST	hvj700619247.h1
Method	BLASTX
NCBI GI	g1353193
BLAST score	665
E value	2.0e-69
Match length	316
% identity	45
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	273470
Contig ID	43885_2.R1011
5'-most EST	ntr700073260.h1
Method	BLASTX
NCBI GI	g4098238
BLAST score	257
E value	3.0e-22
Match length	122
% identity	48
NCBI Description	(U76384) o-methyltransferase [Triticum aestivum]

Seq. No.	273471
Contig ID	43891_1.R1011
5'-most EST	LIB143-013-Q1-E1-B10
Method	BLASTX
NCBI GI	g550438
BLAST score	510
E value	8.0e-52
Match length	126
% identity	85
NCBI Description	(X81829) cytochrome P450 [Zea mays] >gi_1870201_emb_CAA72208_ (Y11404) cytochrome p450 [Zea mays]

Seq. No.	273472
Contig ID	43892_1.R1011
5'-most EST	LIB143-013-Q1-E1-B11
Method	BLASTX
NCBI GI	g1526424
BLAST score	217
E value	3.0e-17
Match length	156
% identity	11
NCBI Description	(D64140) LEA protein in group 3 [Arabidopsis thaliana]

Seq. No.	273473
Contig ID	43896_1.R1011
5'-most EST	LIB143-013-Q1-E1-B4
Method	BLASTX
NCBI GI	g1346487
BLAST score	900
E value	3.0e-97
Match length	195
% identity	91
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_532625 (L35914) malate

synthase [Zea mays]

Seq. No.	273474
Contig ID	43899_1.R1011
5'-most EST	uwc700155052.h1

Seq. No.	273475
Contig ID	43902_1.R1011
5'-most EST	LIB143-013-Q1-E1-C11
Method	BLASTX
NCBI GI	g2467272
BLAST score	294
E value	2.0e-26
Match length	166
% identity	42
NCBI Description	(Z99759) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	273476
Contig ID	43910_1.R1011
5'-most EST	LIB143-013-Q1-E1-D11
Method	BLASTX
NCBI GI	g3128210
BLAST score	501
E value	2.0e-50
Match length	136
% identity	67
NCBI Description	(AC004077) putative cytochrome P450 protein [Arabidopsis thaliana] >gi_3337378 (AC004481) putative cytochrome P450 protein [Arabidopsis thaliana]

Seq. No.	273477
Contig ID	43912_1.R1011
5'-most EST	LIB143-013-Q1-E1-D2

Seq. No.	273478
Contig ID	43914_1.R1011
5'-most EST	uC-zmflB73004d08b1

Seq. No.	273479
Contig ID	43919_1.R1011
5'-most EST	uC-zmflb73199f01b1

Seq. No.	273480
Contig ID	43919_2.R1011
5'-most EST	uC-zmflmo17035d04b1
Method	BLASTX
NCBI GI	g3877580
BLAST score	184
E value	4.0e-13
Match length	136
% identity	39
NCBI Description	(Z67755) F54F7.1 [Caenorhabditis elegans]

Seq. No.	273481
Contig ID	43921_1.R1011
5'-most EST	gct701180666.h1

Seq. No.	273482
Contig ID	43923_1.R1011
5'-most EST	LIB143-013-Q1-E1-E2
Method	BLASTN
NCBI GI	g169800
BLAST score	52
E value	2.0e-20
Match length	56
% identity	98
NCBI Description	Oryza sativa LMW heat shock protein mRNA, complete CDS

Seq. No.	273483
Contig ID	43925_1.R1011
5'-most EST	LIB143-013-Q1-E1-E4
Method	BLASTX
NCBI GI	g4249391
BLAST score	342
E value	4.0e-32
Match length	96
% identity	65
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	273484
Contig ID	43930_1.R1011
5'-most EST	fwa700097691.h1
Method	BLASTX
NCBI GI	g2262105
BLAST score	855
E value	7.0e-92
Match length	321
% identity	51
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	273485
Contig ID	43935_1.R1011
5'-most EST	LIB3059-001-Q1-K2-G8
Method	BLASTX
NCBI GI	g1170092
BLAST score	1156
E value	1.0e-127
Match length	223
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI) >gi_1076807_pir__S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_ (X79515) glutathione transferase [Zea mays] >gi_1094866_prf__2106424A glutathione S-transferase:ISOTYPE=IV [Zea mays]

Seq. No.	273486
Contig ID	43935_3.R1011
5'-most EST	LIB143-024-Q1-E1-A7
Method	BLASTX
NCBI GI	g1170092

BLAST score	282
E value	8.0e-25
Match length	55
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI) >gi_1076807_pir__S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_ (X79515) glutathione transferase [Zea mays] >gi_1094866_prf__2106424A glutathione S-transferase:ISOTYPE=IV [Zea mays]

Seq. No.	273487
Contig ID	43939_1.R1011
5'-most EST	xmt700261176.h1
Method	BLASTX
NCBI GI	g399064
BLAST score	555
E value	4.0e-57
Match length	134
% identity	80
NCBI Description	ASPARAGINE SYNTHASE (GLUTAMINE-HYDROLYZING) (AS) >gi_100980_pir__S25165 asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - garden asparagus >gi_16076_emb_CAA48141_ (X67958) asparagine synthase (glutamine-hydrolysing) [Asparagus officinalis]

Seq. No.	273488
Contig ID	43942_1.R1011
5'-most EST	wyr700243723.h1

Seq. No.	273489
Contig ID	43959_1.R1011
5'-most EST	LIB143-013-Q1-E1-H6
Method	BLASTX
NCBI GI	g2995951
BLAST score	151
E value	1.0e-09
Match length	45
% identity	64
NCBI Description	(AF053564) auxin-induced protein [Mesembryanthemum crystallinum]

Seq. No.	273490
Contig ID	43960_1.R1011
5'-most EST	xsy700209528.h1
Method	BLASTX
NCBI GI	g4388726
BLAST score	1048
E value	1.0e-137
Match length	353
% identity	70
NCBI Description	(AC006413) putative 12-oxophytodienoate-10,11-reductase [Arabidopsis thaliana]

Seq. No.	273491
Contig ID	43964_1.R1011

5'-most EST	uC-zmflb73022d01b1
Method	BLASTX
NCBI GI	g3695388
BLAST score	213
E value	9.0e-17
Match length	92
% identity	45
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	273492
Contig ID	43965_1.R1011
5'-most EST	wty700168731.h1
Method	BLASTX
NCBI GI	g1665817
BLAST score	324
E value	1.0e-29
Match length	192
% identity	37
NCBI Description	(D87466) Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]

Seq. No.	273493
Contig ID	43965_2.R1011
5'-most EST	LIB3069-039-Q1-K1-H10

Seq. No.	273494
Contig ID	43979_1.R1011
5'-most EST	uC-zmflb73255d11b1
Method	BLASTX
NCBI GI	g2827536
BLAST score	363
E value	5.0e-34
Match length	151
% identity	43
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273495
Contig ID	43979_2.R1011
5'-most EST	xdb700337580.h1

Seq. No.	273496
Contig ID	43979_3.R1011
5'-most EST	xmt700259629.h1

Seq. No.	273497
Contig ID	43984_1.R1011
5'-most EST	LIB143-014-Q1-E1-E2

Seq. No.	273498
Contig ID	43989_1.R1011
5'-most EST	uC-zmflmo17202d01b1
Method	BLASTX
NCBI GI	g3757682
BLAST score	519
E value	9.0e-53
Match length	148
% identity	70

NCBI Description	(Y18212) glucan endo-1,3-beta-D-glucosidase [Triticum aestivum]

Seq. No.	273499
Contig ID	44000_1.R1011
5'-most EST	LIB143-054-Q1-E1-E3

Seq. No.	273500
Contig ID	44004_1.R1011
5'-most EST	LIB143-014-Q1-E1-E4

Seq. No.	273501
Contig ID	44006_1.R1011
5'-most EST	uC-zmroteosinte116b04b2
Method	BLASTX
NCBI GI	g542185
BLAST score	325
E value	9.0e-45
Match length	109
% identity	55
NCBI Description	group 3 Lea protein MGL3 - maize >gi_452560 (U05226) group 3 Lea protein MGL3 [Zea mays] >gi_454873_dbj_BAA05550_ (D26552) group 3 Lea protein MGL3 [Zea mays] >gi_2654379_emb_CAA82632.1_ (Z29512) Group 3 Lea protein MGL3 [Zea mays]

Seq. No.	273502
Contig ID	44006_3.R1011
5'-most EST	LIB143-014-Q1-E1-E7
Method	BLASTX
NCBI GI	g542185
BLAST score	625
E value	7.0e-65
Match length	195
% identity	72
NCBI Description	group 3 Lea protein MGL3 - maize >gi_452560 (U05226) group 3 Lea protein MGL3 [Zea mays] >gi_454873_dbj_BAA05550_ (D26552) group 3 Lea protein MGL3 [Zea mays] >gi_2654379_emb_CAA82632.1_ (Z29512) Group 3 Lea protein MGL3 [Zea mays]

Seq. No.	273503
Contig ID	44010_1.R1011
5'-most EST	fdz701166753.h1
Method	BLASTX
NCBI GI	g266944
BLAST score	628
E value	1.0e-65
Match length	124
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2) >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic - tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein L2 [Lycopersicon esculentum]

Seq. No.	273504
Contig ID	44012_1.R1011

5'-most EST	LIB143-014-Q1-E1-F2
Seq. No.	273505
Contig ID	44013_1.R1011
5'-most EST	LIB143-014-Q1-E1-F5
Method	BLASTX
NCBI GI	g2459426
BLAST score	355
E value	1.0e-33
Match length	124
% identity	58
NCBI Description	(AC002332) putative splicing factor U2AF large chain [Arabidopsis thaliana]
Seq. No.	273506
Contig ID	44043_1.R1011
5'-most EST	xtj700378215.h1
Seq. No.	273507
Contig ID	44044_1.R1011
5'-most EST	yyf700347785.h1
Method	BLASTN
NCBI GI	g3850998
BLAST score	34
E value	3.0e-09
Match length	58
% identity	90
NCBI Description	Zea mays pyruvate dehydrogenase E1 beta subunit isoform 1 mRNA, nuclear gene encoding mitochondrial protein, complete cds
Seq. No.	273508
Contig ID	44044_2.R1011
5'-most EST	kem700611724.h1
Seq. No.	273509
Contig ID	44044_3.R1011
5'-most EST	wty700170849.h1
Seq. No.	273510
Contig ID	44055_1.R1011
5'-most EST	uC-zmflb73032a12b1
Method	BLASTX
NCBI GI	g139780
BLAST score	154
E value	9.0e-10
Match length	87
% identity	45
NCBI Description	WOUND-INDUCED PROTEIN 1 >gi_82293_pir__JQ0398 wun1 protein - potato
Seq. No.	273511
Contig ID	44060_1.R1011
5'-most EST	LIB3137-012-Q1-K1-F3
Method	BLASTX
NCBI GI	g2462826
BLAST score	253

E value	2.0e-21
Match length	183
% identity	31
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	273512
Contig ID	44062_1.R1011
5'-most EST	wty700172132.h1
Method	BLASTX
NCBI GI	g3850571
BLAST score	449
E value	3.0e-44
Match length	92
% identity	93
NCBI Description	(AC005278) Similar to gb_U85207 snRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb_AA612141 comes from this gene. [Arabidopsis thaliana]

Seq. No.	273513
Contig ID	44064_1.R1011
5'-most EST	LIB143-015-Q1-E1-C11

Seq. No.	273514
Contig ID	44066_1.R1011
5'-most EST	LIB143-015-Q1-E1-C2
Method	BLASTX
NCBI GI	g4104058
BLAST score	229
E value	1.0e-18
Match length	120
% identity	37
NCBI Description	(AF031195) blue copper-binding protein homolog [Triticum aestivum]

Seq. No.	273515
Contig ID	44077_1.R1011
5'-most EST	xjt700095757.h1

Seq. No.	273516
Contig ID	44078_1.R1011
5'-most EST	uC-zmf1b73196d09b1
Method	BLASTX
NCBI GI	g3386604
BLAST score	649
E value	8.0e-68
Match length	269
% identity	50
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	273517
Contig ID	44082_1.R1011
5'-most EST	LIB143-015-Q1-E1-D8
Method	BLASTX
NCBI GI	g4506043
BLAST score	193
E value	1.0e-14
Match length	83

% identity	42
NCBI Description	prolyl endopeptidase >gi_1346769_sp_P48147_PPCE_HUMAN PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase [Homo sapiens]

Seq. No.	273518
Contig ID	44087_1.R1011
5'-most EST	pmx700088968.h1
Method	BLASTX
NCBI GI	g4006848
BLAST score	306
E value	6.0e-28
Match length	100
% identity	58
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	273519
Contig ID	44088_1.R1011
5'-most EST	LIB143-015-Q1-E1-E2
Method	BLASTX
NCBI GI	g728863
BLAST score	611
E value	9.0e-64
Match length	121
% identity	99
NCBI Description	LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN HYDROXYLASE) >gi_100871_pir__S12043 gene A2 protein - maize >gi_22104_emb_CAA39022_ (X55314) A2 [Zea mays]

Seq. No.	273520
Contig ID	44099_1.R1011
5'-most EST	xay700053567.r1
Method	BLASTX
NCBI GI	g169799
BLAST score	313
E value	1.0e-28
Match length	120
% identity	55
NCBI Description	(M80939) 16.9 kDa heat shock protein [Oryza sativa] >gi_445140_prf__1908439B heat shock protein 16.9B [Oryza sativa]

Seq. No.	273521
Contig ID	44104_1.R1011
5'-most EST	wyr700242574.h1
Method	BLASTX
NCBI GI	g416650
BLAST score	349
E value	8.0e-37
Match length	154
% identity	55
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT35/PCNT111) >gi_100304_pir__S16268 auxin-induced protein (clone pGNT35) - common tobacco

>gi_19797_emb_CAA39706_ (X56265) auxin-induced protein [Nicotiana tabacum] >gi_19801_emb_CAA39710_ (X56269) auxin-induced protein [Nicotiana tabacum]

Seq. No.	273522
Contig ID	44110_1.R1011
5'-most EST	LIB143-015-Q1-E1-G5

Seq. No.	273523
Contig ID	44116_1.R1011
5'-most EST	LIB143-015-Q1-E1-H10

Seq. No.	273524
Contig ID	44117_1.R1011
5'-most EST	fC-zmle700446876f7
Method	BLASTX
NCBI GI	g1150406
BLAST score	333
E value	2.0e-30
Match length	174
% identity	43
NCBI Description	(Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan glucanohydrolase [Pichia angusta]

Seq. No.	273525
Contig ID	44121_1.R1011
5'-most EST	LIB143-015-Q1-E1-H4
Method	BLASTX
NCBI GI	g550452
BLAST score	1351
E value	1.0e-149
Match length	549
% identity	47
NCBI Description	(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]

Seq. No.	273526
Contig ID	44121_2.R1011
5'-most EST	uC-zmflMo17007d09b1
Method	BLASTX
NCBI GI	g4587569
BLAST score	771
E value	4.0e-82
Match length	190
% identity	78
NCBI Description	(AC006550) Identical to gb_U12536 3-methylcrotonyl-CoA carboxylase precursor protein from Arabidopsis thaliana. ESTs gb_H35836, gb_AA651295 and gb_AA721862 come from this gene

Seq. No.	273527
Contig ID	44121_3.R1011
5'-most EST	uC-zmflmo17184f07b1
Method	BLASTX
NCBI GI	g4587569
BLAST score	458
E value	1.0e-57

Match length	137
% identity	84
NCBI Description	(AC006550) Identical to gb_U12536 3-methylcrotonyl-CoA carboxylase precursor protein from Arabidopsis thaliana. ESTs gb_H35836, gb_AA651295 and gb_AA721862 come from this gene

Seq. No.	273528
Contig ID	44125_1.R1011
5'-most EST	LIB143-015-Q1-E1-H8
Method	BLASTX
NCBI GI	g1575709
BLAST score	221
E value	9.0e-18
Match length	76
% identity	46
NCBI Description	(U70479) no arches [Danio rerio]

Seq. No.	273529
Contig ID	44129_1.R1011
5'-most EST	fwa700100013.h1

Seq. No.	273530
Contig ID	44130_1.R1011
5'-most EST	tzu700203456.h1
Method	BLASTN
NCBI GI	g517492
BLAST score	51
E value	1.0e-19
Match length	248
% identity	78
NCBI Description	Z.Mays Zm38 gene, intron

Seq. No.	273531
Contig ID	44140_1.R1011
5'-most EST	uwc700150827.h1
Method	BLASTX
NCBI GI	g3080402
BLAST score	545
E value	8.0e-56
Match length	176
% identity	64
NCBI Description	(AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_ (AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]

Seq. No.	273532
Contig ID	44152_1.R1011
5'-most EST	LIB143-016-Q1-E1-C5
Method	BLASTX
NCBI GI	g2980806
BLAST score	376
E value	7.0e-36
Match length	132
% identity	58
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	273533
Contig ID	44156_1.R1011
5'-most EST	LIB3136-046-Q1-K1-B12

Seq. No.	273534
Contig ID	44162_2.R1011
5'-most EST	pmx700085778.h1

Seq. No.	273535
Contig ID	44163_1.R1011
5'-most EST	uC-zmflmo17221a04b1
Method	BLASTX
NCBI GI	g4056425
BLAST score	688
E value	2.0e-72
Match length	158
% identity	77
NCBI Description	(AC005322) ESTs gb_H36249, gb_AA59732 and gb_AA651219 come from this gene. [Arabidopsis thaliana]

Seq. No.	273536
Contig ID	44165_1.R1011
5'-most EST	LIB143-016-Q1-E1-E11
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	273537
Contig ID	44172_1.R1011
5'-most EST	uwc700150622.h1
Method	BLASTX
NCBI GI	g1865677
BLAST score	510
E value	2.0e-51
Match length	215
% identity	51
NCBI Description	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	273538
Contig ID	44175_1.R1011
5'-most EST	uC-zmflMo17007f02b1
Method	BLASTX
NCBI GI	g3023651
BLAST score	215
E value	5.0e-17
Match length	112
% identity	39
NCBI Description	D-LACTATE DEHYDROGENASE [CYTOCHROME] PRECURSOR (D-LACTATE FERRICYTOCHROME C OXIDOREDUCTASE) (D-LCR) >gi_1076962_pir__S51528 D-lactate dehydrogenase (cytochrome) (EC 1.1.2.4) - yeast (Kluyveromyces marxianus

var. lactis) >gi_602029_emb_CAA50635_ (X71628) D-lactate dehydrogenase (cytochrome) [Kluyveromyces lactis].

Seq. No.	273539
Contig ID	44175_2.R1011
5'-most EST	uC-zmflMo17084a02b1

Seq. No.	273540
Contig ID	44195_1.R1011
5'-most EST	clt70041569.f1
Method	BLASTX
NCBI GI	g2119076
BLAST score	183
E value	7.0e-25
Match length	105
% identity	59
NCBI Description	ribosomal protein S10 - potato mitochondrion

Seq. No.	273541
Contig ID	44202_1.R1011
5'-most EST	LIB143-017-Q1-E1-A2
Method	BLASTX
NCBI GI	g2920839
BLAST score	457
E value	1.0e-45
Match length	115
% identity	73
NCBI Description	(U95136) Os-FIERG2 gene product [Oryza sativa]

Seq. No.	273542
Contig ID	44210_1.R1011
5'-most EST	LIB143-017-Q1-E1-A6

Seq. No.	273543
Contig ID	44230_1.R1011
5'-most EST	LIB3067-009-Q1-K1-D2
Method	BLASTX
NCBI GI	g3915095
BLAST score	1754
E value	0.0e+00
Match length	474
% identity	74
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi_1526537_dbj_BAA13414_ (D87520) cytochrome P450 (CYP73A14) [Glycyrrhiza echinata]

Seq. No.	273544
Contig ID	44230_2.R1011
5'-most EST	uC-zmflmo17126d02b1
Method	BLASTX
NCBI GI	g3915111
BLAST score	385
E value	5.0e-37
Match length	102
% identity	75
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
>gi_1044868_emb_CAA63172_ (X92437) cinnamic acid
4-hydroxylase [Glycine max]

Seq. No.	273545
Contig ID	44230_3.R1011
5'-most EST	uC-zmrob73024g06a1

Seq. No.	273546
Contig ID	44230_6.R1011
5'-most EST	wty700164388.h1
Method	BLASTN
NCBI GI	g3819564
BLAST score	43
E value	5.0e-15
Match length	90
% identity	88
NCBI Description	Hordeum vulgare genomic DNA fragment; clone MWG2112.uni

Seq. No.	273547
Contig ID	44269_1.R1011
5'-most EST	LIB143-017-Q1-E1-G7
Method	BLASTX
NCBI GI	g2766452
BLAST score	506
E value	4.0e-51
Match length	171
% identity	53
NCBI Description	(AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]

Seq. No.	273548
Contig ID	44272_1.R1011
5'-most EST	LIB143-017-Q1-E1-H1
Method	BLASTX
NCBI GI	g3769671
BLAST score	465
E value	1.0e-46
Match length	126
% identity	70
NCBI Description	(AF095284) Tic22 [Pisum sativum]

Seq. No.	273549
Contig ID	44276_1.R1011
5'-most EST	LIB143-017-Q1-E1-H3
Method	BLASTX
NCBI GI	g4454481
BLAST score	197
E value	1.0e-23
Match length	213
% identity	44
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana] >gi_4512647_gb_AAD21702.1_ (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	273550
Contig ID	44276_2.R1011
5'-most EST	LIB83-016-Q1-E1-D6

Method	BLASTX
NCBI GI	g4049350
BLAST score	503
E value	1.0e-50
Match length	187
% identity	50
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	273551
Contig ID	44277_1.R1011
5'-most EST	uC-zmflb73092g12b2

Seq. No.	273552
Contig ID	44284_1.R1011
5'-most EST	LIB143-018-Q1-E1-A10
Method	BLASTX
NCBI GI	g401237
BLAST score	1111
E value	1.0e-122
Match length	242
% identity	86
NCBI Description	UBIQUITIN-ACTIVATING ENZYME E1 2 >gi_170684 (M90663) ubiquitin activating enyme [Triticum aestivum]

Seq. No.	273553
Contig ID	44297_3.R1011
5'-most EST	fdz70l158645.h1

Seq. No.	273554
Contig ID	44297_4.R1011
5'-most EST	zuv70o355964.h1

Seq. No.	273555
Contig ID	44300_1.R1011
5'-most EST	LIB143-018-Q1-E1-F1
Method	BLASTX
NCBI GI	g4468798
BLAST score	725
E value	2.0e-80
Match length	159
% identity	91
NCBI Description	(AJ010440) GST7 protein [Zea mays]

Seq. No.	273556
Contig ID	44301_1.R1011
5'-most EST	LIB143-018-Q1-E1-B6
Method	BLASTX
NCBI GI	g3831463
BLAST score	224
E value	2.0e-18
Match length	60
% identity	65
NCBI Description	(AC005700) unknown protein [Arabidopsis thaliana]

Seq. No.	273557
Contig ID	44313_1.R1011
5'-most EST	uC-zmflb73069a06b1

Method	BLASTX
NCBI GI	g4056615
BLAST score	1048
E value	1.0e-114
Match length	262
% identity	75
NCBI Description	(AF067401) Scl1 protein [Oryza sativa]

Seq. No.	273558
Contig ID	44319_1.R1011
5'-most EST	uC-zmroteosinte016d02b1
Method	BLASTX
NCBI GI	g4512702
BLAST score	1365
E value	1.0e-151
Match length	335
% identity	73
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273559
Contig ID	44326_1.R1011
5'-most EST	LIB84-006-Q1-E1-E11

Seq. No.	273560
Contig ID	44330_1.R1011
5'-most EST	LIB143-035-Q1-E1-C5
Method	BLASTX
NCBI GI	g464986
BLAST score	495
E value	4.0e-50
Match length	113
% identity	80
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	273561
Contig ID	44338_1.R1011
5'-most EST	LIB3067-045-Q1-K1-B5
Method	BLASTX
NCBI GI	g3264767
BLAST score	265
E value	1.0e-22
Match length	66
% identity	73
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	273562
Contig ID	44347_1.R1011

5'-most EST	uC-zmflmo17259f03b1
Seq. No.	273563
Contig ID	44361_1.R1011
5'-most EST	uC-zmflb73144c05b1
Seq. No.	273564
Contig ID	44362_1.R1011
5'-most EST	LIB1443-018-Q1-E1-H8
Method	BLASTX
NCBI GI	g2062167
BLAST score	151
E value	1.0e-09
Match length	61
% identity	54
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
Seq. No.	273565
Contig ID	44363_1.R1011
5'-most EST	LIB3068-022-Q1-K1-F1
Method	BLASTX
NCBI GI	g2655098
BLAST score	415
E value	1.0e-40
Match length	91
% identity	82
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]
Seq. No.	273566
Contig ID	44363_3.R1011
5'-most EST	uC-zmflmo17033a07a1
Seq. No.	273567
Contig ID	44375_1.R1011
5'-most EST	yyf700349334.h1
Method	BLASTX
NCBI GI	g4538905
BLAST score	732
E value	1.0e-77
Match length	188
% identity	71
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]
Seq. No.	273568
Contig ID	44381_1.R1011
5'-most EST	uC-zmflm017025f01b1
Method	BLASTX
NCBI GI	g1617274
BLAST score	784
E value	1.0e-83
Match length	206
% identity	67
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]
Seq. No.	273569
Contig ID	44385_1.R1011

5'-most EST	LIB143-019-Q1-E1-C10
Method	BLASTX
NCBI GI	g3236240
BLAST score	158
E value	1.0e-10
Match length	47
% identity	68
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	273570
Contig ID	44403_1.R1011
5'-most EST	uC-zmroteosinte014f12b1
Method	BLASTX
NCBI GI	g2288999
BLAST score	820
E value	8.0e-88
Match length	187
% identity	74
NCBI Description	(AC002335) electron transfer flavoprotein ubiquinone oxidoreductase isolog [Arabidopsis thaliana]

Seq. No.	273571
Contig ID	44409_1.R1011
5'-most EST	uC-zmflb73091g01b2

Seq. No.	273572
Contig ID	44409_2.R1011
5'-most EST	uC-zmflmo17330g07b1
Method	BLASTX
NCBI GI	g4185133
BLAST score	152
E value	1.0e-09
Match length	89
% identity	43
NCBI Description	(AC005724) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	273573
Contig ID	44417_2.R1011
5'-most EST	LIB143-019-Q1-E1-E8

Seq. No.	273574
Contig ID	44418_1.R1011
5'-most EST	LIB143-019-Q1-E1-E9
Method	BLASTX
NCBI GI	g1418331
BLAST score	370
E value	7.0e-39
Match length	186
% identity	52
NCBI Description	(X95909) receptor like protein kinase [Arabidopsis thaliana]

Seq. No.	273575
Contig ID	44420_1.R1011
5'-most EST	LIB143-021-Q1-E1-D8

Seq. No.	273576
Contig ID	44426_1.R1011
5'-most EST	tfd700572740.h1
Method	BLASTX
NCBI GI	g282995
BLAST score	566
E value	3.0e-58
Match length	183
% identity	67
NCBI Description	seed protein B32E - barley (fragment) >gi_1345530_emb_CAA45538_ (X64254) B32E [Hordeum vulgare]

Seq. No.	273577
Contig ID	44428_1.R1011
5'-most EST	LIB143-019-Q1-E1-F8

Seq. No.	273578
Contig ID	44445_1.R1011
5'-most EST	ntr700073961.h1
Method	BLASTX
NCBI GI	g1171937
BLAST score	821
E value	5.0e-88
Match length	216
% identity	72
NCBI Description	OXALATE OXIDASE PRECURSOR (GERMIN) >gi_516871 (U01963) germin subunit [Hordeum vulgare]

Seq. No.	273579
Contig ID	44447_1.R1011
5'-most EST	LIB143-019-Q1-E1-H6

Seq. No.	273580
Contig ID	44448_1.R1011
5'-most EST	uC-zmflmo17240d03b1
Method	BLASTX
NCBI GI	g1346487
BLAST score	1003
E value	1.0e-109
Match length	264
% identity	84
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_532625 (L35914) malate synthase [Zea mays]

Seq. No.	273581
Contig ID	44448_2.R1011
5'-most EST	uC-zmflb73416a10a1
Method	BLASTX
NCBI GI	g1346487
BLAST score	272
E value	8.0e-24
Match length	50
% identity	100
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_532625 (L35914) malate synthase [Zea mays]

Seq. No.	273582

Contig ID	44449_2.R1011
5'-most EST	uC-zmflmo17327d03b1
Method	BLASTX
NCBI GI	g4104929
BLAST score	265
E value	5.0e-23
Match length	87
% identity	61
NCBI Description	(AF042195) auxin response factor 7 [Arabidopsis thaliana]

Seq. No.	273583
Contig ID	44451_1.R1011
5'-most EST	rv1700456119.h1

Seq. No.	273584
Contig ID	44451_2.R1011
5'-most EST	LIB143-058-Q1-E1-G5

Seq. No.	273585
Contig ID	44458_1.R1011
5'-most EST	uC-zmflb73040c09b1
Method	BLASTX
NCBI GI	g3875381
BLAST score	175
E value	3.0e-12
Match length	140
% identity	34
NCBI Description	(Z47808) cDNA EST EMBL:C10289 comes from this gene; cDNA EST EMBL:C11909 comes from this gene [Caenorhabditis elegans] >gi_3876933_emb_CAA87783_ (Z47809) cDNA EST EMBL:C10289 comes from this gene; cDNA EST EMBL:C11909 comes from this gene [Caenorhabditis elegans]

Seq. No.	273586
Contig ID	44459_1.R1011
5'-most EST	uC-zmroB73017b03b1

Seq. No.	273587
Contig ID	44489_1.R1011
5'-most EST	LIB143-020-Q1-E1-D6
Method	BLASTX
NCBI GI	g2144271
BLAST score	594
E value	9.0e-62
Match length	133
% identity	84
NCBI Description	trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus kitakamiensis (fragment) >gi_1777372_dbj_BAA11578_ (D82814) cinnamic acid 4-hydroxylase [Populus kitakamiensis]

Seq. No.	273588
Contig ID	44495_1.R1011
5'-most EST	uC-zmflb73026c05b1
Method	BLASTX
NCBI GI	g3033386
BLAST score	308
E value	9.0e-28

Match length	159
% identity	43
NCBI Description	(AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No.	273589
Contig ID	44495_2.R1011
5'-most EST	LIB143-020-Q1-E1-E2
Method	BLASTX
NCBI GI	g3033386
BLAST score	325
E value	4.0e-30
Match length	153
% identity	46
NCBI Description	(AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No.	273590
Contig ID	44497_1.R1011
5'-most EST	uC-zmflmo17301g10b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	8.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	273591
Contig ID	44507_1.R1011
5'-most EST	uC-zmflMo17065f03b1
Method	BLASTX
NCBI GI	g4206197
BLAST score	962
E value	1.0e-104
Match length	221
% identity	43
NCBI Description	(AF071527) putative pre-mRNA splicing factor [Arabidopsis thaliana]

Seq. No.	273592
Contig ID	44522_1.R1011
5'-most EST	dyk700104707.h1

Seq. No.	273593
Contig ID	44530_1.R1011
5'-most EST	uC-zmflb73193g01a1
Method	BLASTX
NCBI GI	g2982362
BLAST score	421
E value	3.0e-41
Match length	84
% identity	89
NCBI Description	(AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.	273594
Contig ID	44532_1.R1011
5'-most EST	wen700332025.h1

Seq. No.	273595
Contig ID	44534_1.R1011
5'-most EST	pmx700091760.h1

Seq. No.	273596
Contig ID	44545_1.R1011
5'-most EST	LIB3069-035-Q1-K1-B12

Seq. No.	273597
Contig ID	44548_1.R1011
5'-most EST	xjt700096724.h1
Method	BLASTX
NCBI GI	g4539009
BLAST score	784
E value	2.0e-83
Match length	446
% identity	40
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	273598
Contig ID	44556_1.R1011
5'-most EST	LIB143-021-Q1-E1-C10
Method	BLASTX
NCBI GI	g1421730
BLAST score	522
E value	2.0e-53
Match length	128
% identity	75
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	273599
Contig ID	44558_1.R1011
5'-most EST	LIB148-032-Q1-E1-D6

Seq. No.	273600
Contig ID	44568_1.R1011
5'-most EST	LIB143-021-Q1-E1-D12

Seq. No.	273601
Contig ID	44578_1.R1011
5'-most EST	LIB3059-016-Q1-K1-A12
Method	BLASTX
NCBI GI	g633890
BLAST score	854
E value	1.0e-104
Match length	259
% identity	78
NCBI Description	(S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare]

Seq. No.	273602
Contig ID	44582_2.R1011
5'-most EST	LIB143-021-Q1-E1-E9
Method	BLASTX
NCBI GI	g2668744
BLAST score	438
E value	2.0e-43

Match length	86
% identity	90
NCBI Description	(AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No.	273603
Contig ID	44582_3.R1011
5'-most EST	hvj700619734.h1
Method	BLASTX
NCBI GI	g2668744
BLAST score	320
E value	9.0e-30
Match length	66
% identity	86
NCBI Description	(AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No.	273604
Contig ID	44588_1.R1011
5'-most EST	cyk700049629.f1

Seq. No.	273605
Contig ID	44590_1.R1011
5'-most EST	pwr700450256.h1
Method	BLASTX
NCBI GI	g4467145
BLAST score	339
E value	2.0e-31
Match length	151
% identity	48
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No.	273606
Contig ID	44590_2.R1011
5'-most EST	uC-zmroteosinte057h04b1
Method	BLASTX
NCBI GI	g4467145
BLAST score	349
E value	2.0e-33
Match length	139
% identity	53
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No.	273607
Contig ID	44590_3.R1011
5'-most EST	pwr700449763.h2
Method	BLASTX
NCBI GI	g4467145
BLAST score	196
E value	3.0e-25
Match length	119
% identity	54
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No.	273608
Contig ID	44601_1.R1011

5'-most EST	LIB143-021-Q1-E1-H10
Seq. No.	273609
Contig ID	44602_1.R1011
5'-most EST	uC-zmflmo17185a02b1
Method	BLASTX
NCBI GI	g3426039
BLAST score	449
E value	1.0e-44
Match length	138
% identity	64
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.	273610
Contig ID	44612_1.R1011
5'-most EST	uC-zmflmo17304b06a1
Seq. No.	273611
Contig ID	44636_1.R1011
5'-most EST	ceu700427919.h1
Seq. No.	273612
Contig ID	44640_1.R1011
5'-most EST	xjt700095203.h1
Method	BLASTX
NCBI GI	g20202
BLAST score	879
E value	9.0e-95
Match length	192
% identity	78
NCBI Description	(X56063) chitinase [Oryza sativa]
Seq. No.	273613
Contig ID	44640_2.R1011
5'-most EST	LIB3068-034-Q1-K1-B2
Method	BLASTX
NCBI GI	g500615
BLAST score	863
E value	6.0e-93
Match length	179
% identity	83
NCBI Description	(D16221) endochitinase [Oryza sativa]
Seq. No.	273614
Contig ID	44648_1.R1011
5'-most EST	LIB143-022-Q1-E1-D7
Method	BLASTX
NCBI GI	g2622601
BLAST score	159
E value	2.0e-10
Match length	126
% identity	16
NCBI Description	(AE000909) serine/threonine protein kinase related protein [Methanobacterium thermoautotrophicum]
Seq. No.	273615
Contig ID	44671_1.R1011

5'-most EST	LIB143-022-Q1-E1-F8
Seq. No.	273616
Contig ID	44671_2.R1011
5'-most EST	pmx700087248.h1
Method	BLASTX
NCBI GI	g4508069
BLAST score	954
E value	1.0e-103
Match length	349
% identity	50
NCBI Description	(AC005882) 12246 [Arabidopsis thaliana]
Seq. No.	273617
Contig ID	44673_1.R1011
5'-most EST	LIB143-063-Q1-E1-F1
Method	BLASTX
NCBI GI	g2342686
BLAST score	298
E value	6.0e-27
Match length	91
% identity	64
NCBI Description	(AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb_Z49209). ESTs gb_T44436,gb_42252 come from this gene. [Arabidopsis thaliana]
Seq. No.	273618
Contig ID	44679_1.R1011
5'-most EST	LIB143-022-Q1-E1-G4
Method	BLASTX
NCBI GI	g3056591
BLAST score	365
E value	1.0e-34
Match length	142
% identity	51
NCBI Description	(AC004255) T1F9.12 [Arabidopsis thaliana]
Seq. No.	273619
Contig ID	44690_1.R1011
5'-most EST	LIB143-022-Q1-E1-H4
Seq. No.	273620
Contig ID	44693_1.R1011
5'-most EST	LIB143-022-Q1-E1-H7
Seq. No.	273621
Contig ID	44694_1.R1011
5'-most EST	dyk700104677.h1
Method	BLASTX
NCBI GI	g1170092
BLAST score	546
E value	6.0e-56
Match length	156
% identity	65
NCBI Description	GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI) >gi_1076807_pir__S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione

S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_
(X79515) glutathione transferase [Zea mays]
>gi_1094866_prf__2106424A glutathione
S-transferase:ISOTYPE=IV [Zea mays]

Seq. No.	273622
Contig ID	44694_2.R1011
5'-most EST	hvj700621757.h1
Method	BLASTX
NCBI GI	g1170092
BLAST score	195
E value	3.0e-15
Match length	72
% identity	56
NCBI Description	GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI) >gi_1076807_pir__S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_ (X79515) glutathione transferase [Zea mays] >gi_1094866_prf__2106424A glutathione S-transferase:ISOTYPE=IV [Zea mays]

Seq. No.	273623
Contig ID	44696_1.R1011
5'-most EST	LIB143-027-Q1-E1-C5
Method	BLASTN
NCBI GI	g4185305
BLAST score	82
E value	4.0e-38
Match length	173
% identity	89
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	273624
Contig ID	44704_1.R1011
5'-most EST	uC-zmrob73061a07a1

Seq. No.	273625
Contig ID	44707_1.R1011
5'-most EST	LIB143-023-Q1-E1-B2
Method	BLASTX
NCBI GI	g113497
BLAST score	287
E value	9.0e-26
Match length	75
% identity	69
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_99880_pir__S07472 alpha-galactosidase (EC 3.2.1.22) precursor - guar >gi_18292_emb_CAA32772_ (X14619) alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]

Seq. No.	273626
Contig ID	44709_1.R1011

5'-most EST	pmx700087586.h1
Seq. No.	273627
Contig ID	44709_2.R1011
5'-most EST	xyt700344989.h1
Seq. No.	273628
Contig ID	44715_1.R1011
5'-most EST	pmx700086623.h1
Method	BLASTX
NCBI GI	g2232254
BLAST score	1436
E value	1.0e-160
Match length	352
% identity	76
NCBI Description	(AF005237) old-yellow-enzyme homolog [Catharanthus roseus]
Seq. No.	273629
Contig ID	44724_1.R1011
5'-most EST	vux700157968.h1
Method	BLASTX
NCBI GI	g3582781
BLAST score	262
E value	1.0e-22
Match length	57
% identity	88
NCBI Description	(AF056283) peroxisomal targeting sequence 1 receptor [Nicotiana tabacum]
Seq. No.	273630
Contig ID	44734_1.R1011
5'-most EST	LIB84-012-Q1-E12-A3
Method	BLASTX
NCBI GI	g1773014
BLAST score	811
E value	8.0e-87
Match length	245
% identity	68
NCBI Description	(Y10338) chloride channel Stclc1 [Solanum tuberosum]
Seq. No.	273631
Contig ID	44738_1.R1011
5'-most EST	ceu700430674.h1
Method	BLASTX
NCBI GI	g2911073
BLAST score	462
E value	4.0e-46
Match length	127
% identity	66
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]
Seq. No.	273632
Contig ID	44751_1.R1011
5'-most EST	wyr700242966.h1
Method	BLASTX
NCBI GI	g4538967
BLAST score	751

E value	2.0e-79
Match length	214
% identity	70
NCBI Description	(AL049488) major intrinsic protein (MIP)-like [Arabidopsis thaliana]

Seq. No.	273633
Contig ID	44751_3.R1011
5'-most EST	LIB3067-017-Q1-K1-B11

Seq. No.	273634
Contig ID	44751_4.R1011
5'-most EST	fC-zmf1700352012a1
Method	BLASTX
NCBI GI	g4538967
BLAST score	351
E value	3.0e-33
Match length	105
% identity	70
NCBI Description	(AL049488) major intrinsic protein (MIP)-like [Arabidopsis thaliana]

Seq. No.	273635
Contig ID	44753_1.R1011
5'-most EST	qmh700028417.f1

Seq. No.	273636
Contig ID	44761_1.R1011
5'-most EST	LIB3060-008-Q1-K1-F5

Seq. No.	273637
Contig ID	44763_1.R1011
5'-most EST	hbs701183613.h1
Method	BLASTX
NCBI GI	g2979549
BLAST score	494
E value	8.0e-50
Match length	174
% identity	55
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	273638
Contig ID	44785_1.R1011
5'-most EST	uC-zmroteosinte064h12b1
Method	BLASTX
NCBI GI	g3024756
BLAST score	482
E value	5.0e-48
Match length	346
% identity	33
NCBI Description	TYPE II DNA TOPOISOMERASE VI SUBUNIT B >gi_1926403_emb_CAA71604_ (Y10582) type II DNA topoisomerase subunit B [Sulfolobus shibatae]

Seq. No.	273639
Contig ID	44791_1.R1011

5'-most EST	uC-zmflmo17017g12b1
Method	BLASTX
NCBI GI	g2980770
BLAST score	433
E value	1.0e-42
Match length	153
% identity	57
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	273640
Contig ID	44791_3.R1011
5'-most EST	uC-zmflb73028d05b1
Method	BLASTX
NCBI GI	g2980770
BLAST score	155
E value	3.0e-20
Match length	107
% identity	50
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	273641
Contig ID	44798_1.R1011
5'-most EST	LIB143-024-Q1-E1-B5
Method	BLASTX
NCBI GI	g4220514
BLAST score	166
E value	1.0e-12
Match length	70
% identity	56
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	273642
Contig ID	44800_1.R1011
5'-most EST	wty700168159.h1
Method	BLASTX
NCBI GI	g1488297
BLAST score	726
E value	1.0e-76
Match length	287
% identity	56
NCBI Description	(U63530) osRAD23 [Oryza sativa]

Seq. No.	273643
Contig ID	44800_2.R1011
5'-most EST	uC-zmflmo17309h05b1
Method	BLASTX
NCBI GI	g1488297
BLAST score	430
E value	2.0e-42
Match length	156
% identity	59
NCBI Description	(U63530) osRAD23 [Oryza sativa]

Seq. No.	273644
Contig ID	44800_3.R1011
5'-most EST	hbs701184495.h1

Seq. No.	273645
Contig ID	44802_1.R1011
5'-most EST	LIB143-024-Q1-E1-B9
Method	BLASTN
NCBI GI	g2224809
BLAST score	38
E value	1.0e-11
Match length	42
% identity	98
NCBI Description	Hordeum vulgare gene encoding cysteine proteinase

Seq. No.	273646
Contig ID	44830_1.R1011
5'-most EST	xjt700094387.h1
Method	BLASTX
NCBI GI	g2583123
BLAST score	952
E value	1.0e-103
Match length	241
% identity	72
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	273647
Contig ID	44838_1.R1011
5'-most EST	ymt700223347.h1
Method	BLASTX
NCBI GI	g2880043
BLAST score	237
E value	1.0e-19
Match length	109
% identity	45
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	273648
Contig ID	44842_1.R1011
5'-most EST	cjh700195696.h1

Seq. No.	273649
Contig ID	44842_2.R1011
5'-most EST	LIB3059-030-Q1-K1-B8

Seq. No.	273650
Contig ID	44850_1.R1011
5'-most EST	LIB143-024-Q1-E1-G11

Seq. No.	273651
Contig ID	44858_1.R1011
5'-most EST	LIB143-024-Q1-E1-G9

Seq. No.	273652
Contig ID	44861_1.R1011
5'-most EST	LIB143-024-Q1-E1-H11
Method	BLASTX
NCBI GI	g3522957
BLAST score	553

E value	1.0e-56
Match length	175
% identity	64
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	273653
Contig ID	44885_1.R1011
5'-most EST	uC-zmflb73060d11b1
Method	BLASTX
NCBI GI	g2827537
BLAST score	689
E value	2.0e-72
Match length	253
% identity	55
NCBI Description	(AL021633) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	273654
Contig ID	44891_1.R1011
5'-most EST	uC-zmroteosinte084f01b1

Seq. No.	273655
Contig ID	44895_1.R1011
5'-most EST	LIB143-039-Q1-E1-A12
Method	BLASTX
NCBI GI	g453670
BLAST score	540
E value	2.0e-55
Match length	107
% identity	100
NCBI Description	(L28712) heat shock protein 26 [Zea mays] >gi_227776_prf__1710350A heat shock protein 26 [Zea mays]

Seq. No.	273656
Contig ID	44896_1.R1011
5'-most EST	LIB143-025-Q1-E1-C3
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	273657
Contig ID	44901_1.R1011
5'-most EST	tfd700574835.h1

Seq. No.	273658
Contig ID	44922_1.R1011
5'-most EST	LIB143-025-Q1-E1-E9
Method	BLASTX
NCBI GI	g4103635
BLAST score	348
E value	3.0e-32
Match length	144
% identity	42

NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]
Seq. No.	273659
Contig ID	44926_1.R1011
5'-most EST	cat700019805.r1
Method	BLASTX
NCBI GI	g3763849
BLAST score	410
E value	9.0e-40
Match length	97
% identity	88
NCBI Description	(AB018377) early nodulin [Oryza sativa]
Seq. No.	273660
Contig ID	44933_1.R1011
5'-most EST	yyf700347474.h1
Seq. No.	273661
Contig ID	44941_1.R1011
5'-most EST	fwa700098236.h1
Method	BLASTX
NCBI GI	g4371292
BLAST score	416
E value	5.0e-40
Match length	276
% identity	34
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]
Seq. No.	273662
Contig ID	44958_1.R1011
5'-most EST	LIB143-026-Q1-E1-A11
Seq. No.	273663
Contig ID	44964_1.R1011
5'-most EST	xsy700212912.h1
Seq. No.	273664
Contig ID	44968_1.R1011
5'-most EST	yyf700351483.h1
Seq. No.	273665
Contig ID	44971_1.R1011
5'-most EST	LIB3061-053-Q1-K1-B4
Method	BLASTX
NCBI GI	g4455169
BLAST score	1110
E value	1.0e-121
Match length	471
% identity	48
NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]
Seq. No.	273666
Contig ID	44972_1.R1011
5'-most EST	uC-zmflmo17072f09b1
Seq. No.	273667

Contig ID	44973_1.R1011
5'-most EST	LIB143-026-Q1-E1-B4
Seq. No.	273668
Contig ID	44973_2.R1011
5'-most EST	uwc700152315.h1
Seq. No.	273669
Contig ID	45013_1.R1011
5'-most EST	uC-zmf1b73159d10b2
Seq. No.	273670
Contig ID	45037_1.R1011
5'-most EST	yyf700349895.h1
Method	BLASTX
NCBI GI	g4587681
BLAST score	366
E value	7.0e-35
Match length	92
% identity	73
NCBI Description	(AC007197) hypothetical protein [Arabidopsis thaliana]
Seq. No.	273671
Contig ID	45045_1.R1011
5'-most EST	xdg700405259.h1
Seq. No.	273672
Contig ID	45074_1.R1011
5'-most EST	uC-zmflmo17155c12b1
Seq. No.	273673
Contig ID	45076_1.R1011
5'-most EST	LIB143-044-Q1-E1-F5
Seq. No.	273674
Contig ID	45086_1.R1011
5'-most EST	LIB143-038-Q1-E1-G10
Method	BLASTX
NCBI GI	g4586049
BLAST score	707
E value	3.0e-74
Match length	346
% identity	42
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]
Seq. No.	273675
Contig ID	45087_1.R1011
5'-most EST	fwa700099956.h1
Method	BLASTX
NCBI GI	g2911052
BLAST score	935
E value	1.0e-101
Match length	262
% identity	69
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]
Seq. No.	273676

Contig ID	45091_1.R1011
5'-most EST	uC-zmflb73158d09b2
Method	BLASTX
NCBI GI	g2384758
BLAST score	1050
E value	1.0e-122
Match length	241
% identity	92
NCBI Description	(AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No.	273677
Contig ID	45093_1.R1011
5'-most EST	uC-zmrob73080f06b1
Method	BLASTX
NCBI GI	g4586244
BLAST score	897
E value	2.0e-96
Match length	538
% identity	39
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	273678
Contig ID	45098_1.R1011
5'-most EST	ymt700219006.h1
Method	BLASTX
NCBI GI	g4566505
BLAST score	973
E value	1.0e-106
Match length	211
% identity	85
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	273679
Contig ID	45098_2.R1011
5'-most EST	wty700164293.h1
Method	BLASTX
NCBI GI	g4566505
BLAST score	340
E value	2.0e-40
Match length	115
% identity	77
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	273680
Contig ID	45107_1.R1011
5'-most EST	LIB148-041-Q1-E1-F4
Method	BLASTX
NCBI GI	g4337196
BLAST score	1019
E value	1.0e-111
Match length	255
% identity	76
NCBI Description	(AC006403) putative serine/threonine receptor kinase [Arabidopsis thaliana]

Seq. No.	273681
Contig ID	45107_2.R1011
5'-most EST	LIB3066-053-Q1-K1-B2
Method	BLASTX
NCBI GI	g4337196
BLAST score	724
E value	2.0e-76
Match length	290
% identity	51
NCBI Description	(AC006403) putative serine/threonine receptor kinase [Arabidopsis thaliana]

Seq. No.	273682
Contig ID	45108_1.R1011
5'-most EST	uC-zmroteosinte023f01b2
Method	BLASTX
NCBI GI	g3790677
BLAST score	277
E value	5.0e-24
Match length	285
% identity	28
NCBI Description	(AF099002) similar to human 5'-nucleotidase (SW:P49902) [Caenorhabditis elegans]

Seq. No.	273683
Contig ID	45109_1.R1011
5'-most EST	LIB189-008-Q1-E1-G12

Seq. No.	273684
Contig ID	45111_1.R1011
5'-most EST	LIB3060-032-Q1-K1-F7
Method	BLASTX
NCBI GI	g4455261
BLAST score	518
E value	8.0e-53
Match length	116
% identity	78
NCBI Description	(AL035353) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	273685
Contig ID	45114_1.R1011
5'-most EST	LIB143-028-Q1-E1-A7

Seq. No.	273686
Contig ID	45116_1.R1011
5'-most EST	xsy700213896.h1

Seq. No.	273687
Contig ID	45122_1.R1011
5'-most EST	uC-zmflb73182g10b1

Seq. No.	273688
Contig ID	45127_1.R1011
5'-most EST	LIB143-063-Q1-E1-F4

Seq. No.	273689
Contig ID	45130_1.R1011
5'-most EST	wty700170504.h1
Method	BLASTX
NCBI GI	g3881978
BLAST score	997
E value	1.0e-108
Match length	311
% identity	34
NCBI Description	(Y11348) annexin-like protein [Medicago sativa]

Seq. No.	273690
Contig ID	45133_1.R1011
5'-most EST	LIB143-028-Q1-E1-C6

Seq. No.	273691
Contig ID	45145_1.R1011
5'-most EST	xsy700214966.h1
Method	BLASTX
NCBI GI	g3747026
BLAST score	216
E value	5.0e-17
Match length	78
% identity	46
NCBI Description	(AF093244) import protein Tim9p [Saccharomyces cerevisiae]

Seq. No.	273692
Contig ID	45154_1.R1011
5'-most EST	LIB3069-044-Q1-K1-D11
Method	BLASTX
NCBI GI	g465514
BLAST score	165
E value	2.0e-11
Match length	90
% identity	44
NCBI Description	HYPOTHETICAL 47.4 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION >gi_542308_pir__S39833 hypothetical protein YBL055c - yeast (Saccharomyces cerevisiae) >gi_313743_emb_CAA80792_ (Z23261) YBL0511 [Saccharomyces cerevisiae] >gi_536084_emb_CAA84875_ (Z35816) ORF YBL055c [Saccharomyces cerevisiae]

Seq. No.	273693
Contig ID	45161_1.R1011
5'-most EST	ntr700071884.h1
Method	BLASTN
NCBI GI	g1532070
BLAST score	385
E value	0.0e+00
Match length	786
% identity	88
NCBI Description	Z.mays grp3 mRNA for glycine-rich protein

Seq. No.	273694
Contig ID	45162_1.R1011
5'-most EST	LIB143-028-Q1-E1-G1

Seq. No.	273695
Contig ID	45163_1.R1011
5'-most EST	LIB143-028-Q1-E1-G10

Seq. No.	273696
Contig ID	45167_1.R1011
5'-most EST	LIB143-028-Q1-E1-G4
Method	BLASTX
NCBI GI	g1244566
BLAST score	1170
E value	1.0e-133
Match length	297
% identity	82
NCBI Description	(U39321) acetyl-CoA carboxylase [Triticum aestivum] >gi_1588584_prf__2208491A Ac-CoA carboxylase [Triticum aestivum]

Seq. No.	273697
Contig ID	45168_1.R1011
5'-most EST	cat700020274.r1
Method	BLASTX
NCBI GI	g3426048
BLAST score	523
E value	3.0e-53
Match length	167
% identity	65
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	273698
Contig ID	45169_1.R1011
5'-most EST	tzu700206160.h1

Seq. No.	273699
Contig ID	45174_1.R1011
5'-most EST	LIB3069-055-Q1-K1-B11
Method	BLASTX
NCBI GI	g3819164
BLAST score	272
E value	7.0e-24
Match length	103
% identity	55
NCBI Description	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]

Seq. No.	273700
Contig ID	45177_1.R1011
5'-most EST	uwc700150552.h1
Method	BLASTX
NCBI GI	g2828290
BLAST score	386
E value	3.0e-37
Match length	121
% identity	62
NCBI Description	(AL021687) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 273701

Contig ID	45177_2.R1011
5'-most EST	wty700172171.h1
Method	BLASTX
NCBI GI	g2828290
BLAST score	184
E value	5.0e-14
Match length	60
% identity	62
NCBI Description	(AL021687) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	273702
Contig ID	45181_2.R1011
5'-most EST	uC-zmflb73052c04b1

Seq. No.	273703
Contig ID	45187_1.R1011
5'-most EST	LIB143-029-Q1-E1-A8
Method	BLASTX
NCBI GI	g2145356
BLAST score	256
E value	4.0e-22
Match length	100
% identity	52
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	273704
Contig ID	45193_1.R1011
5'-most EST	pmx700091354.h1

Seq. No.	273705
Contig ID	45193_2.R1011
5'-most EST	ceu700430253.h1

Seq. No.	273706
Contig ID	45193_3.R1011
5'-most EST	wyr700241501.h1

Seq. No.	273707
Contig ID	45202_1.R1011
5'-most EST	LIB143-029-Q1-E1-C12

Seq. No.	273708
Contig ID	45204_1.R1011
5'-most EST	uC-zmflmo17071g07b1
Method	BLASTX
NCBI GI	g2315451
BLAST score	271
E value	3.0e-23
Match length	175
% identity	28
NCBI Description	(AF016448) No definition line found [Caenorhabditis elegans]

Seq. No.	273709
Contig ID	45204_2.R1011
5'-most EST	uC-zmflb73051b08b1

Method	BLASTX
NCBI GI	g2315451
BLAST score	173
E value	5.0e-12
Match length	220
% identity	21
NCBI Description	(AF016448) No definition line found [Caenorhabditis elegans]

Seq. No.	273710
Contig ID	45205_1.R1011
5'-most EST	LIB3067-031-Q1-K1-C10

Seq. No.	273711
Contig ID	45222_1.R1011
5'-most EST	LIB143-029-Q1-E1-E8

Seq. No.	273712
Contig ID	45226_1.R1011
5'-most EST	LIB143-029-Q1-E1-F11

Seq. No.	273713
Contig ID	45229_1.R1011
5'-most EST	LIB143-055-Q1-E1-G1
Method	BLASTX
NCBI GI	g2952328
BLAST score	733
E value	9.0e-78
Match length	183
% identity	75
NCBI Description	(AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza sativa]

Seq. No.	273714
Contig ID	45229_3.R1011
5'-most EST	uC-zmf1b73264a05b1
Method	BLASTX
NCBI GI	g2952328
BLAST score	465
E value	2.0e-46
Match length	118
% identity	75
NCBI Description	(AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza sativa]

Seq. No.	273715
Contig ID	45236_1.R1011
5'-most EST	uC-zmf1b73185a05b1
Method	BLASTX
NCBI GI	g1542941
BLAST score	778
E value	1.0e-82
Match length	237
% identity	65
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No. 273716

Contig ID	45242_1.R1011
5'-most EST	LIB143-042-Q1-E1-D8
Method	BLASTX
NCBI GI	g168467
BLAST score	523
E value	5.0e-53
Match length	113
% identity	96
NCBI Description	(M90554) late embryogenesis abundant protein [Zea mays] >gi_445606_prf__1909353A Emb5 gene [Zea mays]

Seq. No.	273717
Contig ID	45246_1.R1011
5'-most EST	LIB143-029-Q1-E1-H4
Method	BLASTX
NCBI GI	g1362162
BLAST score	489
E value	8.0e-73
Match length	196
% identity	67
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	273718
Contig ID	45252_1.R1011
5'-most EST	LIB3062-053-Q1-K1-C5

Seq. No.	273719
Contig ID	45268_1.R1011
5'-most EST	gct701169002.h1
Method	BLASTX
NCBI GI	g3023956
BLAST score	222
E value	4.0e-18
Match length	80
% identity	6
NCBI Description	VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi_607003 (L28125) beta transducin-like protein [Podospora anserina]

Seq. No.	273720
Contig ID	45273_1.R1011
5'-most EST	LIB143-030-Q1-E1-C3

Seq. No.	273721
Contig ID	45297_1.R1011
5'-most EST	LIB3061-001-Q1-K1-H12

Seq. No.	273722
Contig ID	45300_1.R1011
5'-most EST	LIB143-030-Q1-E1-G4

Seq. No.	273723
Contig ID	45303_1.R1011
5'-most EST	xjt700096317.h1
Method	BLASTX
NCBI GI	g1362162
BLAST score	182

E value	2.0e-13
Match length	44
% identity	77
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	273724
Contig ID	45309_1.R1011
5'-most EST	LIB3067-043-Q1-K1-H5
Method	BLASTX
NCBI GI	g82114
BLAST score	179
E value	5.0e-13
Match length	66
% identity	55
NCBI Description	wound-induced protein - tomato (fragment) >gi_19320_emb_CAA42537_ (X59882) wound induced protein [Lycopersicon esculentum]

Seq. No.	273725
Contig ID	45315_1.R1011
5'-most EST	gwl700614064.h1
Method	BLASTX
NCBI GI	g4580456
BLAST score	277
E value	4.0e-24
Match length	172
% identity	37
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	273726
Contig ID	45323_1.R1011
5'-most EST	LIB189-024-Q1-E1-D3
Method	BLASTX
NCBI GI	g3882355
BLAST score	309
E value	2.0e-33
Match length	96
% identity	77
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana]

Seq. No.	273727
Contig ID	45323_2.R1011
5'-most EST	qmh700029505.f1
Method	BLASTX
NCBI GI	g3882356
BLAST score	325
E value	2.0e-30
Match length	82
% identity	73
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana]

Seq. No.	273728
Contig ID	45336_1.R1011
5'-most EST	xjt700093329.h1

Seq. No.	273729
Contig ID	45338_1.R1011
5'-most EST	LIB143-031-Q1-E1-B9

Seq. No.	273730
Contig ID	45338_2.R1011
5'-most EST	gct701178249.h1

Seq. No.	273731
Contig ID	45339_1.R1011
5'-most EST	LIB143-031-Q1-E1-C1

Seq. No.	273732
Contig ID	45342_1.R1011
5'-most EST	uC-zmflmo17158b02b1
Method	BLASTX
NCBI GI	g3445208
BLAST score	589
E value	5.0e-77
Match length	237
% identity	63
NCBI Description	(AC004786) putative amino-acid acetyltransferase [Arabidopsis thaliana]

Seq. No.	273733
Contig ID	45347_1.R1011
5'-most EST	LIB143-031-Q1-E1-C8
Method	BLASTX
NCBI GI	g3413712
BLAST score	384
E value	3.0e-37
Match length	103
% identity	65
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273734
Contig ID	45352_1.R1011
5'-most EST	LIB143-031-Q1-E1-D3
Method	BLASTX
NCBI GI	g1304227
BLAST score	275
E value	2.0e-24
Match length	98
% identity	49
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	273735
Contig ID	45354_1.R1011
5'-most EST	LIB36-016-Q2-E2-C1
Method	BLASTX
NCBI GI	g4218535
BLAST score	243
E value	4.0e-20
Match length	141

% identity	45
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	273736
Contig ID	45354_2.R1011
5'-most EST	uC-zmflmo17174d02b1

Seq. No.	273737
Contig ID	45354_3.R1011
5'-most EST	sz1700184951.h1

Seq. No.	273738
Contig ID	45354_4.R1011
5'-most EST	wty700172538.h1
Method	BLASTX
NCBI GI	g4218535
BLAST score	322
E value	8.0e-30
Match length	139
% identity	52
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	273739
Contig ID	45358_1.R1011
5'-most EST	LIB143-031-Q1-E1-D9
Method	BLASTX
NCBI GI	g3080390
BLAST score	460
E value	8.0e-46
Match length	121
% identity	72
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	273740
Contig ID	45359_1.R1011
5'-most EST	LIB143-041-Q1-E1-D12
Method	BLASTX
NCBI GI	g3242723
BLAST score	253
E value	8.0e-22
Match length	93
% identity	55
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	273741
Contig ID	45360_1.R1011
5'-most EST	uC-zmroteosinte066f06b1

Seq. No.	273742
Contig ID	45364_1.R1011
5'-most EST	LIB143-031-Q1-E1-E7

Seq. No.	273743
Contig ID	45369_1.R1011
5'-most EST	LIB3137-041-Q1-K1-B12

Seq. No.	273744
Contig ID	45387_1.R1011
5'-most EST	LIB3067-043-Q1-K1-H9
Method	BLASTX
NCBI GI	g4584520
BLAST score	362
E value	2.0e-34
Match length	109
% identity	66
NCBI Description	(AL049607) enoyl-CoA hydratase-like protein [Arabidopsis thaliana]

Seq. No.	273745
Contig ID	45387_2.R1011
5'-most EST	xsy700212138.h1
Method	BLASTX
NCBI GI	g4584520
BLAST score	477
E value	7.0e-48
Match length	158
% identity	61
NCBI Description	(AL049607) enoyl-CoA hydratase-like protein [Arabidopsis thaliana]

Seq. No.	273746
Contig ID	45406_1.R1011
5'-most EST	LIB3061-028-Q1-K1-B1
Method	BLASTX
NCBI GI	g1169469
BLAST score	370
E value	3.0e-35
Match length	60
% identity	100
NCBI Description	EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II) >gi_629848_pir__S47158 metallothionein II - maize >gi_506139_(U10696) Ec metallothionein class II protein [Zea mays] >gi_987123_emb_CAA84233_ (Z34469) class II metallothionein with homology to wheat Ec [Zea mays] >gi_1582362_prf__2118343A metallothionein [Zea mays]

Seq. No.	273747
Contig ID	45411_1.R1011
5'-most EST	LIB143-032-Q1-E1-B7

Seq. No.	273748
Contig ID	45414_1.R1011
5'-most EST	uC-zmf1mo17258e11b1

Seq. No.	273749
Contig ID	45414_2.R1011
5'-most EST	LIB143-032-Q1-E1-C3

Seq. No.	273750
Contig ID	45415_1.R1011
5'-most EST	uC-zmf1b73222e10b1
Method	BLASTX
NCBI GI	g4097573

BLAST score	150
E value	2.0e-09
Match length	65
% identity	40
NCBI Description	(U64917) GMFP7 [Glycine max]

Seq. No.	273751
Contig ID	45415_2.R1011
5'-most EST	LIB143-032-Q1-E1-C11

Seq. No.	273752
Contig ID	45415_3.R1011
5'-most EST	LIB3069-044-Q1-K1-D10

Seq. No.	273753
Contig ID	45420_1.R1011
5'-most EST	nbm700477142.h1

Seq. No.	273754
Contig ID	45420_2.R1011
5'-most EST	LIB3137-017-Q1-K1-G5

Seq. No.	273755
Contig ID	45422_1.R1011
5'-most EST	LIB83-001-Q1-E1-C4
Method	BLASTX
NCBI GI	g1173456
BLAST score	335
E value	6.0e-31
Match length	94
% identity	61
NCBI Description	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	273756
Contig ID	45423_1.R1011
5'-most EST	uC-zmflmo17037e07b1
Method	BLASTX
NCBI GI	g4584957
BLAST score	363
E value	1.0e-34
Match length	107
% identity	73
NCBI Description	(AF077337) heat shock protein 101; 101 kDa heat shock protein [Zea mays]

Seq. No.	273757
Contig ID	45426_1.R1011
5'-most EST	LIB143-033-Q1-E1-D2
Method	BLASTX
NCBI GI	g4510341
BLAST score	242
E value	4.0e-20
Match length	167
% identity	40
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	273758
Contig ID	45434_1.R1011
5'-most EST	LIB3061-021-Q1-K1-D3

Seq. No.	273759
Contig ID	45450_1.R1011
5'-most EST	uC-zmflmo17045a12b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	273760
Contig ID	45450_2.R1011
5'-most EST	nbm700470381.h1
Method	BLASTX
NCBI GI	g1542941
BLAST score	615
E value	7.0e-64
Match length	161
% identity	76
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	273761
Contig ID	45452_1.R1011
5'-most EST	uC-zmflb73361f11a2

Seq. No.	273762
Contig ID	45453_1.R1011
5'-most EST	uC-zmflmo17222f12b1
Method	BLASTX
NCBI GI	g4455304
BLAST score	631
E value	2.0e-65
Match length	357
% identity	39
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273763
Contig ID	45458_1.R1011
5'-most EST	LIB143-032-Q1-E1-H10

Seq. No.	273764
Contig ID	45465_1.R1011
5'-most EST	LIB143-032-Q1-E1-H7
Method	BLASTX
NCBI GI	g4100433
BLAST score	184
E value	3.0e-13
Match length	54
% identity	61
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	273765

Contig ID	45476_1.R1011
5'-most EST	LIB143-033-Q1-E1-A6

Seq. No.	273766
Contig ID	45484_1.R1011
5'-most EST	LIB143-033-Q1-E1-B5
Method	BLASTX
NCBI GI	g2829887
BLAST score	296
E value	1.0e-26
Match length	134
% identity	49
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	273767
Contig ID	45486_1.R1011
5'-most EST	LIB143-033-Q1-E1-C1

Seq. No.	273768
Contig ID	45487_1.R1011
5'-most EST	LIB143-033-Q1-E1-C10

Seq. No.	273769
Contig ID	45511_1.R1011
5'-most EST	LIB3136-019-Q1-K1-C7
Method	BLASTX
NCBI GI	g4191784
BLAST score	383
E value	1.0e-36
Match length	152
% identity	54
NCBI Description	(AC005917) putative WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	273770
Contig ID	45512_2.R1011
5'-most EST	LIB3067-050-Q1-K1-A12
Method	BLASTX
NCBI GI	g1175447
BLAST score	267
E value	8.0e-23
Match length	108
% identity	47
NCBI Description	PUTATIVE ATP-DEPENDENT RNA HELICASE C22F3.08C >gi_2130317_pir__S62423 hypothetical protein SPAC22F3.08c - fission yeast (Schizosaccharomyces pombe) >gi_1008436_emb_CAA91073_ (Z54285) unknown [Schizosaccharomyces pombe]

Seq. No.	273771
Contig ID	45545_1.R1011
5'-most EST	LIB143-034-Q1-E1-A6
Method	BLASTX
NCBI GI	g119791
BLAST score	960
E value	1.0e-104
Match length	281

% identity	68
NCBI Description	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE) >gi_1084385_pir__S22450 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor - Cuphea lanceolata >gi_18046_emb_CAA45866_ (X64566) 3-oxoacyl-[acyl-carrier protein] reductase [Cuphea lanceolata] >gi_228929_prf__1814446A beta ketoacyl-ACP reductase [Cuphea lanceolata]
Seq. No.	273772
Contig ID	45552_1.R1011
5'-most EST	tzu700205883.h1
Method	BLASTX
NCBI GI	g1514643
BLAST score	634
E value	4.0e-66
Match length	218
% identity	55
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
Seq. No.	273773
Contig ID	45559_1.R1011
5'-most EST	uC-zmflmo17084g05a1
Seq. No.	273774
Contig ID	45563_1.R1011
5'-most EST	fxb700397429.h1
Method	BLASTX
NCBI GI	g2190992
BLAST score	472
E value	2.0e-69
Match length	224
% identity	64
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]
Seq. No.	273775
Contig ID	45570_1.R1011
5'-most EST	LIB143-034-Q1-E1-D11
Method	BLASTX
NCBI GI	g2129840
BLAST score	469
E value	4.0e-47
Match length	109
% identity	80
NCBI Description	nucleosome assembly protein 1 - soybean >gi_1161252 (L38856) nucleosome assembly protein 1 [Glycine max]
Seq. No.	273776
Contig ID	45590_1.R1011
5'-most EST	uC-zmflb73301f07a1
Seq. No.	273777
Contig ID	45591_1.R1011
5'-most EST	LIB143-034-Q1-E1-F2
Method	BLASTX

NCBI GI	g4584547
BLAST score	521
E value	5.0e-53
Match length	171
% identity	54
NCBI Description	(AL049608) potassium transporter-like protein [Arabidopsis thaliana]

Seq. No.	273778
Contig ID	45596_1.R1011
5'-most EST	uC-zmroteosinte002h07b1
Method	BLASTX
NCBI GI	g2499946
BLAST score	1019
E value	1.0e-111
Match length	289
% identity	70
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	273779
Contig ID	45609_1.R1011
5'-most EST	LIB143-034-Q1-E1-G9
Method	BLASTX
NCBI GI	g4505823
BLAST score	202
E value	2.0e-28
Match length	110
% identity	58
NCBI Description	pirin >gi_1907076_emb_CAA69194_ (Y07867) pirin [Homo sapiens] >gi_1907078_emb_CAA69195_ (Y07868) pirin [Homo sapiens]

Seq. No.	273780
Contig ID	45628_1.R1011
5'-most EST	xjt700094410.h1
Method	BLASTX
NCBI GI	g4531434
BLAST score	214
E value	5.0e-17
Match length	105
% identity	40
NCBI Description	(AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	273781
Contig ID	45629_1.R1011
5'-most EST	xmt700261950.h1
Method	BLASTX
NCBI GI	g1710748
BLAST score	177
E value	2.0e-12
Match length	131
% identity	33
NCBI Description	40S RIBOSOMAL PROTEIN S1 >gi_1004353 (U05589) ribosomal protein S1 homolog [Homo sapiens]

Seq. No.	273782
Contig ID	45641_1.R1011
5'-most EST	LIB143-035-Q1-E1-C10
Method	BLASTX
NCBI GI	g282994
BLAST score	959
E value	1.0e-104
Match length	235
% identity	76
NCBI Description	Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No.	273783
Contig ID	45655_1.R1011
5'-most EST	LIB143-035-Q1-E1-E1
Method	BLASTX
NCBI GI	g3461820
BLAST score	271
E value	1.0e-23
Match length	132
% identity	40
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	273784
Contig ID	45655_2.R1011
5'-most EST	gct701167714.h1
Method	BLASTX
NCBI GI	g3461820
BLAST score	202
E value	7.0e-16
Match length	44
% identity	73
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	273785
Contig ID	45667_1.R1011
5'-most EST	LIB3067-026-Q1-K1-C11
Method	BLASTX
NCBI GI	g4337192
BLAST score	625
E value	1.0e-64
Match length	248
% identity	51
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273786
Contig ID	45675_1.R1011
5'-most EST	uC-zmflmo17344a10b1
Method	BLASTX
NCBI GI	g3036796
BLAST score	240
E value	1.0e-19
Match length	133
% identity	42
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805858_emb_CAA21478_ (AL031986) putative protein

[Arabidopsis thaliana]

Seq. No.	273787
Contig ID	45675_2.R1011
5'-most EST	fwa700101588.h1

Seq. No.	273788
Contig ID	45675_3.R1011
5'-most EST	LIB3117-006-Q1-K1-G10

Seq. No.	273789
Contig ID	45675_4.R1011
5'-most EST	uC-zmf1b73205b02b2
Method	BLASTX
NCBI GI	g3036796
BLAST score	209
E value	1.0e-16
Match length	96
% identity	45
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805858_emb_CAA21478_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	273790
Contig ID	45677_1.R1011
5'-most EST	LIB143-035-Q1-E1-G5
Method	BLASTX
NCBI GI	g4490303
BLAST score	307
E value	6.0e-28
Match length	82
% identity	67
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	273791
Contig ID	45685_1.R1011
5'-most EST	qmh700027768.f1
Method	BLASTX
NCBI GI	g1168654
BLAST score	1054
E value	1.0e-115
Match length	296
% identity	64
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) - garden asparagus >gi_452712_emb_CAA54525_ (X77319) beta-galactosidase [Asparagus officinalis]

Seq. No.	273792
Contig ID	45685_3.R1011
5'-most EST	uC-zmflmo17068b04b2
Method	BLASTX
NCBI GI	g1168654
BLAST score	199
E value	2.0e-26
Match length	110
% identity	53

NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) - garden asparagus >gi_452712_emb_CAA54525_ (X77319) beta-galactosidase [Asparagus officinalis]
Seq. No.	273793
Contig ID	45690_1.R1011
5'-most EST	LIB3062-026-Q1-K1-B7
Seq. No.	273794
Contig ID	45690_2.R1011
5'-most EST	LIB143-036-Q1-E1-A10
Seq. No.	273795
Contig ID	45703_1.R1011
5'-most EST	fdz701165747.h1
Method	BLASTX
NCBI GI	g2829918
BLAST score	399
E value	8.0e-39
Match length	143
% identity	59
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]
Seq. No.	273796
Contig ID	45721_1.R1011
5'-most EST	uC-zmf1b73122e10b2
Method	BLASTX
NCBI GI	g2275211
BLAST score	299
E value	5.0e-27
Match length	131
% identity	54
NCBI Description	(AC002337) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.	273797
Contig ID	45739_1.R1011
5'-most EST	uC-zmromo17016a10a1
Seq. No.	273798
Contig ID	45751_1.R1011
5'-most EST	LIB143-036-Q1-E1-G8
Seq. No.	273799
Contig ID	45758_1.R1011
5'-most EST	LIB3059-024-Q1-K1-E11
Method	BLASTX
NCBI GI	g3395431
BLAST score	635
E value	4.0e-66
Match length	308
% identity	51
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.	273800
Contig ID	45767_1.R1011

5'-most EST	uC-zmflMo17010g02b1
Method	BLASTX
NCBI GI	g2648355
BLAST score	188
E value	6.0e-14
Match length	146
% identity	33
NCBI Description	(AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]

Seq. No.	273801
Contig ID	45769_1.R1011
5'-most EST	nbm700473796.h1

Seq. No.	273802
Contig ID	45783_1.R1011
5'-most EST	LIB143-037-Q1-E1-C9

Seq. No.	273803
Contig ID	45789_1.R1011
5'-most EST	wty700170543.h1
Method	BLASTX
NCBI GI	g4314376
BLAST score	288
E value	1.0e-25
Match length	112
% identity	53
NCBI Description	(AC006232) similar to PIG-L [Arabidopsis thaliana]

Seq. No.	273804
Contig ID	45791_1.R1011
5'-most EST	xyt700346392.h1
Method	BLASTX
NCBI GI	g3894171
BLAST score	695
E value	4.0e-73
Match length	215
% identity	62
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	273805
Contig ID	45795_1.R1011
5'-most EST	uC-zmflmo17048b05b1

Seq. No.	273806
Contig ID	45797_1.R1011
5'-most EST	nbm700468850.h1

Seq. No.	273807
Contig ID	45797_2.R1011
5'-most EST	yyf700350202.h1

Seq. No.	273808
Contig ID	45797_3.R1011
5'-most EST	wty700165027.h1

Seq. No.	273809
Contig ID	45800_1.R1011
5'-most EST	vux700158854.h1
Method	BLASTX
NCBI GI	g4240031
BLAST score	190
E value	4.0e-14
Match length	102
% identity	40
NCBI Description	(AB018422) DNA binding zinc finger protein (Pspzf) [Pisum sativum]

Seq. No.	273810
Contig ID	45805_1.R1011
5'-most EST	uC-zmroteosinte075e04b1

Seq. No.	273811
Contig ID	45810_2.R1011
5'-most EST	LIB3137-035-Q1-K1-G2

Seq. No.	273812
Contig ID	45823_1.R1011
5'-most EST	wyr700243806.h1

Seq. No.	273813
Contig ID	45827_1.R1011
5'-most EST	LIB143-037-Q1-E1-G12
Method	BLASTX
NCBI GI	g2244998
BLAST score	619
E value	3.0e-64
Match length	164
% identity	69
NCBI Description	(Z97341) similarity to probable transcriptional adaptor ADA2 [Arabidopsis thaliana]

Seq. No.	273814
Contig ID	45830_1.R1011
5'-most EST	xjt700094210.h1
Method	BLASTX
NCBI GI	g3193293
BLAST score	252
E value	3.0e-21
Match length	192
% identity	48
NCBI Description	(AF069298) contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375) [Arabidopsis thaliana]

Seq. No.	273815
Contig ID	45831_1.R1011
5'-most EST	LIB143-068-Q1-E1-E11

Seq. No.	273816
Contig ID	45846_1.R1011
5'-most EST	xmt700263274.h1

Seq. No.	273817
Contig ID	45848_1.R1011
5'-most EST	xsy700214156.h1
Method	BLASTX
NCBI GI	g3785989
BLAST score	558
E value	6.0e-57
Match length	339
% identity	43
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	273818
Contig ID	45856_1.R1011
5'-most EST	LIB143-038-Q1-E1-A8

Seq. No.	273819
Contig ID	45856_2.R1011
5'-most EST	xjt700096648.h1

Seq. No.	273820
Contig ID	45857_1.R1011
5'-most EST	nwy700443371.h1

Seq. No.	273821
Contig ID	45863_1.R1011
5'-most EST	xjt700094726.h1
Method	BLASTX
NCBI GI	g2760844
BLAST score	842
E value	4.0e-90
Match length	365
% identity	46
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273822
Contig ID	45863_3.R1011
5'-most EST	cjh700197706.h1

Seq. No.	273823
Contig ID	45864_1.R1011
5'-most EST	LIB143-038-Q1-E1-B5

Seq. No.	273824
Contig ID	45866_1.R1011
5'-most EST	LIB143-038-Q1-E1-B7
Method	BLASTX
NCBI GI	g2827535
BLAST score	315
E value	8.0e-29
Match length	138
% identity	49
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273825
Contig ID	45866_2.R1011
5'-most EST	rvt700550041.h1

Seq. No.	273826
Contig ID	45871_1.R1011
5'-most EST	LIB143-038-Q1-E1-C11
Method	BLASTX
NCBI GI	g1778095
BLAST score	152
E value	6.0e-10
Match length	41
% identity	73
NCBI Description	(U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	273827
Contig ID	45876_1.R1011
5'-most EST	uC-zmflb73064h01b1
Method	BLASTX
NCBI GI	g1703386
BLAST score	804
E value	7.0e-86
Match length	328
% identity	50
NCBI Description	ACETYLORNITHINE DEACETYLASE (ACETYLORNITHINASE) (AO) (N-ACETYLORNITHINASE) (NAO) >gi_763048 (U23957) N-acetylornithine deacetylase [Dictyostelium discoideum]

Seq. No.	273828
Contig ID	45880_1.R1011
5'-most EST	kem700611044.h1
Method	BLASTX
NCBI GI	g4262225
BLAST score	552
E value	2.0e-56
Match length	185
% identity	55
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No.	273829
Contig ID	45880_2.R1011
5'-most EST	qmh700027084.f1

Seq. No.	273830
Contig ID	45880_3.R1011
5'-most EST	wyr700242780.h1
Method	BLASTX
NCBI GI	g4262225
BLAST score	565
E value	7.0e-58
Match length	177
% identity	58
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No.	273831
Contig ID	45888_1.R1011
5'-most EST	LIB143-038-Q1-E1-E1

Method	BLASTN
NCBI GI	g4514634
BLAST score	345
E value	0.0e+00
Match length	345
% identity	100
NCBI Description	Zea mays ZmRCP1 mRNA for root cap protein 1, complete cds

Seq. No.	273832
Contig ID	45911_1.R1011
5'-most EST	qmh700029517.f1
Method	BLASTX
NCBI GI	g1495804
BLAST score	589
E value	4.0e-61
Match length	158
% identity	69
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	273833
Contig ID	45921_1.R1011
5'-most EST	LIB143-038-Q1-E1-H3

Seq. No.	273834
Contig ID	45923_1.R1011
5'-most EST	LIB143-038-Q1-E1-H5
Method	BLASTX
NCBI GI	g4510373
BLAST score	378
E value	8.0e-36
Match length	143
% identity	48
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	273835
Contig ID	45923_3.R1011
5'-most EST	ntr700077227.h1

Seq. No.	273836
Contig ID	45928_1.R1011
5'-most EST	jfc700968684.h1
Method	BLASTX
NCBI GI	g4510346
BLAST score	300
E value	5.0e-27
Match length	113
% identity	56
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273837
Contig ID	45928_3.R1011
5'-most EST	xjt700093745.h1
Method	BLASTX
NCBI GI	g4510346
BLAST score	179
E value	6.0e-13

Match length	68
% identity	59
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273838
Contig ID	45934_1.R1011
5'-most EST	uC-zmrob73019c04b1
Method	BLASTN
NCBI GI	g22322
BLAST score	47
E value	7.0e-17
Match length	99
% identity	87
NCBI Description	Z.mays mRNA for H2B histone (clone cH2B214)

Seq. No.	273839
Contig ID	45934_2.R1011
5'-most EST	xjt700095280.h1
Method	BLASTN
NCBI GI	g902585
BLAST score	52
E value	4.0e-20
Match length	64
% identity	95
NCBI Description	Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No.	273840
Contig ID	45936_1.R1011
5'-most EST	ymt700223624.h1
Method	BLASTX
NCBI GI	g4262230
BLAST score	228
E value	2.0e-18
Match length	64
% identity	70
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	273841
Contig ID	45957_1.R1011
5'-most EST	xmt700260205.h1

Seq. No.	273842
Contig ID	45963_1.R1011
5'-most EST	ceu700423026.h1
Method	BLASTX
NCBI GI	g4106538
BLAST score	795
E value	4.0e-87
Match length	220
% identity	71
NCBI Description	(AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]

Seq. No.	273843
Contig ID	45979_1.R1011
5'-most EST	LIB143-039-Q1-E1-H12

Seq. No.	273844
Contig ID	45980_1.R1011
5'-most EST	LIB143-039-Q1-E1-H2
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	273845
Contig ID	45982_1.R1011
5'-most EST	LIB143-063-Q1-E1-H9

Seq. No.	273846
Contig ID	45982_2.R1011
5'-most EST	LIB143-039-Q1-E1-H7

Seq. No.	273847
Contig ID	45985_1.R1011
5'-most EST	xjt700094346.h1
Method	BLASTX
NCBI GI	g3915070
BLAST score	1155
E value	1.0e-127
Match length	251
% identity	92
NCBI Description	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) >gi_1841704_emb_CAB06653_ (Z85984) histidyl tRNA Synthetase [Oryza sativa]

Seq. No.	273848
Contig ID	45988_1.R1011
5'-most EST	LIB143-040-Q1-E1-A12

Seq. No.	273849
Contig ID	45994_1.R1011
5'-most EST	LIB3069-004-Q1-K1-C10

Seq. No.	273850
Contig ID	46012_1.R1011
5'-most EST	LIB143-040-Q1-E1-C5

Seq. No.	273851
Contig ID	46013_1.R1011
5'-most EST	uC-zmf1b73272a04b1
Method	BLASTX
NCBI GI	g1087073
BLAST score	694
E value	5.0e-73
Match length	265
% identity	53
NCBI Description	(S79243) calmodulin-binding heat-shock protein, CaMBP [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa] [Nicotiana tabacum]

Seq. No.	273852
Contig ID	46014_1.R1011
5'-most EST	uC-zmflm017214g07b1
Method	BLASTX
NCBI GI	g419789
BLAST score	307
E value	5.0e-28
Match length	99
% identity	61
NCBI Description	hypothetical protein - potato

Seq. No.	273853
Contig ID	46025_1.R1011
5'-most EST	fdz701160519.h1
Method	BLASTX
NCBI GI	g4510425
BLAST score	531
E value	2.0e-54
Match length	126
% identity	79
NCBI Description	(AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	273854
Contig ID	46026_1.R1011
5'-most EST	LIB143-057-Q1-E1-A9
Method	BLASTX
NCBI GI	g3023751
BLAST score	527
E value	1.0e-53
Match length	143
% identity	40
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	273855
Contig ID	46031_1.R1011
5'-most EST	wyr700244209.h1

Seq. No.	273856
Contig ID	46035_1.R1011
5'-most EST	xmt700267963.h1
Method	BLASTX
NCBI GI	g2501196
BLAST score	271
E value	1.0e-23
Match length	47
% identity	98
NCBI Description	GAMMA-ZEATHIONIN

Seq. No.	273857
Contig ID	46035_2.R1011
5'-most EST	xmt700260314.h2
Method	BLASTX
NCBI GI	g2501196

BLAST score	271
E value	8.0e-24
Match length	47
% identity	98
NCBI Description	GAMMA-ZEATHIONIN

Seq. No.	273858
Contig ID	46035_4.R1011
5'-most EST	xmt700258485.h1
Method	BLASTX
NCBI GI	g2501196
BLAST score	271
E value	9.0e-24
Match length	47
% identity	98
NCBI Description	GAMMA-ZEATHIONIN

Seq. No.	273859
Contig ID	46053_1.R1011
5'-most EST	LIB148-058-Q1-E1-A9
Method	BLASTX
NCBI GI	g3426041
BLAST score	616
E value	8.0e-64
Match length	190
% identity	56
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	273860
Contig ID	46053_2.R1011
5'-most EST	LIB148-017-Q1-E1-D6
Method	BLASTX
NCBI GI	g3426041
BLAST score	368
E value	9.0e-35
Match length	145
% identity	47
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	273861
Contig ID	46053_3.R1011
5'-most EST	LIB148-002-Q1-E1-B10
Method	BLASTX
NCBI GI	g3298544
BLAST score	263
E value	6.0e-23
Match length	129
% identity	43
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]

Seq. No.	273862
Contig ID	46070_1.R1011
5'-most EST	uC-zmflmo17179f09b1
Method	BLASTX
NCBI GI	g1771381
BLAST score	254
E value	1.0e-21

Match length	127
% identity	47
NCBI Description	(X95877) phosphoinositide-specific phospholipase C [Nicotiana rustica]

Seq. No.	273863
Contig ID	46086_1.R1011
5'-most EST	LIB83-003-Q1-E1-E1
Method	BLASTX
NCBI GI	g4415942
BLAST score	192
E value	3.0e-14
Match length	147
% identity	34
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273864
Contig ID	46102_1.R1011
5'-most EST	uC-zmflb73070d10b1
Method	BLASTX
NCBI GI	g4504799
BLAST score	1288
E value	1.0e-142
Match length	371
% identity	66
NCBI Description	isovaleryl Coenzyme A dehydrogenase >gi_125051_sp_P26440_IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD) >gi_88038_pir__A37033 isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human >gi_306897 (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens]

Seq. No.	273865
Contig ID	46102_3.R1011
5'-most EST	LIB3137-002-Q1-K1-B4

Seq. No.	273866
Contig ID	46111_1.R1011
5'-most EST	LIB143-041-Q1-E1-F6
Method	BLASTX
NCBI GI	g114182
BLAST score	307
E value	6.0e-28
Match length	85
% identity	66
NCBI Description	CHORISMATE SYNTHASE PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE) >gi_99502_pir__A41197 chorismate synthase (EC 4.6.1.4) - pink corydalis >gi_18256_emb_CAA43034_ (X60544) chorismate synthase [Corydalis sempervirens]

Seq. No.	273867
Contig ID	46130_1.R1011
5'-most EST	LIB143-041-Q1-E1-H2
Method	BLASTN
NCBI GI	g1532070
BLAST score	492
E value	0.0e+00

Match length	569
% identity	97
NCBI Description	Z.mays grp3 mRNA for glycine-rich protein

Seq. No.	273868
Contig ID	46131_1.R1011
5'-most EST	xyt700344947.h1
Method	BLASTN
NCBI GI	g168508
BLAST score	62
E value	6.0e-26
Match length	97
% identity	92
NCBI Description	Maize oleosin KD18 (KD18; L2) gene, complete cds

Seq. No.	273869
Contig ID	46131_2.R1011
5'-most EST	uC-zmflm017093b07b1
Method	BLASTX
NCBI GI	g4455351
BLAST score	620
E value	3.0e-64
Match length	168
% identity	68
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	273870
Contig ID	46131_3.R1011
5'-most EST	wyr700236786.h1
Method	BLASTX
NCBI GI	g4455351
BLAST score	449
E value	2.0e-44
Match length	147
% identity	61
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	273871
Contig ID	46131_5.R1011
5'-most EST	xsy700211307.h1
Method	BLASTX
NCBI GI	g4455351
BLAST score	181
E value	2.0e-13
Match length	52
% identity	56
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	273872
Contig ID	46132_1.R1011
5'-most EST	LIB143-041-Q1-E1-H5
Method	BLASTX
NCBI GI	g3132825
BLAST score	688
E value	1.0e-72
Match length	157
% identity	87

NCBI Description	(AF063403) putative cytosine-5 DNA methyltransferase [Zea mays]

Seq. No.	273873
Contig ID	46148_1.R1011
5'-most EST	xyt700346241.h1
Method	BLASTX
NCBI GI	g4455260
BLAST score	1082
E value	1.0e-118
Match length	232
% identity	85
NCBI Description	(AL035353) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	273874
Contig ID	46153_1.R1011
5'-most EST	uwc700150468.h1
Method	BLASTX
NCBI GI	g4539348
BLAST score	216
E value	2.0e-17
Match length	96
% identity	44
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	273875
Contig ID	46158_1.R1011
5'-most EST	LIB3137-018-Q1-K1-B1

Seq. No.	273876
Contig ID	46163_1.R1011
5'-most EST	uC-zmroteosinte020c08b1

Seq. No.	273877
Contig ID	46169_1.R1011
5'-most EST	vux700161136.h1
Method	BLASTX
NCBI GI	g130940
BLAST score	598
E value	4.0e-62
Match length	125
% identity	87
NCBI Description	PATHOGENESIS-RELATED PROTEIN PRMS PRECURSOR >gi_100906_pir__S14969 pathogenesis-related protein - maize >gi_22454_emb_CAA38223_ (X54325) pathogenesis-related protein [Zea mays]

Seq. No.	273878
Contig ID	46171_1.R1011
5'-most EST	wyr700237789.h1
Method	BLASTX
NCBI GI	g1498055
BLAST score	737
E value	4.0e-78
Match length	144
% identity	99

NCBI Description	(U64437) novel protein [Zea mays]

Seq. No.	273879
Contig ID	46179_1.R1011
5'-most EST	uC-zmflmo17042a05b1
Method	BLASTX
NCBI GI	g3367591
BLAST score	541
E value	1.0e-54
Match length	205
% identity	52
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	273880
Contig ID	46179_2.R1011
5'-most EST	nwy700444591.h1
Method	BLASTN
NCBI GI	g168436
BLAST score	111
E value	4.0e-55
Match length	139
% identity	96
NCBI Description	Zea mays catalase (Cat3) gene, complete cds

Seq. No.	273881
Contig ID	46179_5.R1011
5'-most EST	LIB3061-026-Q1-K1-B1

Seq. No.	273882
Contig ID	46184_1.R1011
5'-most EST	uC-zmroteosinte120a03b2
Method	BLASTX
NCBI GI	g3374509
BLAST score	308
E value	7.0e-28
Match length	231
% identity	34
NCBI Description	(AB016529) Ku70 [Gallus gallus]

Seq. No.	273883
Contig ID	46197_1.R1011
5'-most EST	uC-zmflb73299d09b1
Method	BLASTX
NCBI GI	g3913517
BLAST score	1006
E value	1.0e-109
Match length	296
% identity	66
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1109672 (U33283) 3'(2'),5-diphosphonucleoside 3'(2') phosphohydrolase [Oryza sativa] >gi_1586671_prf__2204308A diphosphonucleoside phosphohydrolase [Oryza sativa]

Seq. No.	273884
Contig ID	46199_1.R1011

5'-most EST	LIB143-042-Q1-E1-G12
Method	BLASTX
NCBI GI	g3413699
BLAST score	190
E value	6.0e-14
Match length	107
% identity	42
NCBI Description	(AC004747) putative heat shock protein [Arabidopsis thaliana]

Seq. No.	273885
Contig ID	46201_1.R1011
5'-most EST	vux700156690.h1

Seq. No.	273886
Contig ID	46221_1.R1011
5'-most EST	LIB143-043-Q1-E1-A2
Method	BLASTX
NCBI GI	g477226
BLAST score	502
E value	7.0e-51
Match length	103
% identity	100
NCBI Description	heat shock protein HSP82 - maize >gi_300083_bbs_130886 (S59780) HSP82=82 kda heat shock protein [Zea mays, seedling, leaves, Peptide, 715 aa] [Zea mays]

Seq. No.	273887
Contig ID	46231_1.R1011
5'-most EST	fC-zmle700426995d2
Method	BLASTX
NCBI GI	g2245066
BLAST score	295
E value	1.0e-26
Match length	105
% identity	53
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	273888
Contig ID	46233_1.R1011
5'-most EST	LIB143-043-Q1-E1-B6

Seq. No.	273889
Contig ID	46234_1.R1011
5'-most EST	LIB143-043-Q1-E1-B7
Method	BLASTX
NCBI GI	g3551247
BLAST score	575
E value	2.0e-59
Match length	134
% identity	85
NCBI Description	(AB012703) 181 [Daucus carota]

Seq. No.	273890
Contig ID	46235_1.R1011
5'-most EST	uC-zmflmo17344d02b1

Seq. No.	273891
Contig ID	46244_1.R1011
5'-most EST	LIB3118-012-Q1-K1-A9
Method	BLASTX
NCBI GI	g2739168
BLAST score	231
E value	4.0e-19
Match length	74
% identity	58
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	273892
Contig ID	46254_1.R1011
5'-most EST	ntr700073691.h1
Method	BLASTX
NCBI GI	g3164222
BLAST score	254
E value	2.0e-21
Match length	123
% identity	43
NCBI Description	(AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205 (AF071527) RMA1 RING zinc finger protein [Arabidopsis thaliana]

Seq. No.	273893
Contig ID	46261_1.R1011
5'-most EST	ntr700071715.h1
Method	BLASTX
NCBI GI	g3763933
BLAST score	584
E value	3.0e-60
Match length	227
% identity	63
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	273894
Contig ID	46266_1.R1011
5'-most EST	uC-zmf1b73184g12b1
Method	BLASTX
NCBI GI	g2642158
BLAST score	1090
E value	1.0e-119
Match length	361
% identity	59
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273895
Contig ID	46274_1.R1011
5'-most EST	ntr700072240.h1
Method	BLASTX
NCBI GI	g4115377
BLAST score	1569
E value	1.0e-175
Match length	416
% identity	72
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	273896
Contig ID	46282_1.R1011
5'-most EST	LIB143-043-Q1-E1-H10
Method	BLASTN
NCBI GI	g1850902
BLAST score	39
E value	1.0e-12
Match length	75
% identity	88
NCBI Description	Z.mays cyp71c4 gene

Seq. No.	273897
Contig ID	46309_1.R1011
5'-most EST	LIB143-044-Q1-E1-C11

Seq. No.	273898
Contig ID	46323_1.R1011
5'-most EST	LIB36-004-Q1-E1-A9
Method	BLASTX
NCBI GI	g1848225
BLAST score	235
E value	2.0e-19
Match length	68
% identity	60
NCBI Description	(U88090) nonspecific lipid transfer protein [Hordeum vulgare]

Seq. No.	273899
Contig ID	46335_1.R1011
5'-most EST	LIB143-044-Q1-E1-E8
Method	BLASTX
NCBI GI	g3142300
BLAST score	287
E value	2.0e-25
Match length	118
% identity	47
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	273900
Contig ID	46337_1.R1011
5'-most EST	LIB143-044-Q1-E1-F10
Method	BLASTX
NCBI GI	g2760345
BLAST score	460
E value	4.0e-46
Match length	96
% identity	26
NCBI Description	(U84967) ubiquitin [Arabidopsis thaliana]

Seq. No.	273901
Contig ID	46343_1.R1011
5'-most EST	uC-zmflmo17215e07b1
Method	BLASTX

NCBI GI	g3367577
BLAST score	150
E value	2.0e-09
Match length	155
% identity	29
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	273902
Contig ID	46353_1.R1011
5'-most EST	LIB143-044-Q1-E1-H1

Seq. No.	273903
Contig ID	46354_1.R1011
5'-most EST	LIB143-044-Q1-E1-H10

Seq. No.	273904
Contig ID	46361_1.R1011
5'-most EST	LIB143-044-Q1-E1-H8

Seq. No.	273905
Contig ID	46361_2.R1011
5'-most EST	uer700581506.h1

Seq. No.	273906
Contig ID	46370_1.R1011
5'-most EST	cjh700195606.h1

Seq. No.	273907
Contig ID	46370_2.R1011
5'-most EST	LIB3062-027-Q1-K1-F6

Seq. No.	273908
Contig ID	46370_4.R1011
5'-most EST	uC-zmf1b73295c10b2

Seq. No.	273909
Contig ID	46372_1.R1011
5'-most EST	LIB3136-057-Q1-K1-A7
Method	BLASTX
NCBI GI	g4432823
BLAST score	414
E value	4.0e-40
Match length	183
% identity	52
NCBI Description	(AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273910
Contig ID	46376_1.R1011
5'-most EST	xjt700096958.h1
Method	BLASTX
NCBI GI	g2129513
BLAST score	777
E value	1.0e-82
Match length	278
% identity	59
NCBI Description	peroxidase (EC 1.11.1.7) A3a precursor - Japanese aspen x large-toothed aspen >gi_1255661_dbj_BAA07240_ (D38050)

peroidase precursor [Populus kitakamiensis]

Seq. No.	273911
Contig ID	46379_1.R1011
5'-most EST	uC-zmflmo17310b07b1
Method	BLASTX
NCBI GI	g2344889
BLAST score	941
E value	1.0e-102
Match length	447
% identity	42
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	273912
Contig ID	46383_1.R1011
5'-most EST	LIB3067-046-Q1-K1-E12

Seq. No.	273913
Contig ID	46383_2.R1011
5'-most EST	wty700164975.h1
Method	BLASTX
NCBI GI	g2244979
BLAST score	474
E value	1.0e-47
Match length	126
% identity	71
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	273914
Contig ID	46396_1.R1011
5'-most EST	ypc700803036.h1
Method	BLASTX
NCBI GI	g2865623
BLAST score	541
E value	3.0e-55
Match length	139
% identity	75
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	273915
Contig ID	46399_1.R1011
5'-most EST	vux700159849.h1
Method	BLASTX
NCBI GI	g3059129
BLAST score	552
E value	2.0e-56
Match length	245
% identity	45
NCBI Description	(AJ000477) cytochrome P450 [Helianthus tuberosus]

Seq. No.	273916
Contig ID	46401_1.R1011
5'-most EST	pwr700451443.h1
Method	BLASTX

NCBI GI	g3021357
BLAST score	288
E value	8.0e-26
Match length	78
% identity	69
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	273917
Contig ID	46442_1.R1011
5'-most EST	LIB143-046-Q1-E1-B3

Seq. No.	273918
Contig ID	46450_2.R1011
5'-most EST	hvj700623212.h1

Seq. No.	273919
Contig ID	46459_1.R1011
5'-most EST	uC-zmflb73082b03a2

Seq. No.	273920
Contig ID	46464_1.R1011
5'-most EST	LIB143-046-Q1-E1-D4

Seq. No.	273921
Contig ID	46469_1.R1011
5'-most EST	LIB143-046-Q1-E1-E1
Method	BLASTX
NCBI GI	g2129929
BLAST score	348
E value	6.0e-33
Match length	121
% identity	53
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 - tomato >gi_1049068 (U28403) RNA polymerase II subunit 2 [Solanum lycopersicum]

Seq. No.	273922
Contig ID	46470_1.R1011
5'-most EST	LIB143-046-Q1-E1-E10
Method	BLASTX
NCBI GI	g3688187
BLAST score	494
E value	6.0e-50
Match length	127
% identity	71
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	273923
Contig ID	46474_1.R1011
5'-most EST	cjh700196009.h1
Method	BLASTX
NCBI GI	g4587686
BLAST score	605
E value	2.0e-62
Match length	256
% identity	54

NCBI Description	(AC007197) dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	273924
Contig ID	46474_4.R1011
5'-most EST	LIB3066-024-Q1-K1-B4
Method	BLASTX
NCBI GI	g4587686
BLAST score	157
E value	2.0e-10
Match length	55
% identity	58
NCBI Description	(AC007197) dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	273925
Contig ID	46474_5.R1011
5'-most EST	ceu700431258.h1

Seq. No.	273926
Contig ID	46482_1.R1011
5'-most EST	uC-zmroteosinte059g08b1
Method	BLASTX
NCBI GI	g2589162
BLAST score	1035
E value	1.0e-113
Match length	215
% identity	94
NCBI Description	(D88451) aldehyde oxidase [Zea mays]

Seq. No.	273927
Contig ID	46484_1.R1011
5'-most EST	uC-zmrob73078f06b1

Seq. No.	273928
Contig ID	46485_1.R1011
5'-most EST	xjt700093733.h1
Method	BLASTX
NCBI GI	g2245034
BLAST score	403
E value	4.0e-39
Match length	118
% identity	68
NCBI Description	(Z97342) enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	273929
Contig ID	46487_1.R1011
5'-most EST	uC-zmflmo17257b11b1

Seq. No.	273930
Contig ID	46496_1.R1011
5'-most EST	xmt700257167.h1
Method	BLASTX
NCBI GI	g3123745
BLAST score	202
E value	1.0e-15
Match length	104
% identity	44
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	273931
Contig ID	46496_2.R1011
5'-most EST	xmt700265767.h1
Seq. No.	273932
Contig ID	46498_1.R1011
5'-most EST	uC-zmflmo17021b11b1
Seq. No.	273933
Contig ID	46498_2.R1011
5'-most EST	uC-zmroteosinte032g03b1
Method	BLASTX
NCBI GI	g2098575
BLAST score	354
E value	5.0e-33
Match length	104
% identity	65
NCBI Description	(AC002115) F25451_2 [Homo sapiens]
Seq. No.	273934
Contig ID	46499_1.R1011
5'-most EST	LIB143-046-Q1-E1-H1
Seq. No.	273935
Contig ID	46500_1.R1011
5'-most EST	fdz701163570.h1
Seq. No.	273936
Contig ID	46501_1.R1011
5'-most EST	LIB3068-061-Q1-K1-H10
Seq. No.	273937
Contig ID	46509_1.R1011
5'-most EST	LIB143-047-Q1-E1-A10
Method	BLASTX
NCBI GI	g3540207
BLAST score	630
E value	1.0e-65
Match length	184
% identity	70
NCBI Description	(AC004260) Putative protein kinase [Arabidopsis thaliana]
Seq. No.	273938
Contig ID	46524_1.R1011
5'-most EST	LIB143-063-Q1-E1-B3
Seq. No.	273939
Contig ID	46533_1.R1011
5'-most EST	rvt700551486.h1
Seq. No.	273940
Contig ID	46537_1.R1011
5'-most EST	wty700166678.h1
Seq. No.	273941
Contig ID	46539_1.R1011

5'-most EST	LIB143-047-Q1-E1-E10
Seq. No.	273942
Contig ID	46563_1.R1011
5'-most EST	pmx700091770.h1
Method	BLASTX
NCBI GI	g1709574
BLAST score	244
E value	9.0e-21
Match length	72
% identity	60
NCBI Description	CARICAIN PRECURSOR (PAPAYA PROTEINASE OMEGA) (PAPAYA PROTEINASE III) (PPIII) (PAPAYA PEPTIDASE A) >gi_484397_pir__JN0633 caricain (EC 3.4.22.30) I precursor - papaya >gi_18098_emb_CAA46862_ (X66060) proteinase omega [Carica papaya]
Seq. No.	273943
Contig ID	46572_1.R1011
5'-most EST	LIB143-047-Q1-E1-H7
Seq. No.	273944
Contig ID	46576_1.R1011
5'-most EST	LIB143-051-Q1-E1-F3
Method	BLASTX
NCBI GI	g100883
BLAST score	155
E value	3.0e-10
Match length	94
% identity	35
NCBI Description	heat shock protein 17.2 - maize >gi_22335_emb_CAA46641_ (X65725) heat shock protein 17.2 [Zea mays]
Seq. No.	273945
Contig ID	46578_1.R1011
5'-most EST	clt700042461.f1
Method	BLASTX
NCBI GI	g3059131
BLAST score	198
E value	2.0e-15
Match length	65
% identity	54
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]
Seq. No.	273946
Contig ID	46579_1.R1011
5'-most EST	clt700046203.f1
Method	BLASTX
NCBI GI	g2494116
BLAST score	424
E value	3.0e-68
Match length	168
% identity	77
NCBI Description	(AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]
Seq. No.	273947

Contig ID	46588_1.R1011
5'-most EST	uC-zmflmo17317g11a1
Seq. No.	273948
Contig ID	46594_1.R1011
5'-most EST	uC-zmflm017092b03b1
Method	BLASTX
NCBI GI	g4263707
BLAST score	650
E value	7.0e-68
Match length	195
% identity	61
NCBI Description	(AC006223) putative 70kD heat shock protein [Arabidopsis thaliana]
Seq. No.	273949
Contig ID	46602_1.R1011
5'-most EST	LIB3136-040-P1-K1-A3
Seq. No.	273950
Contig ID	46631_1.R1011
5'-most EST	LIB148-050-Q1-E1-A8
Method	BLASTX
NCBI GI	g4455359
BLAST score	366
E value	2.0e-34
Match length	183
% identity	50
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]
Seq. No.	273951
Contig ID	46631_2.R1011
5'-most EST	LIB143-048-Q1-E1-F6
Method	BLASTX
NCBI GI	g4455359
BLAST score	222
E value	8.0e-18
Match length	58
% identity	74
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]
Seq. No.	273952
Contig ID	46643_1.R1011
5'-most EST	LIB143-048-Q1-E1-G8
Method	BLASTN
NCBI GI	g12455
BLAST score	302
E value	1.0e-169
Match length	400
% identity	93
NCBI Description	Maize chloroplast rpl16 gene for ribosomal protein L16 exon
Seq. No.	273953
Contig ID	46652_1.R1011
5'-most EST	LIB143-048-Q1-E1-H7
Seq. No.	273954

Contig ID 46654_2.R1011
5'-most EST uC-zmflb73238f02b2

Seq. No. 273955
Contig ID 46654_3.R1011
5'-most EST LIB143-048-Q1-E1-H9

Seq. No. 273956
Contig ID 46662_1.R1011
5'-most EST LIB143-049-Q1-E1-B10

Seq. No. 273957
Contig ID 46665_1.R1011
5'-most EST wyr700238234.h1

Seq. No. 273958
Contig ID 46681_1.R1011
5'-most EST uC-zmflb73052b12b1
Method BLASTX
NCBI GI g4115377
BLAST score 265
E value 3.0e-23
Match length 68
% identity 81
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 273959
Contig ID 46682_1.R1011
5'-most EST LIB3136-037-P1-K1-C2

Seq. No. 273960
Contig ID 46689_1.R1011
5'-most EST wyr700235247.h1
Method BLASTX
NCBI GI g169363
BLAST score 199
E value 3.0e-15
Match length 40
% identity 80
NCBI Description (M75856) PVPR3 [Phaseolus vulgaris]

Seq. No. 273961
Contig ID 46708_1.R1011
5'-most EST LIB143-049-Q1-E1-G3
Method BLASTN
NCBI GI g454880
BLAST score 88
E value 9.0e-42
Match length 205
% identity 87
NCBI Description Rice mRNA for WSI724 protein induced by water stress, complete cds

Seq. No. 273962
Contig ID 46716_1.R1011
5'-most EST hbs701182765.h1

Seq. No.	273963
Contig ID	46732_1.R1011
5'-most EST	LIB143-050-Q1-E1-B12

Seq. No.	273964
Contig ID	46733_1.R1011
5'-most EST	LIB143-050-Q1-E1-B2

Seq. No.	273965
Contig ID	46733_2.R1011
5'-most EST	nbm700469678.h1

Seq. No.	273966
Contig ID	46739_1.R1011
5'-most EST	nbm700477945.h1
Method	BLASTX
NCBI GI	g3033400
BLAST score	1096
E value	1.0e-120
Match length	268
% identity	74
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	273967
Contig ID	46745_1.R1011
5'-most EST	LIB143-050-Q1-E1-C5

Seq. No.	273968
Contig ID	46752_1.R1011
5'-most EST	LIB143-050-Q1-E1-D12

Seq. No.	273969
Contig ID	46773_1.R1011
5'-most EST	LIB143-050-Q1-E1-F5
Method	BLASTX
NCBI GI	g1213118
BLAST score	171
E value	4.0e-12
Match length	68
% identity	46
NCBI Description	(X92984) low molecular weight heat-shock protein [Pseudotsuga menziesii]

Seq. No.	273970
Contig ID	46780_1.R1011
5'-most EST	uC-zmflmo17310f03a1
Method	BLASTX
NCBI GI	g4539403
BLAST score	464
E value	8.0e-46
Match length	124
% identity	68
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	273971
Contig ID	46783_1.R1011

5'-most EST	LIB143-050-Q1-E1-G8
Method	BLASTX
NCBI GI	g2909522
BLAST score	232
E value	6.0e-19
Match length	142
% identity	36
NCBI Description	(AL021932) ufaA1 [Mycobacterium tuberculosis]

Seq. No.	273972
Contig ID	46800_1.R1011
5'-most EST	uC-zmf1Mo17002h06b1
Method	BLASTX
NCBI GI	g3402712
BLAST score	162
E value	4.0e-11
Match length	43
% identity	70
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273973
Contig ID	46800_2.R1011
5'-most EST	xmt700266774.h1

Seq. No.	273974
Contig ID	46803_1.R1011
5'-most EST	LIB143-051-Q1-E1-A9
Method	BLASTX
NCBI GI	g4455328
BLAST score	476
E value	2.0e-47
Match length	116
% identity	74
NCBI Description	(AL035525) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273975
Contig ID	46810_1.R1011
5'-most EST	LIB143-051-Q1-E1-B5
Method	BLASTX
NCBI GI	g2497748
BLAST score	180
E value	3.0e-13
Match length	79
% identity	35
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4) >gi_902058 (U29176) lipid transfer protein precursor [Oryza sativa]

Seq. No.	273976
Contig ID	46813_1.R1011
5'-most EST	LIB143-051-Q1-E1-B9
Method	BLASTX
NCBI GI	g4586113
BLAST score	255
E value	5.0e-22
Match length	99
% identity	48

NCBI Description	(AL049638) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	273977
Contig ID	46817_1.R1011
5'-most EST	uC-zmflmo17150e04b1
Method	BLASTX
NCBI GI	g4220531
BLAST score	192
E value	5.0e-14
Match length	170
% identity	31
NCBI Description	(AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No.	273978
Contig ID	46817_2.R1011
5'-most EST	uC-zmflMo17014b03b1

Seq. No.	273979
Contig ID	46817_4.R1011
5'-most EST	wyr700243402.h1

Seq. No.	273980
Contig ID	46821_1.R1011
5'-most EST	uC-zmflmo17059g12a1

Seq. No.	273981
Contig ID	46823_1.R1011
5'-most EST	LIB143-051-Q1-E1-D1

Seq. No.	273982
Contig ID	46830_1.R1011
5'-most EST	LIB143-051-Q1-E1-D5

Seq. No.	273983
Contig ID	46866_1.R1011
5'-most EST	LIB143-051-Q1-E1-H2

Seq. No.	273984
Contig ID	46868_1.R1011
5'-most EST	rvl700453770.h1
Method	BLASTX
NCBI GI	g3415009
BLAST score	262
E value	2.0e-22
Match length	137
% identity	37
NCBI Description	(AF080245) sesquiterpene synthase [Elaeis oleifera]

Seq. No.	273985
Contig ID	46868_2.R1011
5'-most EST	hvj700621476.h1
Method	BLASTX
NCBI GI	g3415009
BLAST score	374
E value	8.0e-36
Match length	172

% identity	46
NCBI Description	(AF080245) sesquiterpene synthase [Elaeis oleifera]

Seq. No.	273986
Contig ID	46870_1.R1011
5'-most EST	xjt700094843.h1
Method	BLASTX
NCBI GI	g231707
BLAST score	809
E value	1.0e-86
Match length	163
% identity	96
NCBI Description	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG 2 >gi_100668_pir__S22441 protein kinase (EC 2.7.1.37) cdc2 homolog 2 - rice >gi_20345_emb_CAA42923_ (X60375) Rcdc2-2 [Oryza sativa] >gi_228925_prf__1814443B cdc2 protein:ISOTYPE=cdc2Os-2 [Oryza sativa]

Seq. No.	273987
Contig ID	46870_2.R1011
5'-most EST	uC-zmflb73070a11b1
Method	BLASTX
NCBI GI	g115923
BLAST score	1022
E value	1.0e-111
Match length	216
% identity	93
NCBI Description	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG >gi_168511 (M60526) protein cdc2 kinase [Zea mays]

Seq. No.	273988
Contig ID	46870_3.R1011
5'-most EST	hvj700622117.h1
Method	BLASTX
NCBI GI	g115923
BLAST score	521
E value	6.0e-53
Match length	117
% identity	91
NCBI Description	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG >gi_168511 (M60526) protein cdc2 kinase [Zea mays]

Seq. No.	273989
Contig ID	46877_1.R1011
5'-most EST	uC-zmrob73075e06b1
Method	BLASTX
NCBI GI	g2335100
BLAST score	450
E value	2.0e-44
Match length	184
% identity	47
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	273990
Contig ID	46885_1.R1011
5'-most EST	fwa700097484.h1
Method	BLASTX

NCBI GI g4490732
BLAST score 242
E value 2.0e-20
Match length 92
% identity 62
NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No. 273991
Contig ID 46885_2.R1011
5'-most EST LIB143-067-Q1-E1-A10
Method BLASTX
NCBI GI g4490732
BLAST score 257
E value 4.0e-22
Match length 88
% identity 60
NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No. 273992
Contig ID 46899_1.R1011
5'-most EST LIB3060-053-Q1-K1-C7

Seq. No. 273993
Contig ID 46910_1.R1011
5'-most EST LIB143-052-Q1-E1-E11

Seq. No. 273994
Contig ID 46913_1.R1011
5'-most EST jfc700968525.h1

Seq. No. 273995
Contig ID 46918_1.R1011
5'-most EST fC-zmle700441605a5
Method BLASTX
NCBI GI g4584541
BLAST score 1290
E value 1.0e-142
Match length 377
% identity 65
NCBI Description (AL049608) 3-hydroxyisobutyryl-coenzyme A hydrolase-like protein [Arabidopsis thaliana]

Seq. No. 273996
Contig ID 46918_2.R1011
5'-most EST fC-zmle700441605d5

Seq. No. 273997
Contig ID 46924_1.R1011
5'-most EST LIB143-052-Q1-E1-F4

Seq. No. 273998
Contig ID 46930_1.R1011
5'-most EST LIB143-052-Q1-E1-G1
Method BLASTX
NCBI GI g3142295

BLAST score	218
E value	3.0e-17
Match length	118
% identity	42
NCBI Description	(AC002411) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. [Arabidopsis thaliana]

Seq. No.	273999
Contig ID	46936_1.R1011
5'-most EST	LIB3059-027-Q1-K1-E2

Seq. No.	274000
Contig ID	46937_1.R1011
5'-most EST	uC-zmflmo17210e07a1
Method	BLASTX
NCBI GI	g3549656
BLAST score	201
E value	2.0e-15
Match length	84
% identity	46
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	274001
Contig ID	46937_2.R1011
5'-most EST	uer700583944.h1
Method	BLASTX
NCBI GI	g3549656
BLAST score	172
E value	1.0e-12
Match length	68
% identity	50
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	274002
Contig ID	46941_1.R1011
5'-most EST	vux700157966.h1
Method	BLASTN
NCBI GI	g4105124
BLAST score	150
E value	1.0e-78
Match length	251
% identity	98
NCBI Description	Zea mays cell wall invertase (incw4) gene, complete cds

Seq. No.	274003
Contig ID	46948_1.R1011
5'-most EST	uC-zmroteosinte008h12b1

Seq. No.	274004
Contig ID	46948_2.R1011
5'-most EST	uC-zmflb73062f09a1

Seq. No.	274005
Contig ID	46962_1.R1011
5'-most EST	LIB143-053-Q1-E1-D10
Method	BLASTX

NCBI GI	g1931641
BLAST score	245
E value	7.0e-21
Match length	134
% identity	41
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]

Seq. No.	274006
Contig ID	46985_1.R1011
5'-most EST	fdz701161363.h1

Seq. No.	274007
Contig ID	46995_1.R1011
5'-most EST	LIB143-053-Q1-E1-H11

Seq. No.	274008
Contig ID	46996_2.R1011
5'-most EST	LIB143-053-Q1-E1-H12
Method	BLASTX
NCBI GI	g1653033
BLAST score	154
E value	8.0e-18
Match length	143
% identity	43
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	274009
Contig ID	46997_1.R1011
5'-most EST	LIB143-053-Q1-E1-H2
Method	BLASTX
NCBI GI	g2244876
BLAST score	381
E value	1.0e-36
Match length	164
% identity	49
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274010
Contig ID	47005_1.R1011
5'-most EST	uC-zmf1b73237h04b2

Seq. No.	274011
Contig ID	47014_1.R1011
5'-most EST	LIB143-054-Q1-E1-A9

Seq. No.	274012
Contig ID	47016_1.R1011
5'-most EST	qmh700027441.f1
Method	BLASTX
NCBI GI	g3941480
BLAST score	149
E value	4.0e-09
Match length	38
% identity	74
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	274013
Contig ID	47016_3.R1011
5'-most EST	wty700164353.h1

Seq. No.	274014
Contig ID	47029_1.R1011
5'-most EST	uC-zmflB73043c11b1
Method	BLASTX
NCBI GI	g1658503
BLAST score	283
E value	1.0e-24
Match length	308
% identity	31
NCBI Description	(U75467) Atu [Drosophila melanogaster]

Seq. No.	274015
Contig ID	47041_1.R1011
5'-most EST	fdz701164867.h1
Method	BLASTX
NCBI GI	g3121837
BLAST score	497
E value	3.0e-50
Match length	111
% identity	82
NCBI Description	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_2182104_emb_CAA63004_ (X91909) CDP-diacylglycerol synthetase [Solanum tuberosum]

Seq. No.	274016
Contig ID	47041_2.R1011
5'-most EST	gct701174081.h1
Method	BLASTX
NCBI GI	g3121837
BLAST score	429
E value	4.0e-42
Match length	91
% identity	84
NCBI Description	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_2182104_emb_CAA63004_ (X91909) CDP-diacylglycerol synthetase [Solanum tuberosum]

Seq. No.	274017
Contig ID	47041_3.R1011
5'-most EST	uer700580213.h1
Method	BLASTX
NCBI GI	g3121837
BLAST score	640
E value	4.0e-67
Match length	138
% identity	83
NCBI Description	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE

SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_2182104_emb_CAA63004_ (X91909) CDP-diacylglycerol synthetase [Solanum tuberosum]

Seq. No.	274018
Contig ID	47051_1.R1011
5'-most EST	LIB3060-015-Q1-K1-A7

Seq. No.	274019
Contig ID	47080_1.R1011
5'-most EST	uC-zmflb73230d10b2
Method	BLASTX
NCBI GI	g465945
BLAST score	151
E value	4.0e-09
Match length	239
% identity	28
NCBI Description	HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III >gi_630670_pir__S44837 K02D10.1 protein - Caenorhabditis elegans >gi_289686 (L14710) homology with 4-nitrophenylphosphatase and mouse synaptosomal associated protein 25; putative [Caenorhabditis elegans]

Seq. No.	274020
Contig ID	47089_1.R1011
5'-most EST	uC-zmflmo17268a06b1

Seq. No.	274021
Contig ID	47103_1.R1011
5'-most EST	LIB143-055-Q1-E1-B7

Seq. No.	274022
Contig ID	47107_1.R1011
5'-most EST	LIB143-055-Q1-E1-C11
Method	BLASTX
NCBI GI	g1200239
BLAST score	333
E value	2.0e-67
Match length	155
% identity	84
NCBI Description	(X87690) GAMyb protein [Hordeum vulgare]

Seq. No.	274023
Contig ID	47109_1.R1011
5'-most EST	qmh700027501.f1
Method	BLASTX
NCBI GI	g1197461
BLAST score	932
E value	1.0e-101
Match length	241
% identity	77
NCBI Description	(X78819) casein kinase I [Arabidopsis thaliana]

Seq. No.	274024
Contig ID	47117_1.R1011

5'-most EST	uC-zmflb73088h11b2
Seq. No.	274025
Contig ID	47120_1.R1011
5'-most EST	wty700163870.h1
Method	BLASTX
NCBI GI	g4530066
BLAST score	219
E value	2.0e-17
Match length	161
% identity	29
NCBI Description	(AF060544) androgen receptor associated protein 54 [Homo sapiens]
Seq. No.	274026
Contig ID	47123_1.R1011
5'-most EST	LIB143-055-Q1-E1-E12
Method	BLASTX
NCBI GI	g3355486
BLAST score	420
E value	7.0e-41
Match length	113
% identity	74
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.	274027
Contig ID	47128_1.R1011
5'-most EST	mwy700442378.h1
Method	BLASTX
NCBI GI	g2244899
BLAST score	148
E value	2.0e-09
Match length	88
% identity	39
NCBI Description	(Z97338) similar to UFD1 protein [Arabidopsis thaliana]
Seq. No.	274028
Contig ID	47135_1.R1011
5'-most EST	LIB3069-008-Q1-K1-A5
Seq. No.	274029
Contig ID	47152_1.R1011
5'-most EST	LIB3067-047-Q1-K1-F2
Method	BLASTX
NCBI GI	g4586246
BLAST score	1276
E value	1.0e-141
Match length	418
% identity	57
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]
Seq. No.	274030
Contig ID	47156_1.R1011
5'-most EST	LIB143-056-Q1-E1-A10
Seq. No.	274031
Contig ID	47158_1.R1011

5'-most EST	wty700168817.h1
Seq. No.	274032
Contig ID	47163_1.R1011
5'-most EST	uC-zmroteosinte035c04b2
Method	BLASTX
NCBI GI	g3059131
BLAST score	497
E value	3.0e-50
Match length	154
% identity	57
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]
Seq. No.	274033
Contig ID	47170_1.R1011
5'-most EST	LIB143-056-Q1-E1-C1
Seq. No.	274034
Contig ID	47173_1.R1011
5'-most EST	zuv700354427.h1
Method	BLASTX
NCBI GI	g2190419
BLAST score	352
E value	3.0e-33
Match length	81
% identity	81
NCBI Description	(Y13632) dem [Lycopersicon esculentum]
Seq. No.	274035
Contig ID	47188_1.R1011
5'-most EST	uC-zmflmo17037e12b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	7.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	274036
Contig ID	47188_2.R1011
5'-most EST	xsy700207451.h1
Seq. No.	274037
Contig ID	47192_1.R1011
5'-most EST	LIB3067-044-Q1-K1-D6
Seq. No.	274038
Contig ID	47208_1.R1011
5'-most EST	hbs701183244.h1
Method	BLASTX
NCBI GI	g4432844
BLAST score	174
E value	3.0e-20
Match length	143
% identity	40
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	274039
Contig ID	47213_1.R1011
5'-most EST	fC-zmfl700464992a2

Seq. No.	274040
Contig ID	47215_1.R1011
5'-most EST	uC-zmflmo17202a10b1
Method	BLASTX
NCBI GI	g1877397
BLAST score	991
E value	1.0e-112
Match length	217
% identity	88
NCBI Description	(Y11591) shaggy-like kinase [Ricinus communis]

Seq. No.	274041
Contig ID	47215_2.R1011
5'-most EST	LIB143-057-Q1-E1-A1
Method	BLASTX
NCBI GI	g2129739
BLAST score	1075
E value	1.0e-117
Match length	221
% identity	90
NCBI Description	shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947) shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No.	274042
Contig ID	47215_3.R1011
5'-most EST	xmt700267777.h1
Method	BLASTX
NCBI GI	g2129739
BLAST score	383
E value	8.0e-37
Match length	84
% identity	87
NCBI Description	shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947) shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No.	274043
Contig ID	47215_4.R1011
5'-most EST	LIB3069-030-Q1-K1-G11
Method	BLASTX
NCBI GI	g1480078
BLAST score	263
E value	2.0e-24
Match length	79
% identity	80
NCBI Description	(X99696) shaggy-like protein kinase iota [Arabidopsis thaliana] >gi_2444277 (AF019927) GSK3/shaggy-like protein kinase [Arabidopsis thaliana]

Seq. No.	274044
Contig ID	47219_1.R1011
5'-most EST	uC-zmrob73006a11b1
Method	BLASTX
NCBI GI	g2598589
BLAST score	291
E value	1.0e-49
Match length	188
% identity	51
NCBI Description	(Y15367) MtN19 [Medicago truncatula]

Seq. No.	274045
Contig ID	47228_1.R1011
5'-most EST	dyk700105716.h1
Method	BLASTX
NCBI GI	g2662310
BLAST score	478
E value	4.0e-48
Match length	113
% identity	83
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]

Seq. No.	274046
Contig ID	47242_1.R1011
5'-most EST	LIB143-057-Q1-E1-C6

Seq. No.	274047
Contig ID	47247_1.R1011
5'-most EST	gct701176057.h1

Seq. No.	274048
Contig ID	47251_1.R1011
5'-most EST	tzu700201809.h1
Method	BLASTX
NCBI GI	g4322940
BLAST score	279
E value	2.0e-24
Match length	98
% identity	29
NCBI Description	(AF096299) DNA-binding protein 2 [Nicotiana tabacum]

Seq. No.	274049
Contig ID	47256_1.R1011
5'-most EST	LIB143-057-Q1-E1-E1
Method	BLASTX
NCBI GI	g4263696
BLAST score	337
E value	2.0e-31
Match length	142
% identity	51
NCBI Description	(AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274050
Contig ID	47279_1.R1011
5'-most EST	pmx700085750.h1
Method	BLASTX
NCBI GI	g4585993

BLAST score	503
E value	6.0e-51
Match length	143
% identity	62
NCBI Description	(AC005287) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	274051
Contig ID	47281_1.R1011
5'-most EST	yyf700348315.h1

Seq. No.	274052
Contig ID	47293_1.R1011
5'-most EST	uC-zmflb73134g10b1

Seq. No.	274053
Contig ID	47303_1.R1011
5'-most EST	LIB143-061-Q1-E1-E9

Seq. No.	274054
Contig ID	47316_1.R1011
5'-most EST	wyr700244333.h1
Method	BLASTX
NCBI GI	g3695408
BLAST score	148
E value	1.0e-14
Match length	62
% identity	71
NCBI Description	(AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable wound-induced protein [Arabidopsis thaliana]

Seq. No.	274055
Contig ID	47317_1.R1011
5'-most EST	LIB143-058-Q1-E1-C3
Method	BLASTX
NCBI GI	g3096922
BLAST score	308
E value	3.0e-28
Match length	131
% identity	51
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	274056
Contig ID	47319_1.R1011
5'-most EST	xsy700212459.h1
Method	BLASTX
NCBI GI	g4063002
BLAST score	178
E value	8.0e-13
Match length	156
% identity	33
NCBI Description	(AB021703) fr [Neurospora crassa]

Seq. No.	274057
Contig ID	47323_1.R1011

5'-most EST	LIB143-058-Q1-E1-D1
Method	BLASTX
NCBI GI	g4539303
BLAST score	207
E value	3.0e-16
Match length	77
% identity	53
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	274058
Contig ID	47331_1.R1011
5'-most EST	uC-zmflmo17297b03b1
Method	BLASTX
NCBI GI	g2815292
BLAST score	565
E value	7.0e-58
Match length	190
% identity	57
NCBI Description	(Y15962) Germin-like protein 1 [Hordeum vulgare]

Seq. No.	274059
Contig ID	47339_1.R1011
5'-most EST	hvj700623362.h1
Method	BLASTX
NCBI GI	g4432814
BLAST score	874
E value	1.0e-111
Match length	385
% identity	46
NCBI Description	(AC006593) unknown protein [Arabidopsis thaliana]

Seq. No.	274060
Contig ID	47348_1.R1011
5'-most EST	LIB143-058-Q1-E1-F6

Seq. No.	274061
Contig ID	47350_1.R1011
5'-most EST	uC-zmflmo17273e11b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	8.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	274062
Contig ID	47350_6.R1011
5'-most EST	uC-zmflb73028h10b1

Seq. No.	274063
Contig ID	47352_1.R1011
5'-most EST	xjt700093365.h1
Method	BLASTX
NCBI GI	g1001430
BLAST score	161
E value	8.0e-11

Match length	54
% identity	61
NCBI Description	(D63999) ORF1 [Synechocystis sp.]

Seq. No.	274064
Contig ID	47364_1.R1011
5'-most EST	uC-zmflb73202g09b1
Method	BLASTX
NCBI GI	g478740
BLAST score	478
E value	5.0e-48
Match length	121
% identity	82
NCBI Description	phenylalanine ammonia-lyase (EC 4.1.3.5) - rice

Seq. No.	274065
Contig ID	47373_1.R1011
5'-most EST	zuv70o354745.h1
Method	BLASTX
NCBI GI	g2924509
BLAST score	270
E value	3.0e-23
Match length	147
% identity	43
NCBI Description	(AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No.	274066
Contig ID	47381_1.R1011
5'-most EST	ntr70o076364.h1

Seq. No.	274067
Contig ID	47388_1.R1011
5'-most EST	LIB143-059-Q1-E1-B3
Method	BLASTX
NCBI GI	g3738323
BLAST score	440
E value	2.0e-43
Match length	126
% identity	64
NCBI Description	(AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274068
Contig ID	47388_2.R1011
5'-most EST	uC-zmflb73319b01b1

Seq. No.	274069
Contig ID	47412_1.R1011
5'-most EST	LIB143-059-Q1-E1-E1

Seq. No.	274070
Contig ID	47419_1.R1011
5'-most EST	LIB3061-055-Q1-K1-F9
Method	BLASTX
NCBI GI	g4105101
BLAST score	230
E value	4.0e-19

Match length	98
% identity	51
NCBI Description	(AF043086) dehydrin 11 [Hordeum vulgare]

Seq. No.	274071
Contig ID	47422_1.R1011
5'-most EST	ceu700433005.h1
Method	BLASTX
NCBI GI	g1351945
BLAST score	745
E value	8.0e-79
Match length	204
% identity	68
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA2 >gi_533709 (U12546) APETALA2 protein [Arabidopsis thaliana] >gi_2464888_emb_CAB16765.1_ (Z99707) APETALA2 protein [Arabidopsis thaliana]

Seq. No.	274072
Contig ID	47422_2.R1011
5'-most EST	wyr700237359.h1

Seq. No.	274073
Contig ID	47422_4.R1011
5'-most EST	uC-zmroB73013c05b1

Seq. No.	274074
Contig ID	47424_1.R1011
5'-most EST	tzu700205612.h1

Seq. No.	274075
Contig ID	47424_2.R1011
5'-most EST	uC-zmroteosinte083f04b1

Seq. No.	274076
Contig ID	47437_1.R1011
5'-most EST	uC-zmflmo17303b04b1
Method	BLASTX
NCBI GI	g2443881
BLAST score	359
E value	8.0e-34
Match length	168
% identity	48
NCBI Description	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]

Seq. No.	274077
Contig ID	47442_1.R1011
5'-most EST	ceu700426716.h1
Method	BLASTX
NCBI GI	g1173618
BLAST score	190
E value	3.0e-14
Match length	128
% identity	38
NCBI Description	(U33885) CCAAT-binding factor B subunit homolog [Brassica napus] >gi_1336841_bbs_176378 (S81261) CCAAT-binding factor

B subunit, CBF-B subunit=HAP2 subunit homolog {alternatively spliced, shorter form} [Brassica napus, cv. Westar, Peptide, 303 aa] [Brassica napus]

Seq. No.	274078
Contig ID	47447_1.R1011
5'-most EST	LIB143-059-Q1-E1-H6
Method	BLASTX
NCBI GI	g2649345
BLAST score	252
E value	2.0e-21
Match length	91
% identity	49
NCBI Description	(AE001019) tryptophan synthase, subunit beta (trpB-1) [Archaeoglobus fulgidus]

Seq. No.	274079
Contig ID	47447_2.R1011
5'-most EST	uC-zmflb73151b03a2

Seq. No.	274080
Contig ID	47449_1.R1011
5'-most EST	uwc700153158.h1
Method	BLASTX
NCBI GI	g1215812
BLAST score	403
E value	5.0e-39
Match length	161
% identity	48
NCBI Description	(D38170) probenazole-inducible protein PBZ1 [Oryza sativa] >gi_2780343_dbj_BAA24277_ (D82066) PBZ1 [Oryza sativa]

Seq. No.	274081
Contig ID	47461_1.R1011
5'-most EST	uC-zmflb73300b08b1
Method	BLASTX
NCBI GI	g4314378
BLAST score	749
E value	3.0e-79
Match length	337
% identity	42
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	274082
Contig ID	47461_3.R1011
5'-most EST	LIB3060-035-Q1-K1-D8
Method	BLASTX
NCBI GI	g2129636
BLAST score	195
E value	7.0e-15
Match length	75
% identity	52
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	274083
Contig ID	47468_1.R1011

5'-most EST	qmh700029981.f1
Method	BLASTX
NCBI GI	g169459
BLAST score	262
E value	1.0e-22
Match length	96
% identity	49
NCBI Description	(M18538) pop3 peptide [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No.	274084
Contig ID	47473_1.R1011
5'-most EST	LIB143-060-Q1-E1-C3

Seq. No.	274085
Contig ID	47475_1.R1011
5'-most EST	uC-zmflmo17220b11b1
Method	BLASTX
NCBI GI	g3510249
BLAST score	191
E value	2.0e-14
Match length	115
% identity	35
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	274086
Contig ID	47480_1.R1011
5'-most EST	xjt700092546.h1

Seq. No.	274087
Contig ID	47491_1.R1011
5'-most EST	uC-zmflm017086h06b1

Seq. No.	274088
Contig ID	47495_1.R1011
5'-most EST	LIB143-060-Q1-E1-E7

Seq. No.	274089
Contig ID	47500_1.R1011
5'-most EST	LIB143-060-Q1-E1-F4
Method	BLASTX
NCBI GI	g2224810
BLAST score	220
E value	9.0e-18
Match length	81
% identity	54
NCBI Description	(Z97022) cysteine proteinase [Hordeum vulgare]

Seq. No.	274090
Contig ID	47504_1.R1011
5'-most EST	LIB143-060-Q1-E1-G1

Seq. No.	274091
Contig ID	47511_1.R1011
5'-most EST	fwa700099721.h1

Seq. No.	274092

Contig ID	47521_1.R1011
5'-most EST	wty700172434.h1
Seq. No.	274093
Contig ID	47522_1.R1011
5'-most EST	uC-zmrob73080d09b1
Method	BLASTX
NCBI GI	g2160189
BLAST score	350
E value	6.0e-33
Match length	158
% identity	48
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]
Seq. No.	274094
Contig ID	47531_1.R1011
5'-most EST	uC-zmflb73251d01b3
Seq. No.	274095
Contig ID	47531_2.R1011
5'-most EST	pmx700084593.h1
Seq. No.	274096
Contig ID	47543_1.R1011
5'-most EST	uC-zmflb73078g12b2
Seq. No.	274097
Contig ID	47544_1.R1011
5'-most EST	dyk700106363.h1
Method	BLASTX
NCBI GI	g2564237
BLAST score	220
E value	7.0e-18
Match length	84
% identity	50
NCBI Description	(Y10112) omega-6 desaturase [Gossypium hirsutum]
Seq. No.	274098
Contig ID	47548_1.R1011
5'-most EST	LIB143-061-Q1-E1-B9
Seq. No.	274099
Contig ID	47551_1.R1011
5'-most EST	ntr700073218.h1
Method	BLASTX
NCBI GI	g2444271
BLAST score	395
E value	3.0e-38
Match length	177
% identity	40
NCBI Description	(AF019637) putative amino acid or GABA permease [Arabidopsis thaliana]
Seq. No.	274100
Contig ID	47553_1.R1011

5'-most EST	uC-zmrob73002h04b1
Seq. No.	274101
Contig ID	47562_1.R1011
5'-most EST	LIB3136-054-Q1-K1-E9
Seq. No.	274102
Contig ID	47563_1.R1011
5'-most EST	fdz701165755.h1
Seq. No.	274103
Contig ID	47564_1.R1011
5'-most EST	nbm700464708.h1
Method	BLASTX
NCBI GI	g2467272
BLAST score	498
E value	5.0e-50
Match length	224
% identity	28
NCBI Description	(Z99759) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	274104
Contig ID	47564_2.R1011
5'-most EST	uC-zmromo17017b02a1
Seq. No.	274105
Contig ID	47567_1.R1011
5'-most EST	LIB143-061-Q1-E1-D9
Method	BLASTX
NCBI GI	g560610
BLAST score	178
E value	1.0e-12
Match length	73
% identity	42
NCBI Description	trypsin inhibitor, WTI [Triticum aestivum=wheat, variety San Pastore, endosperm, Peptide, 71 aa]
Seq. No.	274106
Contig ID	47567_3.R1011
5'-most EST	wyr700235413.h1
Seq. No.	274107
Contig ID	47583_1.R1011
5'-most EST	LIB143-061-Q1-E1-F6
Method	BLASTX
NCBI GI	g2500649
BLAST score	164
E value	2.0e-18
Match length	169
% identity	34
NCBI Description	PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)
Seq. No.	274108
Contig ID	47586_1.R1011
5'-most EST	xsy700213271.h1
Method	BLASTX

NCBI GI	g2632252
BLAST score	475
E value	3.0e-47
Match length	215
% identity	46
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	274109
Contig ID	47586_2.R1011
5'-most EST	ymt700223309.h1
Method	BLASTN
NCBI GI	g485376
BLAST score	83
E value	5.0e-39
Match length	91
% identity	99
NCBI Description	Zea mays alpha-3-tubulin gene, complete cds

Seq. No.	274110
Contig ID	47593_1.R1011
5'-most EST	LIB143-061-Q1-E1-G5

Seq. No.	274111
Contig ID	47595_1.R1011
5'-most EST	LIB143-061-Q1-E1-G7

Seq. No.	274112
Contig ID	47602_1.R1011
5'-most EST	xsy700208175.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	3.0e-10
Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	274113
Contig ID	47609_1.R1011
5'-most EST	LIB143-062-Q1-E1-A1
Method	BLASTX
NCBI GI	g4056437
BLAST score	169
E value	7.0e-12
Match length	79
% identity	48
NCBI Description	(AC005990) Strong similarity to PFAM PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	274114
Contig ID	47610_1.R1011
5'-most EST	LIB143-062-Q1-E1-A10
Method	BLASTX
NCBI GI	g550438
BLAST score	208
E value	2.0e-16
Match length	80

% identity	54
NCBI Description	(X81829) cytochrome P450 [Zea mays] >gi_1870201_emb_CAA72208_ (Y11404) cytochrome p450 [Zea mays]
Seq. No.	274115
Contig ID	47617_1.R1011
5'-most EST	ntr700074867.h1
Seq. No.	274116
Contig ID	47627_1.R1011
5'-most EST	rvl700457013.h1
Seq. No.	274117
Contig ID	47630_1.R1011
5'-most EST	uer700583920.h1
Method	BLASTX
NCBI GI	g2190992
BLAST score	613
E value	2.0e-63
Match length	220
% identity	53
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]
Seq. No.	274118
Contig ID	47637_1.R1011
5'-most EST	uC-zmflb73116d03b2
Method	BLASTX
NCBI GI	g2979552
BLAST score	361
E value	6.0e-34
Match length	186
% identity	43
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]
Seq. No.	274119
Contig ID	47647_1.R1011
5'-most EST	uC-zmroteosinte041a12b1
Method	BLASTX
NCBI GI	g3550661
BLAST score	587
E value	2.0e-60
Match length	206
% identity	57
NCBI Description	(AJ001310) 39 kDa EF-Hand containing protein [Solanum tuberosum]
Seq. No.	274120
Contig ID	47652_1.R1011
5'-most EST	uC-zmflmo17367a08a1
Seq. No.	274121
Contig ID	47652_2.R1011
5'-most EST	LIB143-062-Q1-E1-E3
Seq. No.	274122

Contig ID	47654_1.R1011
5'-most EST	LIB3066-055-Q1-K1-C4
Method	BLASTX
NCBI GI	g2623298
BLAST score	795
E value	8.0e-85
Match length	216
% identity	69
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	274123
Contig ID	47654_2.R1011
5'-most EST	LIB3066-054-Q1-K1-E2
Method	BLASTX
NCBI GI	g2623298
BLAST score	1188
E value	1.0e-131
Match length	274
% identity	78
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	274124
Contig ID	47654_4.R1011
5'-most EST	xmt700262606.h1
Method	BLASTX
NCBI GI	g2623298
BLAST score	589
E value	4.0e-61
Match length	122
% identity	85
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	274125
Contig ID	47656_1.R1011
5'-most EST	uer700577275.h1
Method	BLASTX
NCBI GI	g4376650
BLAST score	209
E value	1.0e-16
Match length	68
% identity	59
NCBI Description	(AE001621) GcpE Protein [Chlamydia pneumoniae]

Seq. No.	274126
Contig ID	47663_1.R1011
5'-most EST	LIB3066-011-Q1-K1-C10
Method	BLASTX
NCBI GI	g3150410
BLAST score	424
E value	1.0e-41
Match length	148
% identity	55
NCBI Description	(AC004165) unknown protein [Arabidopsis thaliana]

Seq. No.	274127
Contig ID	47681_1.R1011
5'-most EST	LIB143-062-Q1-E1-H10
Method	BLASTX
NCBI GI	g3482979
BLAST score	519
E value	1.0e-52
Match length	143
% identity	65
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana] >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274128
Contig ID	47685_1.R1011
5'-most EST	uC-zmflb73157c03b2
Method	BLASTX
NCBI GI	g3293551
BLAST score	384
E value	1.0e-36
Match length	314
% identity	31
NCBI Description	(AF072697) SHYC [Mus musculus]

Seq. No.	274129
Contig ID	47715_1.R1011
5'-most EST	uC-zmflmo17059c05b1
Method	BLASTX
NCBI GI	g4185136
BLAST score	796
E value	6.0e-85
Match length	285
% identity	51
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	274130
Contig ID	47721_1.R1011
5'-most EST	LIB143-063-Q1-E1-D2
Method	BLASTX
NCBI GI	g2130135
BLAST score	434
E value	1.0e-42
Match length	83
% identity	93
NCBI Description	heat shock factor (clone hsfc) - maize (fragment)

Seq. No.	274131
Contig ID	47732_1.R1011
5'-most EST	uC-zmflMo17006g04b1
Method	BLASTX
NCBI GI	g4406820
BLAST score	295
E value	2.0e-26
Match length	118
% identity	50
NCBI Description	(AC006201) putative ras superfamily member [Arabidopsis

thaliana]

Seq. No.	274132
Contig ID	47736_1.R1011
5'-most EST	LIB143-063-Q1-E1-E8
Method	BLASTX
NCBI GI	g1723231
BLAST score	189
E value	8.0e-14
Match length	120
% identity	36
NCBI Description	HYPOTHETICAL 27.1 KD PROTEIN C1D4.09C IN CHROMOSOME I >gi_1177342_emb_CAA93218_ (Z69239) unknown [Schizosaccharomyces pombe]

Seq. No.	274133
Contig ID	47739_2.R1011
5'-most EST	LIB143-063-Q1-E1-F11

Seq. No.	274134
Contig ID	47744_1.R1011
5'-most EST	pmx700083772.h1
Method	BLASTX
NCBI GI	g417482
BLAST score	1187
E value	1.0e-130
Match length	364
% identity	61
NCBI Description	PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir__JQ2254 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta chain - garden pea >gi_169049 (L08664) farnesyl-protein transferase beta-subunit [Pisum sativum]

Seq. No.	274135
Contig ID	47746_1.R1011
5'-most EST	uer700580028.h1
Method	BLASTX
NCBI GI	g3746059
BLAST score	633
E value	6.0e-66
Match length	227
% identity	56
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	274136
Contig ID	47753_1.R1011
5'-most EST	LIB143-063-Q1-E1-G2
Method	BLASTX
NCBI GI	g3850568
BLAST score	201
E value	1.0e-15
Match length	125
% identity	39

NCBI Description	(AC005278) Similar to hypothetical protein SPAC2F7.14c gi_1052797 from Schizosaccharomyces pombe cosmid gb_Z50142. [Arabidopsis thaliana]
Seq. No.	274137
Contig ID	47764_1.R1011
5'-most EST	LIB84-023-Q1-E1-D3
Method	BLASTX
NCBI GI	g2506931
BLAST score	243
E value	2.0e-20
Match length	154
% identity	35
NCBI Description	APYRASE PRECURSOR (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE) >gi_2129977_pir__JC4616 apyrase (EC 3.6.1.5) - potato >gi_1381633 (U58597) ATP-diphosphohydrolase [Solanum tuberosum]
Seq. No.	274138
Contig ID	47765_1.R1011
5'-most EST	uC-zmf1b73303f11b1
Method	BLASTX
NCBI GI	g4455285
BLAST score	275
E value	4.0e-24
Match length	106
% identity	76
NCBI Description	(AL035527) hypothetical protein [Arabidopsis thaliana]
Seq. No.	274139
Contig ID	47800_1.R1011
5'-most EST	wty700171765.h1
Method	BLASTX
NCBI GI	g2648379
BLAST score	164
E value	5.0e-11
Match length	98
% identity	42
NCBI Description	(AE000956) isochorismatase (entB) [Archaeoglobus fulgidus]
Seq. No.	274140
Contig ID	47804_1.R1011
5'-most EST	tzu700203312.h1
Method	BLASTX
NCBI GI	g4337046
BLAST score	217
E value	3.0e-17
Match length	60
% identity	70
NCBI Description	(AF124162) molybdopterin synthase sulphurylase [Nicotiana plumbaginifolia]
Seq. No.	274141
Contig ID	47804_2.R1011
5'-most EST	ymt700224203.h1
Method	BLASTX

NCBI GI	g4337040
BLAST score	1007
E value	1.0e-110
Match length	263
% identity	73
NCBI Description	(AF124159) molybdopterin synthase sulphurylase [Arabidopsis thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin synthase sulphurylase [Arabidopsis thaliana]

Seq. No.	274142
Contig ID	47806_1.R1011
5'-most EST	vux700157303.h1
Method	BLASTX
NCBI GI	g1373392
BLAST score	392
E value	6.0e-38
Match length	87
% identity	77
NCBI Description	(U57787) permatin precursor [Avena sativa]

Seq. No.	274143
Contig ID	47812_1.R1011
5'-most EST	uC-zmflmo17057a11b1

Seq. No.	274144
Contig ID	47812_2.R1011
5'-most EST	uC-zmflmo17140f07a1

Seq. No.	274145
Contig ID	47813_1.R1011
5'-most EST	LIB143-064-Q1-E1-E5
Method	BLASTX
NCBI GI	g2244994
BLAST score	919
E value	1.0e-99
Match length	206
% identity	80
NCBI Description	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No.	274146
Contig ID	47816_1.R1011
5'-most EST	vux700157483.h1

Seq. No.	274147
Contig ID	47827_1.R1011
5'-most EST	LIB143-064-Q1-E1-G11
Method	BLASTX
NCBI GI	g4455208
BLAST score	234
E value	2.0e-19
Match length	83
% identity	53
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	274148
Contig ID	47832_1.R1011

5'-most EST	uC-zmflb73286d04b1
Method	BLASTN
NCBI GI	g4234841
BLAST score	122
E value	9.0e-62
Match length	270
% identity	92
NCBI Description	Zea mays copia-like retrotransposon Sto-1, partial sequence

Seq. No.	274149
Contig ID	47850_1.R1011
5'-most EST	uC-zmflmo17130h03b1
Method	BLASTX
NCBI GI	g2827002
BLAST score	435
E value	4.0e-43
Match length	91
% identity	90
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	274150
Contig ID	47857_1.R1011
5'-most EST	LIB143-065-Q1-E1-B4

Seq. No.	274151
Contig ID	47860_1.R1011
5'-most EST	gct701175666.h1
Method	BLASTX
NCBI GI	g4115538
BLAST score	400
E value	7.0e-39
Match length	138
% identity	58
NCBI Description	(AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No.	274152
Contig ID	47862_1.R1011
5'-most EST	pmx700089135.h1
Method	BLASTX
NCBI GI	g2146739
BLAST score	1022
E value	1.0e-111
Match length	270
% identity	73
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No.	274153
Contig ID	47869_1.R1011
5'-most EST	LIB3068-008-Q1-K1-A8
Method	BLASTX
NCBI GI	g4115379
BLAST score	267
E value	3.0e-23
Match length	89
% identity	60

NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]
Seq. No.	274154
Contig ID	47879_1.R1011
5'-most EST	dyk700103191.h1
Method	BLASTX
NCBI GI	g3021357
BLAST score	232
E value	3.0e-19
Match length	85
% identity	58
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]
Seq. No.	274155
Contig ID	47880_1.R1011
5'-most EST	ntr700076977.h1
Method	BLASTX
NCBI GI	g4163997
BLAST score	1311
E value	1.0e-158
Match length	338
% identity	75
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]
Seq. No.	274156
Contig ID	47886_1.R1011
5'-most EST	LIB3137-036-Q1-K1-E3
Seq. No.	274157
Contig ID	47890_1.R1011
5'-most EST	LIB36-014-Q1-E1-D4
Seq. No.	274158
Contig ID	47897_1.R1011
5'-most EST	LIB3061-052-Q1-K1-D3
Method	BLASTX
NCBI GI	g1255852
BLAST score	341
E value	9.0e-32
Match length	221
% identity	36
NCBI Description	(U53339) simmilar to enoyl-CoA hydratases [Caenorhabditis elegans]
Seq. No.	274159
Contig ID	47902_1.R1011
5'-most EST	uC-zmf1mo17217e08b1
Seq. No.	274160
Contig ID	47908_1.R1011
5'-most EST	xjt700096252.h1
Seq. No.	274161
Contig ID	47919_1.R1011

5'-most EST	uwc700151156.h1
Seq. No.	274162
Contig ID	47920_1.R1011
5'-most EST	LIB3069-042-Q1-K1-C3
Method	BLASTX
NCBI GI	g4586038
BLAST score	380
E value	2.0e-36
Match length	117
% identity	67
NCBI Description	(AC007109) putative heat shock protein [Arabidopsis thaliana]
Seq. No.	274163
Contig ID	47920_2.R1011
5'-most EST	yyf700350678.h1
Method	BLASTX
NCBI GI	g2842490
BLAST score	344
E value	3.0e-32
Match length	114
% identity	61
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.	274164
Contig ID	47934_1.R1011
5'-most EST	LIB143-066-Q1-E1-B7
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	274165
Contig ID	47944_1.R1011
5'-most EST	LIB143-066-Q1-E1-C8
Seq. No.	274166
Contig ID	47948_1.R1011
5'-most EST	kem700611202.h1
Method	BLASTX
NCBI GI	g4337207
BLAST score	269
E value	1.0e-27
Match length	141
% identity	52
NCBI Description	(AC006403) putative zinc-finger protein [Arabidopsis thaliana] >gi_4585205_gb_AAD25324.1_AF095588_1 (AF095588) C2H2 zinc finger protein FZF [Arabidopsis thaliana]
Seq. No.	274167
Contig ID	47966_1.R1011
5'-most EST	xjt700093879.h1
Method	BLASTX

NCBI GI	g4038055
BLAST score	176
E value	1.0e-12
Match length	102
% identity	42
NCBI Description	(AC005897) putative cytochrome P450 [Arabidopsis thaliana] >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	274168
Contig ID	47973_1.R1011
5'-most EST	pwr700450189.h1

Seq. No.	274169
Contig ID	47980_1.R1011
5'-most EST	uC-zmflmo17247b01a1

Seq. No.	274170
Contig ID	47988_1.R1011
5'-most EST	LIB143-067-Q1-E1-H3
Method	BLASTX
NCBI GI	g3292849
BLAST score	265
E value	1.0e-22
Match length	140
% identity	45
NCBI Description	(AJ007582) arginine methyltransferase [Arabidopsis thaliana]

Seq. No.	274171
Contig ID	47990_1.R1011
5'-most EST	LIB143-066-Q1-E1-H5

Seq. No.	274172
Contig ID	47991_1.R1011
5'-most EST	LIB143-066-Q1-E1-H6

Seq. No.	274173
Contig ID	47999_1.R1011
5'-most EST	pmx700084509.h1

Seq. No.	274174
Contig ID	48024_1.R1011
5'-most EST	pmx700091784.h1

Seq. No.	274175
Contig ID	48032_1.R1011
5'-most EST	LIB143-067-Q1-E1-E3

Seq. No.	274176
Contig ID	48035_1.R1011
5'-most EST	uC-zmflb73095e01b1
Method	BLASTX
NCBI GI	g2735017
BLAST score	936
E value	1.0e-101
Match length	203

% identity	90
NCBI Description	(U82481) KI domain interacting kinase 1 [Zea mays]

Seq. No.	274177
Contig ID	48050_1.R1011
5'-most EST	xyt700343354.h1

Seq. No.	274178
Contig ID	48066_1.R1011
5'-most EST	LIB3118-002-Q1-K1-C1
Method	BLASTX
NCBI GI	g2114207
BLAST score	486
E value	1.0e-48
Match length	113
% identity	85
NCBI Description	(D86744) glutaredoxin [Oryza sativa]

Seq. No.	274179
Contig ID	48067_1.R1011
5'-most EST	LIB143-067-Q1-E1-H9

Seq. No.	274180
Contig ID	48073_1.R1011
5'-most EST	wyr700244150.h1

Seq. No.	274181
Contig ID	48073_3.R1011
5'-most EST	hvj700621320.h1

Seq. No.	274182
Contig ID	48074_1.R1011
5'-most EST	LIB143-068-Q1-E1-A4
Method	BLASTX
NCBI GI	g2462822
BLAST score	367
E value	4.0e-35
Match length	127
% identity	60
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274183
Contig ID	48088_1.R1011
5'-most EST	fwa700100861.h1
Method	BLASTX
NCBI GI	g1352461
BLAST score	446
E value	2.0e-44
Match length	94
% identity	93
NCBI Description	IN2-2 PROTEIN

Seq. No.	274184
Contig ID	48088_2.R1011
5'-most EST	wyr700243664.h1
Method	BLASTX
NCBI GI	g728744

BLAST score	316
E value	2.0e-29
Match length	70
% identity	83
NCBI Description	AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390 auxin-induced protein - common tobacco >gi_19799_emb_CAA39708_ (X56267) auxin-induced protein [Nicotiana tabacum]

Seq. No.	274185
Contig ID	48093_1.R1011
5'-most EST	LIB3136-004-Q1-K1-D12
Method	BLASTX
NCBI GI	g2827715
BLAST score	596
E value	9.0e-62
Match length	194
% identity	9
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	274186
Contig ID	48096_1.R1011
5'-most EST	uC-zmflb73063h12b1
Method	BLASTN
NCBI GI	g435941
BLAST score	103
E value	1.0e-50
Match length	239
% identity	86
NCBI Description	Oryza sativa Nipponbare bZIP DNA-binding factor (osZIP-1a) mRNA, complete cds

Seq. No.	274187
Contig ID	48096_2.R1011
5'-most EST	uC-zmflb73317g02b1
Method	BLASTX
NCBI GI	g435942
BLAST score	281
E value	8.0e-25
Match length	77
% identity	69
NCBI Description	(U04295) DNA-binding factor of bZIP class [Oryza sativa]

Seq. No.	274188
Contig ID	48096_3.R1011
5'-most EST	uC-zmflmo17197h06b1
Method	BLASTX
NCBI GI	g435942
BLAST score	223
E value	4.0e-18
Match length	100
% identity	51
NCBI Description	(U04295) DNA-binding factor of bZIP class [Oryza sativa]

Seq. No.	274189
Contig ID	48098_1.R1011

5'-most EST	LIB143-068-Q1-E1-D2
Seq. No.	274190
Contig ID	48109_1.R1011
5'-most EST	LIB143-068-Q1-E1-E4
Method	BLASTX
NCBI GI	g3876615
BLAST score	424
E value	4.0e-48
Match length	241
% identity	45
NCBI Description	(Z74031) Similarity to Yeast D-lactate dehydrogenase (SW:DLD1_YEAST); cDNA EST EMBL:C12235 comes from this gene; cDNA EST EMBL:C12916 comes from this gene; cDNA EST EMBL:C10532 comes from this gene; cDNA EST EMBL:C10979 comes f
Seq. No.	274191
Contig ID	48111_1.R1011
5'-most EST	LIB3066-010-Q1-K1-A1
Seq. No.	274192
Contig ID	48116_1.R1011
5'-most EST	wyr700242618.h1
Seq. No.	274193
Contig ID	48142_1.R1011
5'-most EST	tym700023114.f1
Seq. No.	274194
Contig ID	48149_1.R1011
5'-most EST	LIB148-008-Q1-E1-D12
Method	BLASTX
NCBI GI	g4204263
BLAST score	146
E value	6.0e-09
Match length	40
% identity	65
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]
Seq. No.	274195
Contig ID	48149_2.R1011
5'-most EST	LIB148-043-Q1-E1-H6
Seq. No.	274196
Contig ID	48157_1.R1011
5'-most EST	LIB148-041-Q1-E1-F8
Method	BLASTX
NCBI GI	g2342735
BLAST score	374
E value	1.0e-35
Match length	111
% identity	68
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.	274197
Contig ID	48159_1.R1011

5'-most EST	LIB148-007-Q1-E1-E4
Method	BLASTX
NCBI GI	g4204263
BLAST score	367
E value	1.0e-34
Match length	147
% identity	48
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	274198
Contig ID	48159_2.R1011
5'-most EST	LIB148-028-Q1-E1-F10
Method	BLASTN
NCBI GI	g22458
BLAST score	86
E value	2.0e-40
Match length	86
% identity	100
NCBI Description	Z.mays pollen specific mRNA C-terminal (clone 4H7)

Seq. No.	274199
Contig ID	48164_1.R1011
5'-most EST	LIB3066-037-Q1-K1-C6
Method	BLASTX
NCBI GI	g2239262
BLAST score	2413
E value	0.0e+00
Match length	534
% identity	78
NCBI Description	(Y13285) pectin methylesterase-like protein [Zea mays]

Seq. No.	274200
Contig ID	48164_2.R1011
5'-most EST	LIB3066-017-Q1-K1-G9
Method	BLASTX
NCBI GI	g4455337
BLAST score	443
E value	6.0e-44
Match length	144
% identity	58
NCBI Description	(AL035525) pectinesterase-like protein [Arabidopsis thaliana]

Seq. No.	274201
Contig ID	48165_1.R1011
5'-most EST	LIB148-001-Q1-E1-C11
Method	BLASTX
NCBI GI	g3798740
BLAST score	179
E value	2.0e-12
Match length	158
% identity	32
NCBI Description	(AB011261) supercoiling factor [Drosophila melanogaster]

Seq. No.	274202
Contig ID	48175_1.R1011
5'-most EST	LIB148-025-Q1-E1-C5

Seq. No.	274203
Contig ID	48180_1.R1011
5'-most EST	LIB3067-044-Q1-K1-H6

Seq. No.	274204
Contig ID	48180_2.R1011
5'-most EST	LIB148-011-Q1-E1-A5

Seq. No.	274205
Contig ID	48182_1.R1011
5'-most EST	LIB3066-013-Q1-K1-E4

Seq. No.	274206
Contig ID	48182_2.R1011
5'-most EST	LIB148-044-Q1-E1-A3

Seq. No.	274207
Contig ID	48182_3.R1011
5'-most EST	LIB148-041-Q1-E1-E9

Seq. No.	274208
Contig ID	48183_1.R1011
5'-most EST	LIB3066-053-Q1-K1-B8

Seq. No.	274209
Contig ID	48184_1.R1011
5'-most EST	LIB148-033-Q1-E1-D12

Seq. No.	274210
Contig ID	48189_1.R1011
5'-most EST	LIB148-001-Q1-E1-E12

Seq. No.	274211
Contig ID	48194_1.R1011
5'-most EST	LIB148-009-Q1-E1-D6
Method	BLASTX
NCBI GI	g2281085
BLAST score	393
E value	1.0e-49
Match length	168
% identity	61
NCBI Description	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	274212
Contig ID	48201_1.R1011
5'-most EST	LIB148-005-Q1-E1-F6
Method	BLASTX
NCBI GI	g4539383
BLAST score	555
E value	9.0e-57
Match length	224
% identity	48
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	274213
Contig ID	48207_1.R1011
5'-most EST	LIB148-001-Q1-E1-F8

Seq. No.	274214
Contig ID	48215_1.R1011
5'-most EST	LIB3066-003-Q1-K1-F11
Method	BLASTX
NCBI GI	g3367520
BLAST score	857
E value	5.0e-92
Match length	248
% identity	65
NCBI Description	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb_D12522 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	274215
Contig ID	48215_2.R1011
5'-most EST	LIB148-051-Q1-E1-C12

Seq. No.	274216
Contig ID	48215_3.R1011
5'-most EST	LIB148-022-Q1-E1-C8
Method	BLASTX
NCBI GI	g4580398
BLAST score	611
E value	3.0e-63
Match length	176
% identity	64
NCBI Description	(AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No.	274217
Contig ID	48221_1.R1011
5'-most EST	LIB148-001-Q1-E1-H12

Seq. No.	274218
Contig ID	48222_1.R1011
5'-most EST	uC-zmroteosinte006d10b1
Method	BLASTX
NCBI GI	g1705450
BLAST score	416
E value	3.0e-40
Match length	220
% identity	42
NCBI Description	BEM46 PROTEIN >gi_987287 (U29892) temperature sensitive supressor of Saccharomyces cerevisiae bem1/bud5 [Schizosaccharomyces pombe]

Seq. No.	274219
Contig ID	48222_2.R1011
5'-most EST	uC-zmflmo17399e08a1

Seq. No.	274220
Contig ID	48227_1.R1011
5'-most EST	LIB148-018-Q1-E1-G3

Method	BLASTX
NCBI GI	g2293568
BLAST score	286
E value	1.0e-25
Match length	87
% identity	64
NCBI Description	(AF012897) HvB12D homolog [Oryza sativa]

Seq. No.	274221
Contig ID	48228_1.R1011
5'-most EST	LIB148-030-Q1-E1-A12
Method	BLASTX
NCBI GI	g2104536
BLAST score	733
E value	9.0e-78
Match length	193
% identity	64
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	274222
Contig ID	48246_1.R1011
5'-most EST	LIB3066-047-Q1-K1-C9
Method	BLASTX
NCBI GI	g4539330
BLAST score	1182
E value	1.0e-130
Match length	290
% identity	78
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	274223
Contig ID	48257_1.R1011
5'-most EST	LIB148-033-Q1-E1-B1
Method	BLASTX
NCBI GI	g533692
BLAST score	176
E value	2.0e-12
Match length	54
% identity	57
NCBI Description	(U12150) protease inhibitor [Glycine max]

Seq. No.	274224
Contig ID	48266_1.R1011
5'-most EST	LIB148-065-Q1-E1-F1

Seq. No.	274225
Contig ID	48267_1.R1011
5'-most EST	uC-zmflb73174c08b1
Method	BLASTX
NCBI GI	g2982243
BLAST score	383
E value	2.0e-36
Match length	154
% identity	54
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	274226
Contig ID	48267_2.R1011
5'-most EST	xjt700094030.h1
Method	BLASTX
NCBI GI	g2982243
BLAST score	279
E value	8.0e-25
Match length	82
% identity	63
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	274227
Contig ID	48289_1.R1011
5'-most EST	hbs701181820.h1

Seq. No.	274228
Contig ID	48291_1.R1011
5'-most EST	LIB148-002-Q1-E1-F5
Method	BLASTX
NCBI GI	g4218120
BLAST score	374
E value	2.0e-35
Match length	341
% identity	29
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	274229
Contig ID	48298_1.R1011
5'-most EST	LIB148-002-Q1-E1-G12

Seq. No.	274230
Contig ID	48301_1.R1011
5'-most EST	LIB148-030-Q1-E1-D5
Method	BLASTX
NCBI GI	g3183989
BLAST score	322
E value	1.0e-29
Match length	185
% identity	42
NCBI Description	(AJ005172) P69E protein [Lycopersicon esculentum]

Seq. No.	274231
Contig ID	48308_1.R1011
5'-most EST	uC-zmflmo17161e10b1
Method	BLASTN
NCBI GI	g312180
BLAST score	157
E value	1.0e-82
Match length	197
% identity	95
NCBI Description	Z.mays GapC4 gene

Seq. No.	274232
Contig ID	48309_1.R1011
5'-most EST	LIB148-002-Q1-E1-H11

Method	BLASTX
NCBI GI	g4218011
BLAST score	1120
E value	1.0e-123
Match length	319
% identity	71
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	274233
Contig ID	48316_1.R1011
5'-most EST	LIB3066-033-Q1-K1-C12

Seq. No.	274234
Contig ID	48345_1.R1011
5'-most EST	LIB148-013-Q1-E1-D8
Method	BLASTX
NCBI GI	g1084442
BLAST score	631
E value	3.0e-78
Match length	353
% identity	43
NCBI Description	cellulase (EC 3.2.1.4) - European elder >gi_575404_emb_CAA52343_ (X74290) cellulase [Sambucus nigra]

Seq. No.	274235
Contig ID	48358_1.R1011
5'-most EST	xyt700343803.h1
Method	BLASTX
NCBI GI	g3850587
BLAST score	434
E value	2.0e-42
Match length	222
% identity	51
NCBI Description	(AC005278) Strong similarity to gi_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No.	274236
Contig ID	48361_1.R1011
5'-most EST	LIB148-003-Q1-E1-D8
Method	BLASTX
NCBI GI	g2213632
BLAST score	428
E value	4.0e-42
Match length	124
% identity	64
NCBI Description	(AC000103) F21J9.24 [Arabidopsis thaliana]

Seq. No.	274237
Contig ID	48377_1.R1011
5'-most EST	LIB148-003-Q1-E1-F7
Method	BLASTX
NCBI GI	g3152590
BLAST score	441

E value	1.0e-43
Match length	112
% identity	71
NCBI Description	(AC002986) Similar to protein serine/threonine kinase NPK15 gb_D31737 from Nicotiana tabacum. [Arabidopsis thaliana]

Seq. No.	274238
Contig ID	48379_1.R1011
5'-most EST	uC-zmflb73298d02b1
Method	BLASTX
NCBI GI	g3928097
BLAST score	713
E value	4.0e-75
Match length	296
% identity	47
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	274239
Contig ID	48379_2.R1011
5'-most EST	LIB3137-015-Q1-K1-F1
Method	BLASTX
NCBI GI	g3928097
BLAST score	213
E value	5.0e-17
Match length	76
% identity	51
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	274240
Contig ID	48392_1.R1011
5'-most EST	uC-zmrob73006e01b1
Method	BLASTX
NCBI GI	g1362066
BLAST score	620
E value	3.0e-66
Match length	190
% identity	71
NCBI Description	small GTP-binding protein - garden pea >gi_871510_emb_CAA90080_ (Z49900) small GTP-binding protein [Pisum sativum]

Seq. No.	274241
Contig ID	48392_3.R1011
5'-most EST	uC-zmflmo17078b03b1
Method	BLASTX
NCBI GI	g1370190
BLAST score	633
E value	7.0e-66
Match length	152
% identity	80
NCBI Description	(Z73944) RAB8A [Lotus japonicus]

Seq. No.	274242
Contig ID	48394_1.R1011
5'-most EST	clt700042945.f1

Seq. No.	274243
Contig ID	48399_1.R1011
5'-most EST	LIB3066-008-Q1-K1-E11
Method	BLASTX
NCBI GI	g2244956
BLAST score	181
E value	2.0e-13
Match length	90
% identity	41
NCBI Description	(Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No.	274244
Contig ID	48422_1.R1011
5'-most EST	LIB3066-018-Q1-K1-D11
Method	BLASTX
NCBI GI	g1546692
BLAST score	438
E value	5.0e-43
Match length	205
% identity	44
NCBI Description	(X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No.	274245
Contig ID	48427_1.R1011
5'-most EST	LIB3066-011-Q1-K1-G3

Seq. No.	274246
Contig ID	48430_1.R1011
5'-most EST	LIB148-004-Q1-E1-C9
Method	BLASTX
NCBI GI	g3204125
BLAST score	192
E value	2.0e-14
Match length	64
% identity	59
NCBI Description	(AJ006766) putative Pi starvation-induced protein [Cicer arietinum]

Seq. No.	274247
Contig ID	48442_1.R1011
5'-most EST	uC-zmroteosinte031g07b1

Seq. No.	274248
Contig ID	48449_1.R1011
5'-most EST	uC-zmflb73167c04b2
Method	BLASTX
NCBI GI	g4468813
BLAST score	311
E value	4.0e-28
Match length	103
% identity	55
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	274249
Contig ID	48449_2.R1011

5'-most EST	LIB3060-048-Q1-K1-F3
Method	BLASTX
NCBI GI	g4468813
BLAST score	623
E value	9.0e-65
Match length	211
% identity	55
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	274250
Contig ID	48452_1.R1011
5'-most EST	uC-zmflmo17057d09b1
Method	BLASTX
NCBI GI	g4455359
BLAST score	400
E value	1.0e-38
Match length	267
% identity	38
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	274251
Contig ID	48461_1.R1011
5'-most EST	LIB3066-046-Q1-K1-A4
Method	BLASTX
NCBI GI	g4585976
BLAST score	467
E value	1.0e-46
Match length	149
% identity	60
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	274252
Contig ID	48484_1.R1011
5'-most EST	LIB3066-002-Q1-K1-F4

Seq. No.	274253
Contig ID	48499_1.R1011
5'-most EST	LIB148-006-Q1-E1-G4
Method	BLASTX
NCBI GI	g3776559
BLAST score	892
E value	8.0e-96
Match length	424
% identity	46
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	274254
Contig ID	48509_1.R1011
5'-most EST	LIB3066-011-Q1-K1-E11
Method	BLASTX
NCBI GI	g2459424
BLAST score	617
E value	5.0e-64
Match length	242

% identity	51
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	274255
Contig ID	48522_1.R1011
5'-most EST	LIB148-044-Q1-E1-D7

Seq. No.	274256
Contig ID	48527_1.R1011
5'-most EST	LIB148-018-Q1-E1-A8
Method	BLASTX
NCBI GI	g2642215
BLAST score	162
E value	9.0e-11
Match length	40
% identity	72
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]

Seq. No.	274257
Contig ID	48529_1.R1011
5'-most EST	uC-zmflmo17132c12b1

Seq. No.	274258
Contig ID	48553_1.R1011
5'-most EST	LIB148-052-Q1-E1-A4
Method	BLASTX
NCBI GI	g2493493
BLAST score	313
E value	2.0e-28
Match length	144
% identity	44
NCBI Description	SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1) >gi_619352_bbs_153538 CP-MII.1=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324 aa]

Seq. No.	274259
Contig ID	48564_1.R1011
5'-most EST	LIB148-011-Q1-E1-E2
Method	BLASTX
NCBI GI	g1076386
BLAST score	454
E value	5.0e-45
Match length	97
% identity	85
NCBI Description	protein kinase ADK1 - Arabidopsis thaliana >gi_1216484 (U48779) dual specificity kinase 1 [Arabidopsis thaliana]

Seq. No.	274260
Contig ID	48564_2.R1011
5'-most EST	LIB148-021-Q1-E1-H6
Method	BLASTX
NCBI GI	g1103318
BLAST score	301
E value	3.0e-27
Match length	68
% identity	78

NCBI Description	(X78818) casein kinase I [Arabidopsis thaliana] >gi_2244791_emb_CAB10213.1_ (Z97336) casein kinase I [Arabidopsis thaliana]

Seq. No.	274261
Contig ID	48565_1.R1011
5'-most EST	LIB148-024-Q1-E1-G7
Method	BLASTX
NCBI GI	g2459424
BLAST score	357
E value	6.0e-34
Match length	129
% identity	53
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	274262
Contig ID	48570_1.R1011
5'-most EST	LIB148-018-Q1-E1-F2
Method	BLASTX
NCBI GI	g3450842
BLAST score	227
E value	1.0e-18
Match length	82
% identity	51
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	274263
Contig ID	48575_1.R1011
5'-most EST	cyk70O052242.f1
Method	BLASTX
NCBI GI	g4468993
BLAST score	359
E value	5.0e-34
Match length	92
% identity	72
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	274264
Contig ID	48594_1.R1011
5'-most EST	LIB3066-014-Q1-K1-H6
Method	BLASTX
NCBI GI	g282965
BLAST score	227
E value	2.0e-18
Match length	74
% identity	53
NCBI Description	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia >gi_20565_emb_CAA78388_ (Z13998) protein 3 [Petunia x hybrida]

Seq. No.	274265
Contig ID	48596_2.R1011
5'-most EST	LIB3066-017-Q1-K1-B4

Seq. No.	274266
Contig ID	48596_3.R1011

5'-most EST	LIB148-036-Q1-E1-A6
Seq. No.	274267
Contig ID	48607_1.R1011
5'-most EST	LIB148-025-Q1-E1-B10
Seq. No.	274268
Contig ID	48611_1.R1011
5'-most EST	uC-zmflb73143f09b1
Method	BLASTX
NCBI GI	g4206640
BLAST score	647
E value	1.0e-67
Match length	180
% identity	72
NCBI Description	(AF072858) zinc transporter ZAT [Arabidopsis thaliana]
Seq. No.	274269
Contig ID	48611_2.R1011
5'-most EST	uC-zmflmo17077d07b1
Method	BLASTX
NCBI GI	g3510254
BLAST score	252
E value	2.0e-21
Match length	87
% identity	60
NCBI Description	(AC005310) putative zinc transporter [Arabidopsis thaliana]
Seq. No.	274270
Contig ID	48617_1.R1011
5'-most EST	uC-zmflmo17075h04a1
Method	BLASTX
NCBI GI	g2231312
BLAST score	146
E value	6.0e-09
Match length	71
% identity	52
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]
Seq. No.	274271
Contig ID	48617_2.R1011
5'-most EST	uwc700153220.h1
Method	BLASTX
NCBI GI	g1370174
BLAST score	442
E value	7.0e-44
Match length	104
% identity	83
NCBI Description	(Z73936) RAB1Y [Lotus japonicus]
Seq. No.	274272
Contig ID	48624_1.R1011
5'-most EST	LIB148-033-Q1-E1-E4
Method	BLASTX
NCBI GI	g2723471
BLAST score	1537
E value	1.0e-171

Match length	441
% identity	67
NCBI Description	(D87819) sucrose transporter [Oryza sativa]

Seq. No.	274273
Contig ID	48634_1.R1011
5'-most EST	LIB148-006-Q1-E1-F6
Method	BLASTX
NCBI GI	g3152560
BLAST score	350
E value	8.0e-33
Match length	133
% identity	50
NCBI Description	(AC002986) Strong similarity to ser/thr protein kinases, especially gb_X97980 from solanum berthaultii, gb_X90990 from solanum tuberosum and gb_D10909 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	274274
Contig ID	48636_1.R1011
5'-most EST	LIB148-061-Q1-E1-B12

Seq. No.	274275
Contig ID	48639_1.R1011
5'-most EST	LIB148-032-Q1-E1-G12

Seq. No.	274276
Contig ID	48649_1.R1011
5'-most EST	uC-zmflmo17240d08b1
Method	BLASTX
NCBI GI	g3702323
BLAST score	1307
E value	1.0e-147
Match length	382
% identity	68
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	274277
Contig ID	48678_1.R1011
5'-most EST	LIB148-007-Q1-E1-C1

Seq. No.	274278
Contig ID	48682_1.R1011
5'-most EST	LIB148-007-Q1-E1-C2

Seq. No.	274279
Contig ID	48700_1.R1011
5'-most EST	uC-zmflmo17048a03b1
Method	BLASTX
NCBI GI	g4063750
BLAST score	387
E value	2.0e-37
Match length	135
% identity	55
NCBI Description	(AC005851) putative indole-3-acetate beta-glucosyltransferase synthetase [Arabidopsis thaliana]

Seq. No. 274280
Contig ID 48700_2.R1011
5'-most EST fxb700397577.h1

Seq. No. 274281
Contig ID 48714_1.R1011
5'-most EST LIB148-007-Q1-E1-F4
Method BLASTX
NCBI GI g2829889
BLAST score 529
E value 1.0e-53
Match length 167
% identity 66
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 274282
Contig ID 48718_1.R1011
5'-most EST LIB148-007-Q1-E1-F9
Method BLASTX
NCBI GI g4512667
BLAST score 608
E value 7.0e-63
Match length 176
% identity 65
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 274283
Contig ID 48732_1.R1011
5'-most EST LIB148-046-Q1-E1-D2

Seq. No. 274284
Contig ID 48750_1.R1011
5'-most EST LIB148-045-Q1-E1-B6
Method BLASTX
NCBI GI g3015488
BLAST score 400
E value 1.0e-38
Match length 202
% identity 43
NCBI Description (U58474) receptor-like protein kinase [Lycopersicon esculentum]

Seq. No. 274285
Contig ID 48784_1.R1011
5'-most EST nbm700468664.h1
Method BLASTX
NCBI GI g3075399
BLAST score 264
E value 2.0e-22
Match length 275
% identity 28
NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No. 274286
Contig ID 48796_1.R1011
5'-most EST LIB3066-029-Q1-K1-E12
Method BLASTN

NCBI GI	g22264
BLAST score	151
E value	3.0e-79
Match length	155
% identity	99
NCBI Description	Maize DNA for Ds(bz-wm) controlling element (Ds1-related)

Seq. No.	274287
Contig ID	48799_1.R1011
5'-most EST	uC-zmflb73147b05b1

Seq. No.	274288
Contig ID	48803_1.R1011
5'-most EST	LIB1488-030-Q1-E1-G8

Seq. No.	274289
Contig ID	48820_1.R1011
5'-most EST	LIB1488-008-Q1-E1-H5

Seq. No.	274290
Contig ID	48823_1.R1011
5'-most EST	LIB3066-003-Q1-K1-A2

Seq. No.	274291
Contig ID	48823_2.R1011
5'-most EST	LIB1488-039-Q1-E1-H5
Method	BLASTX
NCBI GI	g4646203
BLAST score	570
E value	5.0e-69
Match length	301
% identity	45
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No.	274292
Contig ID	48829_1.R1011
5'-most EST	LIB1488-009-Q1-E1-A3
Method	BLASTX
NCBI GI	g130718
BLAST score	180
E value	6.0e-13
Match length	101
% identity	33
NCBI Description	ACID PHOSPHATASE PRECURSOR 1 >gi_170370 (M83211) acid phosphatase type 1 [Lycopersicon esculentum] >gi_170372 (M67474) acid phosphatase type 5 [Lycopersicon esculentum] >gi_445121_prf__1908427A acid phosphatase 1 [Lycopersicon esculentum]

Seq. No.	274293
Contig ID	48842_1.R1011
5'-most EST	LIB1488-009-Q1-E1-B5
Method	BLASTX
NCBI GI	g4490737
BLAST score	145
E value	4.0e-09

Match length	75
% identity	48
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	274294
Contig ID	48850_1.R1011
5'-most EST	LIB3066-030-Q1-K1-C4
Method	BLASTX
NCBI GI	g3036807
BLAST score	355
E value	1.0e-33
Match length	123
% identity	61
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana]

Seq. No.	274295
Contig ID	48851_1.R1011
5'-most EST	pmx700091036.h1

Seq. No.	274296
Contig ID	48876_1.R1011
5'-most EST	LIB148-064-Q1-E1-F6
Method	BLASTX
NCBI GI	g2398681
BLAST score	346
E value	3.0e-50
Match length	134
% identity	71
NCBI Description	(Y14798) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	274297
Contig ID	48882_1.R1011
5'-most EST	LIB148-038-Q1-E1-G1
Method	BLASTX
NCBI GI	g3935148
BLAST score	246
E value	2.0e-20
Match length	78
% identity	59
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	274298
Contig ID	48883_1.R1011
5'-most EST	LIB148-052-Q1-E1-H9
Method	BLASTX
NCBI GI	g4006902
BLAST score	305
E value	3.0e-27
Match length	276
% identity	31
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	274299
Contig ID	48885_1.R1011
5'-most EST	LIB148-009-Q1-E1-F5
Method	BLASTX

NCBI GI	g4335763
BLAST score	396
E value	2.0e-38
Match length	157
% identity	48
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	274300
Contig ID	48892_1.R1011
5'-most EST	LIB148-030-Q1-E1-B6
Method	BLASTX
NCBI GI	g3805765
BLAST score	601
E value	3.0e-62
Match length	178
% identity	68
NCBI Description	(AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No.	274301
Contig ID	48918_1.R1011
5'-most EST	LIB148-010-Q1-E1-A9
Method	BLASTX
NCBI GI	g4415931
BLAST score	514
E value	5.0e-52
Match length	161
% identity	61
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	274302
Contig ID	48919_1.R1011
5'-most EST	LIB148-010-Q1-E1-B1

Seq. No.	274303
Contig ID	48920_1.R1011
5'-most EST	LIB148-014-Q1-E1-E11
Method	BLASTX
NCBI GI	g639722
BLAST score	571
E value	8.0e-78
Match length	208
% identity	71
NCBI Description	(L27484) calcium-dependent protein kinase [Zea mays]

Seq. No.	274304
Contig ID	48920_2.R1011
5'-most EST	LIB3066-011-Q1-K1-A3
Method	BLASTX
NCBI GI	g639722
BLAST score	1539
E value	1.0e-172
Match length	356
% identity	80
NCBI Description	(L27484) calcium-dependent protein kinase [Zea mays]

Seq. No.	274305
Contig ID	48934_1.R1011
5'-most EST	xsy700209607.h1
Method	BLASTX
NCBI GI	g3935187
BLAST score	1497
E value	1.0e-167
Match length	436
% identity	67
NCBI Description	(AC004557) F17L21.30 [Arabidopsis thaliana]

Seq. No.	274306
Contig ID	48934_2.R1011
5'-most EST	wyr700235267.h1
Method	BLASTX
NCBI GI	g3935187
BLAST score	540
E value	5.0e-55
Match length	170
% identity	63
NCBI Description	(AC004557) F17L21.30 [Arabidopsis thaliana]

Seq. No.	274307
Contig ID	48934_3.R1011
5'-most EST	LIB148-029-Q1-E1-E9
Method	BLASTX
NCBI GI	g3513727
BLAST score	202
E value	8.0e-16
Match length	63
% identity	68
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	274308
Contig ID	48940_1.R1011
5'-most EST	LIB148-010-Q1-E1-D11
Method	BLASTX
NCBI GI	g4531442
BLAST score	788
E value	5.0e-84
Match length	331
% identity	51
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274309
Contig ID	48943_1.R1011
5'-most EST	LIB148-012-Q1-E1-B5

Seq. No.	274310
Contig ID	48948_1.R1011
5'-most EST	LIB148-022-Q1-E1-F3
Method	BLASTX
NCBI GI	g1364059

BLAST score	292
E value	3.0e-26
Match length	130
% identity	44
NCBI Description	dioscorin class A precursor - Dioscorea cayenensis >gi_433463_emb_CAA53781_ (X76187) storage protein [Dioscorea cayenensis]

Seq. No.	274311
Contig ID	48960_1.R1011
5'-most EST	LIB148-036-Q1-E1-E2

Seq. No.	274312
Contig ID	48966_1.R1011
5'-most EST	LIB148-028-Q1-E1-D6
Method	BLASTX
NCBI GI	g3183991
BLAST score	320
E value	9.0e-30
Match length	160
% identity	46
NCBI Description	(AJ005173) P69F protein [Lycopersicon esculentum]

Seq. No.	274313
Contig ID	48972_1.R1011
5'-most EST	LIB3066-023-Q1-K1-E11
Method	BLASTN
NCBI GI	g454880
BLAST score	57
E value	3.0e-23
Match length	133
% identity	92
NCBI Description	Rice mRNA for WSI724 protein induced by water stress, complete cds

Seq. No.	274314
Contig ID	48984_1.R1011
5'-most EST	LIB3068-020-Q1-K1-C3
Method	BLASTX
NCBI GI	g3540179
BLAST score	666
E value	1.0e-69
Match length	246
% identity	52
NCBI Description	(AC004122) putative amino acid permease [Arabidopsis thaliana]

Seq. No.	274315
Contig ID	48985_1.R1011
5'-most EST	LIB3137-013-Q1-K1-D11

Seq. No.	274316
Contig ID	48999_1.R1011
5'-most EST	uC-zmflb73201h04b1

Seq. No.	274317
Contig ID	49031_1.R1011

5'-most EST	LIB148-052-Q1-E1-F6
Seq. No.	274318
Contig ID	49033_1.R1011
5'-most EST	uC-zmflmo17018a01a1
Method	BLASTX
NCBI GI	g4467156
BLAST score	1086
E value	1.0e-118
Match length	318
% identity	63
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]
Seq. No.	274319
Contig ID	49033_2.R1011
5'-most EST	uC-zmflb73126h04a1
Method	BLASTX
NCBI GI	g4467156
BLAST score	179
E value	6.0e-13
Match length	54
% identity	63
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]
Seq. No.	274320
Contig ID	49033_3.R1011
5'-most EST	LIB3066-027-Q1-K1-H1
Method	BLASTX
NCBI GI	g4467156
BLAST score	678
E value	3.0e-71
Match length	178
% identity	69
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]
Seq. No.	274321
Contig ID	49040_1.R1011
5'-most EST	nbm70l0467327.h1
Method	BLASTX
NCBI GI	g3047114
BLAST score	371
E value	3.0e-35
Match length	178
% identity	45
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	274322
Contig ID	49043_1.R1011
5'-most EST	LIB148-037-Q1-E1-F5
Method	BLASTX
NCBI GI	g4539351
BLAST score	283
E value	3.0e-25
Match length	88
% identity	62
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	274323
Contig ID	49046_1.R1011
5'-most EST	LIB3066-034-Q1-K1-H4
Method	BLASTX
NCBI GI	g4191774
BLAST score	298
E value	9.0e-27
Match length	113
% identity	54
NCBI Description	(AC005917) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	274324
Contig ID	49048_1.R1011
5'-most EST	LIB148-035-Q1-E1-A9
Method	BLASTX
NCBI GI	g3868853
BLAST score	171
E value	1.0e-11
Match length	117
% identity	36
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No.	274325
Contig ID	49048_3.R1011
5'-most EST	LIB148-025-Q1-E1-E9

Seq. No.	274326
Contig ID	49049_1.R1011
5'-most EST	LIB148-011-Q1-E1-F5
Method	BLASTX
NCBI GI	g4567229
BLAST score	157
E value	1.0e-10
Match length	69
% identity	39
NCBI Description	(AC007119) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	274327
Contig ID	49051_1.R1011
5'-most EST	LIB148-011-Q1-E1-F8

Seq. No.	274328
Contig ID	49057_1.R1011
5'-most EST	LIB148-011-Q1-E1-G2

Seq. No.	274329
Contig ID	49062_1.R1011
5'-most EST	LIB148-011-Q1-E1-G7
Method	BLASTX
NCBI GI	g4337196
BLAST score	223
E value	8.0e-18
Match length	159
% identity	31
NCBI Description	(AC006403) putative serine/threonine receptor kinase

[Arabidopsis thaliana]

Seq. No.	274330
Contig ID	49067_1.R1011
5'-most EST	LIB148-042-Q1-E1-C7

Seq. No.	274331
Contig ID	49070_1.R1011
5'-most EST	pwr700452780.h1
Method	BLASTN
NCBI GI	g4185305
BLAST score	50
E value	8.0e-19
Match length	88
% identity	53
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	274332
Contig ID	49097_1.R1011
5'-most EST	LIB148-012-Q1-E1-B9
Method	BLASTX
NCBI GI	g1706318
BLAST score	565
E value	2.0e-58
Match length	136
% identity	79
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) (ERT D1) >gi_1362098_pir__S56177 probable glutamate decarboxylase - tomato >gi_995555_emb_CAA56812_ (X80840) homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon [Lycopersicon esculentum]

Seq. No.	274333
Contig ID	49102_1.R1011
5'-most EST	LIB148-012-Q1-E1-C3
Method	BLASTX
NCBI GI	g4567310
BLAST score	187
E value	9.0e-14
Match length	81
% identity	52
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	274334
Contig ID	49104_1.R1011
5'-most EST	LIB148-012-Q1-E1-C5
Method	BLASTX
NCBI GI	g1834353
BLAST score	269
E value	3.0e-23
Match length	198
% identity	40
NCBI Description	(Y10986) hypothetical protein 194 [Arabidopsis thaliana]

Seq. No.	274335
Contig ID	49105_1.R1011
5'-most EST	hvj70̄0624540.h1
Method	BLASTX
NCBI GI	g1170745
BLAST score	349
E value	8.0e-33
Match length	111
% identity	59
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326 (M88321) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167328 (M88322) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	274336
Contig ID	49109_1.R1011
5'-most EST	LIB148̄-012-Q1-E1-D11
Method	BLASTX
NCBI GI	g3252806
BLAST score	162
E value	6.0e-11
Match length	86
% identity	36
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274337
Contig ID	49129_1.R1011
5'-most EST	LIB148̄-012-Q1-E1-E9
Method	BLASTX
NCBI GI	g4006878
BLAST score	425
E value	8.0e-42
Match length	154
% identity	51
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	274338
Contig ID	49140_1.R1011
5'-most EST	LIB148̄-012-Q1-E1-F8

Seq. No.	274339
Contig ID	49146_1.R1011
5'-most EST	LIB148̄-012-Q1-E1-G2
Method	BLASTX
NCBI GI	g4539303
BLAST score	334
E value	4.0e-31
Match length	132
% identity	52
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	274340
Contig ID	49148_1.R1011
5'-most EST	LIB148̄-033-Q1-E1-D8
Method	BLASTX
NCBI GI	g2760326
BLAST score	192

E value	2.0e-14
Match length	103
% identity	42
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	274341
Contig ID	49154_1.R1011
5'-most EST	LIB148-012-Q1-E1-H1
Method	BLASTX
NCBI GI	g3360289
BLAST score	675
E value	9.0e-71
Match length	216
% identity	60
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	274342
Contig ID	49156_1.R1011
5'-most EST	LIB148-012-Q1-E1-H11
Method	BLASTX
NCBI GI	g2244771
BLAST score	417
E value	9.0e-41
Match length	204
% identity	48
NCBI Description	(Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No.	274343
Contig ID	49179_1.R1011
5'-most EST	LIB148-030-Q1-E1-D8
Method	BLASTX
NCBI GI	g2335096
BLAST score	464
E value	5.0e-46
Match length	333
% identity	36
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274344
Contig ID	49184_1.R1011
5'-most EST	LIB148-013-Q1-E1-B5
Method	BLASTX
NCBI GI	g2829898
BLAST score	178
E value	6.0e-13
Match length	80
% identity	40
NCBI Description	(AC002311) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	274345
Contig ID	49188_1.R1011
5'-most EST	LIB3066-044-Q1-K1-C5

Seq. No.	274346
Contig ID	49199_1.R1011
5'-most EST	qmh70O029165.f1

Method	BLASTX
NCBI GI	g401190
BLAST score	410
E value	8.0e-40
Match length	102
% identity	78
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_100715_pir__S25551 thaumatin-like protein - rice >gi_20376_emb_CAA48278_ (X68197) thaumatin-like protein [Oryza sativa]

Seq. No.	274347
Contig ID	49199_2.R1011
5'-most EST	LIB148-013-Q1-E1-C9
Method	BLASTX
NCBI GI	g3290006
BLAST score	652
E value	3.0e-68
Match length	151
% identity	82
NCBI Description	(U82201) pathogenesis related protein-5 [Zea mays]

Seq. No.	274348
Contig ID	49202_1.R1011
5'-most EST	LIB148-013-Q1-E1-D11
Method	BLASTX
NCBI GI	g1346756
BLAST score	239
E value	4.0e-20
Match length	71
% identity	68
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 3 >gi_421852_pir__S31087 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP3) - Arabidopsis thaliana >gi_166799 (M93410) phosphoprotein phosphatase 1 [Arabidopsis thaliana]

Seq. No.	274349
Contig ID	49206_1.R1011
5'-most EST	LIB148-049-Q1-E1-D12
Method	BLASTX
NCBI GI	g4544464
BLAST score	166
E value	3.0e-11
Match length	154
% identity	29
NCBI Description	(AC006580) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	274350
Contig ID	49227_1.R1011
5'-most EST	LIB148-044-Q1-E1-E4
Method	BLASTX
NCBI GI	g4490706
BLAST score	388
E value	3.0e-37
Match length	124
% identity	58

NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	274351
Contig ID	49236_1.R1011
5'-most EST	LIB3066-020-Q1-K1-D6

Seq. No.	274352
Contig ID	49239_1.R1011
5'-most EST	LIB3066-035-Q1-K1-F12
Method	BLASTX
NCBI GI	g2529672
BLAST score	273
E value	7.0e-24
Match length	101
% identity	50
NCBI Description	(AC002535) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	274353
Contig ID	49254_1.R1011
5'-most EST	LIB148-013-Q1-E1-H7

Seq. No.	274354
Contig ID	49267_1.R1011
5'-most EST	LIB148-014-Q1-E1-A9

Seq. No.	274355
Contig ID	49287_1.R1011
5'-most EST	uC-zmrob73053f04a1
Method	BLASTX
NCBI GI	g4586054
BLAST score	158
E value	1.0e-10
Match length	63
% identity	57
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	274356
Contig ID	49288_1.R1011
5'-most EST	LIB3066-006-Q1-K1-E5

Seq. No.	274357
Contig ID	49294_1.R1011
5'-most EST	LIB148-014-Q1-E1-D5
Method	BLASTX
NCBI GI	g4417304
BLAST score	400
E value	1.0e-38
Match length	111
% identity	61
NCBI Description	(AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]

Seq. No.	274358
Contig ID	49306_1.R1011
5'-most EST	LIB148-030-Q1-E1-B1

Seq. No.	274359
Contig ID	49310_1.R1011
5'-most EST	LIB148-035-Q1-E1-C6
Seq. No.	274360
Contig ID	49315_1.R1011
5'-most EST	LIB148-025-Q1-E1-G3
Method	BLASTX
NCBI GI	g4099090
BLAST score	621
E value	2.0e-64
Match length	179
% identity	61
NCBI Description	(U83178) unknown [Arabidopsis thaliana]
Seq. No.	274361
Contig ID	49325_1.R1011
5'-most EST	LIB3137-050-Q1-K1-H1
Seq. No.	274362
Contig ID	49338_1.R1011
5'-most EST	zuv700355402.h1
Method	BLASTX
NCBI GI	g4539351
BLAST score	361
E value	2.0e-34
Match length	148
% identity	51
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	274363
Contig ID	49341_1.R1011
5'-most EST	uC-zmflb73092d12b2
Seq. No.	274364
Contig ID	49355_2.R1011
5'-most EST	LIB148-036-Q1-E1-F9
Method	BLASTX
NCBI GI	g3128224
BLAST score	270
E value	1.0e-23
Match length	139
% identity	43
NCBI Description	(AC004077) putative protein serine/threonine kinase [Arabidopsis thaliana]
Seq. No.	274365
Contig ID	49358_1.R1011
5'-most EST	nwy700444319.h1
Seq. No.	274366
Contig ID	49358_2.R1011
5'-most EST	uC-zmflmo17330d03b1
Seq. No.	274367
Contig ID	49365_1.R1011
5'-most EST	LIB3066-048-Q1-K1-B7

Seq. No.	274368
Contig ID	49374_1.R1011
5'-most EST	dyk700103756.h1
Method	BLASTX
NCBI GI	g4585996
BLAST score	291
E value	7.0e-26
Match length	155
% identity	37
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	274369
Contig ID	49376_1.R1011
5'-most EST	LIB148-015-Q1-E1-D1
Method	BLASTX
NCBI GI	g2829911
BLAST score	346
E value	9.0e-33
Match length	121
% identity	56
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	274370
Contig ID	49401_1.R1011
5'-most EST	LIB148-015-Q1-E1-F3
Method	BLASTX
NCBI GI	g2291232
BLAST score	736
E value	9.0e-78
Match length	308
% identity	50
NCBI Description	(AF016427) similar to the AAA family of ATPases [Caenorhabditis elegans]

Seq. No.	274371
Contig ID	49402_1.R1011
5'-most EST	uC-zmrob73022e03a1
Method	BLASTX
NCBI GI	g2493321
BLAST score	562
E value	4.0e-94
Match length	314
% identity	55
NCBI Description	L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO) >gi_2129952_pir__S66353 L-ascorbate oxidase (EC 1.10.3.3) precursor - common tobacco >gi_599594_dbj_BAA07734_ (D43624) ascorbate oxidase precursor [Nicotiana tabacum]

Seq. No.	274372
Contig ID	49435_1.R1011
5'-most EST	LIB148-016-Q1-E1-A2

Seq. No.	274373
Contig ID	49436_1.R1011
5'-most EST	LIB148-049-Q1-E1-D8
Method	BLASTX

NCBI GI	g3892058
BLAST score	150
E value	1.0e-09
Match length	78
% identity	37
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No.	274374
Contig ID	49438_1.R1011
5'-most EST	LIB3066-026-Q1-K1-G9

Seq. No.	274375
Contig ID	49443_1.R1011
5'-most EST	LIB148-016-Q1-E1-D3

Seq. No.	274376
Contig ID	49456_1.R1011
5'-most EST	LIB148-016-Q1-E1-C3

Seq. No.	274377
Contig ID	49480_1.R1011
5'-most EST	LIB148-025-Q1-E1-G8
Method	BLASTX
NCBI GI	g4417291
BLAST score	235
E value	3.0e-19
Match length	96
% identity	53
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274378
Contig ID	49502_1.R1011
5'-most EST	uC-zmflb73029c09b1
Method	BLASTX
NCBI GI	g3287695
BLAST score	632
E value	4.0e-66
Match length	141
% identity	86
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	274379
Contig ID	49508_1.R1011
5'-most EST	uC-zmflmo17245c09a1

Seq. No.	274380
Contig ID	49512_1.R1011
5'-most EST	LIB148-016-Q1-E1-H9
Method	BLASTX
NCBI GI	g2739366
BLAST score	200
E value	1.0e-15
Match length	138
% identity	38

NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]
Seq. No.	274381
Contig ID	49524_1.R1011
5'-most EST	uC-zmflmo17126f10b1
Seq. No.	274382
Contig ID	49536_1.R1011
5'-most EST	LIB148-044-Q1-E1-C8
Seq. No.	274383
Contig ID	49573_1.R1011
5'-most EST	LIB148-017-Q1-E1-F2
Method	BLASTX
NCBI GI	g1890776
BLAST score	261
E value	2.0e-22
Match length	223
% identity	29
NCBI Description	(U88574) syringomycin biosynthesis enzyme [Pseudomonas syringae pv. syringae]
Seq. No.	274384
Contig ID	49578_1.R1011
5'-most EST	LIB3066-001-Q1-K1-G12
Seq. No.	274385
Contig ID	49586_1.R1011
5'-most EST	LIB148-017-Q1-E1-G3
Method	BLASTX
NCBI GI	g2880046
BLAST score	175
E value	2.0e-12
Match length	96
% identity	42
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.	274386
Contig ID	49591_1.R1011
5'-most EST	uC-zmflb73011h01b1
Method	BLASTX
NCBI GI	g4262154
BLAST score	592
E value	1.0e-60
Match length	234
% identity	51
NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]
Seq. No.	274387
Contig ID	49600_1.R1011
5'-most EST	xyt700346223.h1
Method	BLASTX
NCBI GI	g4337191
BLAST score	668
E value	4.0e-70
Match length	183

% identity	69
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274388
Contig ID	49600_2.R1011
5'-most EST	LIB3062-023-Q1-K1-A5
Method	BLASTX
NCBI GI	g2980764
BLAST score	292
E value	4.0e-26
Match length	84
% identity	61
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	274389
Contig ID	49608_1.R1011
5'-most EST	LIB3066-032-Q1-K1-B6
Method	BLASTX
NCBI GI	g4417291
BLAST score	459
E value	2.0e-45
Match length	174
% identity	55
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274390
Contig ID	49613_1.R1011
5'-most EST	pwf70321767.h1
Method	BLASTX
NCBI GI	g2388582
BLAST score	1311
E value	1.0e-179
Match length	481
% identity	65
NCBI Description	(AC000098) Contains similarity to Rattus O-GlcNAc transferase (gb_U76557). [Arabidopsis thaliana]

Seq. No.	274391
Contig ID	49618_1.R1011
5'-most EST	LIB148-018-Q1-E1-B2
Method	BLASTX
NCBI GI	g2398679
BLAST score	903
E value	1.0e-97
Match length	191
% identity	88
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	274392
Contig ID	49618_2.R1011
5'-most EST	LIB3066-011-Q1-K1-D4
Method	BLASTX
NCBI GI	g2398679
BLAST score	720
E value	3.0e-76
Match length	150

% identity	90
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	274393
Contig ID	49628_1.R1011
5'-most EST	bdu700382670.h1

Seq. No.	274394
Contig ID	49632_1.R1011
5'-most EST	LIB148-018-Q1-E1-C8
Method	BLASTX
NCBI GI	g1707015
BLAST score	278
E value	5.0e-48
Match length	140
% identity	69
NCBI Description	(U78721) protein phosphatase 2C isolog [Arabidopsis thaliana]

Seq. No.	274395
Contig ID	49642_1.R1011
5'-most EST	LIB148-018-Q1-E1-D9
Method	BLASTX
NCBI GI	g4455192
BLAST score	281
E value	7.0e-25
Match length	155
% identity	40
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	274396
Contig ID	49645_1.R1011
5'-most EST	LIB148-022-Q1-E1-F1
Method	BLASTX
NCBI GI	g3108161
BLAST score	846
E value	8.0e-91
Match length	237
% identity	67
NCBI Description	(AF061106) putative monosaccharide transporter 1 [Petunia x hybrida]

Seq. No.	274397
Contig ID	49652_1.R1011
5'-most EST	LIB3066-008-Q1-K1-H11
Method	BLASTX
NCBI GI	g99733
BLAST score	664
E value	9.0e-70
Match length	190
% identity	68
NCBI Description	hypothetical protein H1flk - Arabidopsis thaliana (fragment) >gi_16482_emb_CAA44318_ (X62461) H1flk [Arabidopsis thaliana]

Seq. No.	274398

Contig ID	49661_1.R1011
5'-most EST	LIB3066-053-Q1-K1-E12
Method	BLASTX
NCBI GI	g3785983
BLAST score	238
E value	5.0e-20
Match length	91
% identity	49
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274399
Contig ID	49680_1.R1011
5'-most EST	LIB3066-014-Q1-K1-A4
Method	BLASTX
NCBI GI	g2827623
BLAST score	886
E value	1.0e-108
Match length	330
% identity	62
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	274400
Contig ID	49700_1.R1011
5'-most EST	LIB148-019-Q1-E1-B6

Seq. No.	274401
Contig ID	49706_1.R1011
5'-most EST	ymt700223244.h1
Method	BLASTX
NCBI GI	g732003
BLAST score	236
E value	2.0e-19
Match length	146
% identity	42
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2125977_pir__I84534 outer membrane lipoprotein - Escherichia coli >gi_536993 (U14003) ORF_f177 [Escherichia coli] >gi_717134 (U21726) lipocalin precursor [Escherichia coli] >gi_1790592 (AE000487) outer membrane lipoprotein (lipocalin) [Escherichia coli]

Seq. No.	274402
Contig ID	49706_4.R1011
5'-most EST	gct701177618.h1

Seq. No.	274403
Contig ID	49721_1.R1011
5'-most EST	LIB148-062-Q1-E1-A6

Seq. No.	274404
Contig ID	49729_1.R1011
5'-most EST	LIB3066-021-Q1-K1-H5
Method	BLASTX
NCBI GI	g2914706
BLAST score	445
E value	3.0e-44
Match length	118

% identity	67
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	274405
Contig ID	49754_1.R1011
5'-most EST	LIB148-036-Q1-E1-F6
Method	BLASTX
NCBI GI	g728483
BLAST score	173
E value	3.0e-12
Match length	60
% identity	53
NCBI Description	(L41046) endo-1,4-beta-glucanase [Pisum sativum]

Seq. No.	274406
Contig ID	49766_1.R1011
5'-most EST	LIB148-020-Q1-E1-A10
Method	BLASTX
NCBI GI	g4506725
BLAST score	704
E value	2.0e-75
Match length	143
% identity	91
NCBI Description	ribosomal protein S4, X-linked >gi_1350997_sp_P12750_RS4_HUMAN 40S RIBOSOMAL PROTEIN S4, X ISOFORM (SINGLE COPY ABUNDANT MRNA PROTEIN) (SCR10) >gi_70870_pir__R3RT4 ribosomal protein S4 - rat >gi_70871_pir__R3HU4X ribosomal protein S4.X - human >gi_1083572_pir__A55276 ribosomal protein S4 - western wild mouse >gi_2148029_pir__I48169 ribosomal protein S4 - hamster (Mesocricetus sp.) >gi_57135_emb_CAA32427_ (X14210) ribosomal protein S4 (AA 1 - 263) [Rattus rattus] >gi_200864 (M73436) ribosomal protein S4 [Mus musculus] >gi_220321_dbj_BAA01858_ (D11087) ribosomal protein S4 [Mesocricetus sp.] >gi_337510 (M58458) ribosomal protein S4X isoform [Homo sapiens] >gi_2791861 (AF041428) ribosomal protein s4 X isoform [Homo sapiens] >gi_4115718_dbj_BAA36501_ (AB015610) ribosomal protein S4X [Chlorocebus aethiops]

Seq. No.	274407
Contig ID	49823_2.R1011
5'-most EST	ntr700073880.h1
Method	BLASTX
NCBI GI	g3341699
BLAST score	189
E value	3.0e-14
Match length	81
% identity	46
NCBI Description	(AC003672) putative giberellin beta-hydroxylase [Arabidopsis thaliana]

Seq. No.	274408
Contig ID	49830_1.R1011
5'-most EST	LIB148-020-Q1-E1-G12
Method	BLASTX
NCBI GI	g417719

BLAST score	1217
E value	1.0e-134
Match length	243
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_2144763_pir__R3HUS3 ribosomal protein S3 - human >gi_233042_bbs_42659 (S42658) S3 ribosomal protein [human, colon, Peptide, 243 aa] [Homo sapiens] >gi_555941 (U14990) ribosomal protein S3 [Homo sapiens] >gi_555943 (U14991) ribosomal protein S3 [Homo sapiens] >gi_555945 (U14992) ribosomal protein S3 [Homo sapiens]

Seq. No.	274409
Contig ID	49833_1.R1011
5'-most EST	LIB3066-001-Q1-K1-D5
Method	BLASTX
NCBI GI	g4581150
BLAST score	498
E value	2.0e-50
Match length	170
% identity	59
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274410
Contig ID	49837_1.R1011
5'-most EST	LIB1488-036-Q1-E1-D5

Seq. No.	274411
Contig ID	49843_1.R1011
5'-most EST	uC-zmflmo17269a02a1

Seq. No.	274412
Contig ID	49859_1.R1011
5'-most EST	LIB1488-021-Q1-E1-B6

Seq. No.	274413
Contig ID	49860_1.R1011
5'-most EST	LIB1488-021-Q1-E1-B7

Seq. No.	274414
Contig ID	49865_1.R1011
5'-most EST	LIB3066-056-Q1-K1-C1
Method	BLASTX
NCBI GI	g2739382
BLAST score	284
E value	4.0e-25
Match length	206
% identity	33
NCBI Description	(AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	274415
Contig ID	49877_1.R1011
5'-most EST	LIB1488-063-Q1-E1-C6

Seq. No.	274416
Contig ID	49899_1.R1011

5'-most EST	LIB148-021-Q1-E1-F2
Method	BLASTX
NCBI GI	g4544384
BLAST score	258
E value	7.0e-22
Match length	66
% identity	80
NCBI Description	(AC007047) unknown protein [Arabidopsis thaliana]

Seq. No.	274417
Contig ID	49902_1.R1011
5'-most EST	LIB3062-019-Q1-K1-D9

Seq. No.	274418
Contig ID	49904_1.R1011
5'-most EST	LIB3066-020-Q1-K1-E7
Method	BLASTX
NCBI GI	g1669599
BLAST score	314
E value	3.0e-28
Match length	116
% identity	58
NCBI Description	(D88746) AR791 [Arabidopsis thaliana]

Seq. No.	274419
Contig ID	49912_1.R1011
5'-most EST	uC-zmflmo170112g11b1
Method	BLASTX
NCBI GI	g4467146
BLAST score	1026
E value	1.0e-111
Match length	456
% identity	45
NCBI Description	(AL035540) galactosidase like protein [Arabidopsis thaliana]

Seq. No.	274420
Contig ID	49933_1.R1011
5'-most EST	dyk700105747.h1

Seq. No.	274421
Contig ID	49943_1.R1011
5'-most EST	LIB3066-029-Q1-K1-F7
Method	BLASTX
NCBI GI	g1706082
BLAST score	564
E value	6.0e-58
Match length	173
% identity	61
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	274422
Contig ID	49951_1.R1011
5'-most EST	LIB1480-022-Q1-E1-C11
Method	BLASTX
NCBI GI	g4337202
BLAST score	370
E value	3.0e-35
Match length	166
% identity	47
NCBI Description	(AC006403) putative endosperm-specific protein [Arabidopsis thaliana]

Seq. No.	274423
Contig ID	49953_1.R1011
5'-most EST	LIB1480-022-Q1-E1-C2
Method	BLASTX
NCBI GI	g2760326
BLAST score	339
E value	7.0e-32
Match length	124
% identity	50
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	274424
Contig ID	49956_1.R1011
5'-most EST	LIB1480-022-Q1-E1-C7
Method	BLASTX
NCBI GI	g2642446
BLAST score	590
E value	7.0e-61
Match length	166
% identity	69
NCBI Description	(AC002391) similar to auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	274425
Contig ID	49958_1.R1011
5'-most EST	ceu700433990.h2

Seq. No.	274426
Contig ID	49967_1.R1011
5'-most EST	LIB1480-027-Q1-E1-D10

Seq. No.	274427
Contig ID	49988_1.R1011
5'-most EST	LIB3066-004-Q1-K1-B1

Seq. No.	274428
Contig ID	49990_1.R1011
5'-most EST	zuv700356216.h1
Method	BLASTX
NCBI GI	g2388565
BLAST score	214
E value	5.0e-17
Match length	117
% identity	43
NCBI Description	(AC000098) Similar to Prunus pectinesterase (gb_X95991).

[Arabidopsis thaliana]

Seq. No.	274429
Contig ID	50004_1.R1011
5'-most EST	LIB148-036-Q1-E1-G4
Method	BLASTX
NCBI GI	g2924781
BLAST score	612
E value	1.0e-63
Match length	159
% identity	70
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	274430
Contig ID	50023_1.R1011
5'-most EST	LIB148-032-Q1-E1-E12

Seq. No.	274431
Contig ID	50024_1.R1011
5'-most EST	uC-zmflb73298h04b1

Seq. No.	274432
Contig ID	50033_1.R1011
5'-most EST	LIB148-023-Q1-E1-B8
Method	BLASTX
NCBI GI	g4538945
BLAST score	511
E value	1.0e-51
Match length	122
% identity	74
NCBI Description	(AL049483) putative thioredoxin [Arabidopsis thaliana]

Seq. No.	274433
Contig ID	50034_1.R1011
5'-most EST	LIB3066-002-Q1-K1-B8
Method	BLASTX
NCBI GI	g4309731
BLAST score	202
E value	2.0e-15
Match length	131
% identity	40
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274434
Contig ID	50056_1.R1011
5'-most EST	LIB148-023-Q1-E1-E1
Method	BLASTX
NCBI GI	g2281094
BLAST score	215
E value	3.0e-17
Match length	118
% identity	39
NCBI Description	(AC002333) molybdenum cofactor biosynthesis protein E isolog [Arabidopsis thaliana] >gi_4469121_emb_CAB38428_ (AJ133519) molybdopterin synthase large subunit [Arabidopsis thaliana]

Seq. No.	274435
Contig ID	50062_1.R1011
5'-most EST	LIB148-023-Q1-E1-E5
Method	BLASTX
NCBI GI	g115506
BLAST score	221
E value	7.0e-18
Match length	111
% identity	41
NCBI Description	CALMODULIN >gi_71688_pir__MCKM calmodulin - Chlamydomonas reinhardtii >gi_167411 (M20729) calmodulin [Chlamydomonas reinhardtii]

Seq. No.	274436
Contig ID	50065_1.R1011
5'-most EST	uC-zmflb73196h08b1
Method	BLASTX
NCBI GI	g4580398
BLAST score	1139
E value	1.0e-125
Match length	322
% identity	69
NCBI Description	(AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No.	274437
Contig ID	50065_2.R1011
5'-most EST	uC-zmflmo17048e03b1

Seq. No.	274438
Contig ID	50103_1.R1011
5'-most EST	LIB148-024-Q1-E1-A4

Seq. No.	274439
Contig ID	50115_1.R1011
5'-most EST	LIB148-024-Q1-E1-C2
Method	BLASTX
NCBI GI	g4454051
BLAST score	695
E value	2.0e-73
Match length	187
% identity	67
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	274440
Contig ID	50124_1.R1011
5'-most EST	zuv700356072.h1

Seq. No.	274441
Contig ID	50132_1.R1011
5'-most EST	LIB36-001-Q1-E1-A2
Method	BLASTX
NCBI GI	g1370188
BLAST score	1010
E value	1.0e-110

Match length	205
% identity	91
NCBI Description	(Z73943) RAB7D [Lotus japonicus]

Seq. No.	274442
Contig ID	50136_1.R1011
5'-most EST	LIB148-035-Q1-E1-B4

Seq. No.	274443
Contig ID	50143_1.R1011
5'-most EST	LIB148-024-Q1-E1-E6

Seq. No.	274444
Contig ID	50167_1.R1011
5'-most EST	LIB148-024-Q1-E1-H1
Method	BLASTX
NCBI GI	g2245125
BLAST score	157
E value	2.0e-10
Match length	39
% identity	77
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274445
Contig ID	50233_1.R1011
5'-most EST	uC-zmf1b73189d11b1

Seq. No.	274446
Contig ID	50233_2.R1011
5'-most EST	xjt700095295.h1
Method	BLASTX
NCBI GI	g1575296
BLAST score	478
E value	7.0e-48
Match length	100
% identity	84
NCBI Description	(U58919) beta-carotene hydroxylase [Arabidopsis thaliana]

Seq. No.	274447
Contig ID	50233_3.R1011
5'-most EST	LIB148-025-Q1-E1-F2
Method	BLASTX
NCBI GI	g1575296
BLAST score	268
E value	3.0e-26
Match length	74
% identity	80
NCBI Description	(U58919) beta-carotene hydroxylase [Arabidopsis thaliana]

Seq. No.	274448
Contig ID	50233_4.R1011
5'-most EST	fC-zmle700426259d3

Seq. No.	274449
Contig ID	50243_1.R1011
5'-most EST	LIB148-025-Q1-E1-G11

Seq. No.	274450
Contig ID	50251_1.R1011
5'-most EST	bdu700383007.h1
Method	BLASTX
NCBI GI	g3080420
BLAST score	319
E value	2.0e-29
Match length	81
% identity	70
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	274451
Contig ID	50254_1.R1011
5'-most EST	mwy700440963.h1
Method	BLASTX
NCBI GI	g3395439
BLAST score	435
E value	1.0e-42
Match length	238
% identity	40
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274452
Contig ID	50277_1.R1011
5'-most EST	LIB148-026-Q1-E1-B7

Seq. No.	274453
Contig ID	50279_1.R1011
5'-most EST	LIB148-048-Q1-E1-H9
Method	BLASTX
NCBI GI	g4415931
BLAST score	318
E value	3.0e-32
Match length	142
% identity	58
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	274454
Contig ID	50286_1.R1011
5'-most EST	pmx700083475.h1
Method	BLASTX
NCBI GI	g4204265
BLAST score	540
E value	6.0e-55
Match length	218
% identity	50
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	274455
Contig ID	50313_1.R1011
5'-most EST	LIB3066-014-Q1-K1-B1
Method	BLASTX
NCBI GI	g2832300
BLAST score	782

E value	3.0e-83
Match length	200
% identity	74
NCBI Description	(AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus roseus]

Seq. No.	274456
Contig ID	50313_3.R1011
5'-most EST	LIB148-058-Q1-E1-F6
Method	BLASTX
NCBI GI	g1076283
BLAST score	299
E value	2.0e-31
Match length	105
% identity	68
NCBI Description	adenylylsulfate kinase (EC 2.7.1.25) precursor - Arabidopsis thaliana >gi_414737_emb_CAA53426_ (X75782) APS kinase [Arabidopsis thaliana] >gi_450235 (U05238) APS kinase [Arabidopsis thaliana] >gi_1575322 (U59759) APS kinase [Arabidopsis thaliana] >gi_3252812 (AC004705) APS kinase [Arabidopsis thaliana]

Seq. No.	274457
Contig ID	50357_1.R1011
5'-most EST	LIB148-027-Q1-E1-B5
Method	BLASTX
NCBI GI	g4200165
BLAST score	310
E value	3.0e-28
Match length	81
% identity	70
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	274458
Contig ID	50372_1.R1011
5'-most EST	LIB148-027-Q1-E1-D11
Method	BLASTX
NCBI GI	g4582467
BLAST score	718
E value	5.0e-76
Match length	218
% identity	61
NCBI Description	(AC007071) putative calcium dependent protein kinase; contains protein kinase domain [Arabidopsis thaliana] >gi_4589951_gb_AAD26469.1_AC007169_1 (AC007169) putative calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	274459
Contig ID	50384_1.R1011
5'-most EST	LIB148-027-Q1-E1-E11

Seq. No.	274460
Contig ID	50399_1.R1011
5'-most EST	bdu700382963.h1
Method	BLASTX
NCBI GI	g3868853
BLAST score	316

E value	5.0e-29
Match length	93
% identity	60
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No.	274461
Contig ID	50419_1.R1011
5'-most EST	tzu700205347.h1
Method	BLASTX
NCBI GI	g1854443
BLAST score	416
E value	1.0e-52
Match length	168
% identity	64
NCBI Description	(D83970) CPRD8 protein [Vigna unguiculata]

Seq. No.	274462
Contig ID	50438_1.R1011
5'-most EST	uC-zmflmo17070c02b1
Method	BLASTX
NCBI GI	g1304599
BLAST score	430
E value	7.0e-42
Match length	314
% identity	32
NCBI Description	(U41315) ZNF127-Xp [Homo sapiens]

Seq. No.	274463
Contig ID	50454_1.R1011
5'-most EST	LIB148-028-Q1-E1-C7
Method	BLASTX
NCBI GI	g4505823
BLAST score	346
E value	9.0e-33
Match length	116
% identity	59
NCBI Description	pirin >gi_1907076_emb_CAA69194_ (Y07867) pirin [Homo sapiens] >gi_1907078_emb_CAA69195_ (Y07868) pirin [Homo sapiens]

Seq. No.	274464
Contig ID	50461_1.R1011
5'-most EST	LIB148-028-Q1-E1-E5
Method	BLASTX
NCBI GI	g3367520
BLAST score	363
E value	2.0e-34
Match length	129
% identity	53
NCBI Description	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb_D12522 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	274465
Contig ID	50466_1.R1011
5'-most EST	LIB148-046-Q1-E1-B11
Method	BLASTX

NCBI GI	g4567250
BLAST score	307
E value	2.0e-27
Match length	205
% identity	53
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274466
Contig ID	50507_1.R1011
5'-most EST	pmx700089219.h1
Method	BLASTX
NCBI GI	g2132388
BLAST score	151
E value	2.0e-09
Match length	88
% identity	42
NCBI Description	PHO85 protein - yeast (Saccharomyces cerevisiae) >gi_1163103 (U43503) Lph16p [Saccharomyces cerevisiae]

Seq. No.	274467
Contig ID	50515_1.R1011
5'-most EST	ymt700219013.h1
Method	BLASTX
NCBI GI	g731834
BLAST score	184
E value	2.0e-13
Match length	149
% identity	38
NCBI Description	HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION >gi_1077790_pir__S49797 hypothetical protein YIL083c - yeast (Saccharomyces cerevisiae) >gi_577131_emb_CAA86711.1_ (Z46728) YI9910.13c, unknown orf, len: 365, CAI: 0.17 [Saccharomyces cerevisiae]

Seq. No.	274468
Contig ID	50554_1.R1011
5'-most EST	wyr700235821.h1
Method	BLASTX
NCBI GI	g2213594
BLAST score	722
E value	3.0e-76
Match length	173
% identity	72
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	274469
Contig ID	50564_1.R1011
5'-most EST	LIB3060-012-Q1-K1-B5

Seq. No.	274470
Contig ID	50569_1.R1011
5'-most EST	LIB148-029-Q1-E1-F9
Method	BLASTN
NCBI GI	g600117
BLAST score	794
E value	0.0e+00
Match length	1048

% identity	37
NCBI Description	Z.mays (B73) gene for extensin-like protein

Seq. No.	274471
Contig ID	50583_1.R1011
5'-most EST	LIB3066-042-Q1-K1-C8
Method	BLASTX
NCBI GI	g2746086
BLAST score	590
E value	3.0e-61
Match length	139
% identity	76
NCBI Description	(AF025292) putative high-affinity potassium transporter [Hordeum vulgare]

Seq. No.	274472
Contig ID	50603_1.R1011
5'-most EST	uC-zmflb73111d03a1

Seq. No.	274473
Contig ID	50617_1.R1011
5'-most EST	LIB148-030-Q1-E1-B2

Seq. No.	274474
Contig ID	50619_1.R1011
5'-most EST	LIB3066-033-Q1-K1-A2

Seq. No.	274475
Contig ID	50624_1.R1011
5'-most EST	LIB148-030-Q1-E1-C10
Method	BLASTX
NCBI GI	g2335096
BLAST score	368
E value	5.0e-35
Match length	135
% identity	57
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274476
Contig ID	50626_1.R1011
5'-most EST	LIB3136-010-Q1-K1-C8

Seq. No.	274477
Contig ID	50628_1.R1011
5'-most EST	LIB148-030-Q1-E1-C4

Seq. No.	274478
Contig ID	50636_1.R1011
5'-most EST	LIB3066-024-Q1-K1-G5
Method	BLASTX
NCBI GI	g4581116
BLAST score	504
E value	6.0e-51
Match length	126
% identity	65
NCBI Description	(AC005825) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	274479
Contig ID	50662_1.R1011
5'-most EST	LIB148-034-Q1-E1-C5
Method	BLASTX
NCBI GI	g2459447
BLAST score	450
E value	7.0e-45
Match length	138
% identity	64
NCBI Description	(AC002332) putative Mlo protein [Arabidopsis thaliana]

Seq. No.	274480
Contig ID	50671_1.R1011
5'-most EST	LIB148-030-Q1-E1-G9
Method	BLASTX
NCBI GI	g2911040
BLAST score	508
E value	2.0e-51
Match length	193
% identity	55
NCBI Description	(AL021961) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	274481
Contig ID	50672_1.R1011
5'-most EST	LIB148-030-Q1-E1-G11

Seq. No.	274482
Contig ID	50674_1.R1011
5'-most EST	wyr70242403.h1
Method	BLASTX
NCBI GI	g4115931
BLAST score	1113
E value	1.0e-156
Match length	370
% identity	77
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	274483
Contig ID	50682_1.R1011
5'-most EST	yyf70347769.h1

Seq. No.	274484
Contig ID	50726_1.R1011
5'-most EST	ceu70427360.h1
Method	BLASTX
NCBI GI	g3540190
BLAST score	385
E value	7.0e-37
Match length	167
% identity	44
NCBI Description	(AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	274485
Contig ID	50792_1.R1011

5'-most EST	tzu700202948.h1
Method	BLASTN
NCBI GI	g2832242
BLAST score	42
E value	2.0e-14
Match length	46
% identity	98
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	274486
Contig ID	50796_1.R1011
5'-most EST	uC-zmflmo17138f07b1

Seq. No.	274487
Contig ID	50796_2.R1011
5'-most EST	uC-zmflmo17258e01b1

Seq. No.	274488
Contig ID	50796_3.R1011
5'-most EST	LIB3069-036-Q1-K1-C12

Seq. No.	274489
Contig ID	50798_1.R1011
5'-most EST	LIB148-032-Q1-E1-E9
Method	BLASTN
NCBI GI	g2341023
BLAST score	42
E value	2.0e-14
Match length	62
% identity	92
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	274490
Contig ID	50826_1.R1011
5'-most EST	LIB148-032-Q1-E1-H3

Seq. No.	274491
Contig ID	50831_2.R1011
5'-most EST	LIB148-040-Q1-E1-H4
Method	BLASTX
NCBI GI	g4539351
BLAST score	443
E value	1.0e-43
Match length	188
% identity	48
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	274492
Contig ID	50876_1.R1011
5'-most EST	LIB3066-054-Q1-K1-A7
Method	BLASTX
NCBI GI	g4210504
BLAST score	342
E value	6.0e-32
Match length	184
% identity	39

NCBI Description	(AC002392) putative cadmium-transporting ATPase [Arabidopsis thaliana]

Seq. No.	274493
Contig ID	50886_1.R1011
5'-most EST	LIB3137-033-Q1-K1-A12
Method	BLASTX
NCBI GI	g4220537
BLAST score	170
E value	6.0e-12
Match length	44
% identity	75
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	274494
Contig ID	50905_1.R1011
5'-most EST	LIB148-033-Q1-E1-G9
Method	BLASTX
NCBI GI	g3858935
BLAST score	227
E value	1.0e-18
Match length	64
% identity	61
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	274495
Contig ID	50909_1.R1011
5'-most EST	ypc700804561.h1
Method	BLASTX
NCBI GI	g2146746
BLAST score	693
E value	5.0e-73
Match length	154
% identity	85
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No.	274496
Contig ID	50929_1.R1011
5'-most EST	LIB148-048-Q1-E1-C4
Method	BLASTX
NCBI GI	g1871593
BLAST score	205
E value	8.0e-16
Match length	218
% identity	30
NCBI Description	(Z92669) lipC [Mycobacterium tuberculosis]

Seq. No.	274497
Contig ID	50935_1.R1011
5'-most EST	LIB148-034-Q1-E1-B5

Seq. No.	274498
Contig ID	50950_2.R1011

5'-most EST	nwy700444496.h1
Method	BLASTX
NCBI GI	g2408103
BLAST score	433
E value	1.0e-42
Match length	161
% identity	48
NCBI Description	(AJ001587) sid3 [Schizosaccharomyces pombe]

Seq. No.	274499
Contig ID	50954_1.R1011
5'-most EST	LIB3066-056-Q1-K1-H6
Method	BLASTX
NCBI GI	g3786005
BLAST score	773
E value	4.0e-82
Match length	239
% identity	43
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	274500
Contig ID	50954_2.R1011
5'-most EST	ntr700075768.h1
Method	BLASTX
NCBI GI	g3786005
BLAST score	546
E value	8.0e-56
Match length	167
% identity	66
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	274501
Contig ID	50961_1.R1011
5'-most EST	LIB148-034-Q1-E1-D7
Method	BLASTN
NCBI GI	g22378
BLAST score	201
E value	1.0e-109
Match length	369
% identity	98
NCBI Description	Z.mays gene for nucleic acid binding protein

Seq. No.	274502
Contig ID	50966_1.R1011
5'-most EST	LIB3067-002-Q1-K1-D9

Seq. No.	274503
Contig ID	50986_1.R1011
5'-most EST	LIB148-034-Q1-E1-G5

Seq. No.	274504
Contig ID	51008_1.R1011
5'-most EST	uC-zmflm017025d03b1
Method	BLASTX
NCBI GI	g4490325

BLAST score	562
E value	2.0e-57
Match length	149
% identity	72
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274505
Contig ID	51023_1.R1011
5'-most EST	LIB148-035-Q1-E1-C4
Method	BLASTX
NCBI GI	g1871186
BLAST score	537
E value	4.0e-55
Match length	126
% identity	80
NCBI Description	(U90439) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	274506
Contig ID	51028_1.R1011
5'-most EST	rvt700551726.h1
Method	BLASTX
NCBI GI	g3510254
BLAST score	236
E value	9.0e-20
Match length	107
% identity	52
NCBI Description	(AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	274507
Contig ID	51064_1.R1011
5'-most EST	LIB148-035-Q1-E1-G3

Seq. No.	274508
Contig ID	51113_1.R1011
5'-most EST	LIB148-036-Q1-E1-D12
Method	BLASTX
NCBI GI	g3264769
BLAST score	564
E value	4.0e-58
Match length	160
% identity	62
NCBI Description	(AF071894) late embryogenesis-like protein [Prunus armeniaca]

Seq. No.	274509
Contig ID	51121_1.R1011
5'-most EST	LIB3068-057-Q1-K1-B3

Seq. No.	274510
Contig ID	51141_1.R1011
5'-most EST	LIB148-036-Q1-E1-F8

Seq. No.	274511
Contig ID	51144_1.R1011
5'-most EST	LIB3059-020-Q1-K1-G1
Method	BLASTX
NCBI GI	g3047123

BLAST score	442
E value	1.0e-43
Match length	116
% identity	72
NCBI Description	(AF058919) similar to the family of glycosyl hydrolases [Arabidopsis thaliana]

Seq. No.	274512
Contig ID	51160_1.R1011
5'-most EST	LIB148-036-Q1-E1-H6
Method	BLASTX
NCBI GI	g1706110
BLAST score	292
E value	8.0e-49
Match length	198
% identity	55
NCBI Description	NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) >gi_1143713 (U13632) non-green plastid phosphate/triose-phosphate translocator precursor [Brassica oleracea]

Seq. No.	274513
Contig ID	51212_1.R1011
5'-most EST	LIB148-037-Q1-E1-E6

Seq. No.	274514
Contig ID	51232_1.R1011
5'-most EST	LIB3066-024-Q1-K1-D8

Seq. No.	274515
Contig ID	51277_1.R1011
5'-most EST	LIB148-038-Q1-E1-C6
Method	BLASTX
NCBI GI	g3421384
BLAST score	563
E value	9.0e-58
Match length	227
% identity	51
NCBI Description	(AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No.	274516
Contig ID	51302_1.R1011
5'-most EST	LIB148-038-Q1-E1-E7
Method	BLASTX
NCBI GI	g4468993
BLAST score	544
E value	9.0e-56
Match length	166
% identity	64
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	274517
Contig ID	51307_1.R1011
5'-most EST	LIB148-065-Q1-E1-H6
Method	BLASTX
NCBI GI	g2335096

BLAST score	210
E value	3.0e-16
Match length	222
% identity	33
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274518
Contig ID	51336_1.R1011
5'-most EST	LIB148-038-Q1-E1-H6
Method	BLASTX
NCBI GI	g1888357
BLAST score	693
E value	5.0e-73
Match length	170
% identity	75
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	274519
Contig ID	51347_1.R1011
5'-most EST	LIB148-039-Q1-E1-A5
Method	BLASTX
NCBI GI	g3810602
BLAST score	275
E value	2.0e-24
Match length	98
% identity	48
NCBI Description	(AC005398) PR-1-like protein [Arabidopsis thaliana] >gi_4263816_gb_AAD15459_ (AC006067) putative pathogenesis related-1 (PR1) protein [Arabidopsis thaliana]

Seq. No.	274520
Contig ID	51354_1.R1011
5'-most EST	LIB148-039-Q1-E1-C11
Method	BLASTX
NCBI GI	g2760830
BLAST score	471
E value	2.0e-47
Match length	123
% identity	70
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	274521
Contig ID	51390_1.R1011
5'-most EST	uC-zmflmo17265a11b1
Method	BLASTX
NCBI GI	g4468993
BLAST score	591
E value	4.0e-61
Match length	128
% identity	82
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	274522
Contig ID	51437_1.R1011

5'-most EST	LIB3069-055-Q1-K1-F6
Method	BLASTX
NCBI GI	g4512667
BLAST score	1345
E value	1.0e-156
Match length	346
% identity	78
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	274523
Contig ID	51437_2.R1011
5'-most EST	nbm700477373.h1
Method	BLASTX
NCBI GI	g4512667
BLAST score	376
E value	3.0e-55
Match length	159
% identity	69
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	274524
Contig ID	51443_1.R1011
5'-most EST	LIB148-040-Q1-E1-B12

Seq. No.	274525
Contig ID	51475_1.R1011
5'-most EST	LIB148-057-Q1-E1-H8
Method	BLASTX
NCBI GI	g4539389
BLAST score	255
E value	5.0e-22
Match length	99
% identity	47
NCBI Description	(AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No.	274526
Contig ID	51478_1.R1011
5'-most EST	uC-zmroteosinte042c10b1
Method	BLASTX
NCBI GI	g3367593
BLAST score	447
E value	4.0e-44
Match length	166
% identity	48
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi_3805841_emb_CAA21461_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	274527
Contig ID	51488_1.R1011
5'-most EST	LIB3066-007-Q1-K1-H9

Seq. No.	274528
Contig ID	51489_1.R1011
5'-most EST	uC-zmroteosinte086b12b1

Seq. No.	274529

Contig ID	51489_2.R1011
5'-most EST	uC-zmflb73260a06b2
Seq. No.	274530
Contig ID	51496_1.R1011
5'-most EST	LIB148-040-Q1-E1-H1
Seq. No.	274531
Contig ID	51499_1.R1011
5'-most EST	wty700168088.h1
Seq. No.	274532
Contig ID	51517_1.R1011
5'-most EST	LIB148-041-Q1-E1-B2
Method	BLASTX
NCBI GI	g1707940
BLAST score	149
E value	1.0e-09
Match length	79
% identity	48
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_2130036_pir__S61479 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small chain B - barley >gi_1143502_emb_CAA88450_ (Z48563) ADP-glucose pyrophosphorylase small subunit [Hordeum vulgare]
Seq. No.	274533
Contig ID	51533_1.R1011
5'-most EST	LIB3062-002-Q1-K2-C6
Method	BLASTX
NCBI GI	g4587616
BLAST score	280
E value	7.0e-25
Match length	94
% identity	56
NCBI Description	(AC006951) hypothetical protein [Arabidopsis thaliana]
Seq. No.	274534
Contig ID	51540_1.R1011
5'-most EST	fwa700099308.h1
Method	BLASTX
NCBI GI	g2330797
BLAST score	256
E value	8.0e-22
Match length	125
% identity	39
NCBI Description	(Z98601) zinc finger protein [Schizosaccharomyces pombe]
Seq. No.	274535
Contig ID	51540_2.R1011
5'-most EST	LIB3136-014-Q1-K1-G12
Seq. No.	274536
Contig ID	51544_1.R1011

5'-most EST	LIB3066-021-Q1-K1-D1
Seq. No.	274537
Contig ID	51565_1.R1011
5'-most EST	uC-zmflmo17161e05b1
Seq. No.	274538
Contig ID	51577_1.R1011
5'-most EST	LIB148-041-Q1-E1-H12
Seq. No.	274539
Contig ID	51587_1.R1011
5'-most EST	LIB148-042-Q1-E1-A11
Seq. No.	274540
Contig ID	51591_1.R1011
5'-most EST	LIB148-042-Q1-E1-A4
Method	BLASTX
NCBI GI	g2739374
BLAST score	569
E value	1.0e-58
Match length	159
% identity	69
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.	274541
Contig ID	51627_1.R1011
5'-most EST	nbm700473586.h1
Seq. No.	274542
Contig ID	51639_1.R1011
5'-most EST	LIB148-042-Q1-E1-F2
Method	BLASTX
NCBI GI	g4204263
BLAST score	161
E value	6.0e-11
Match length	44
% identity	64
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]
Seq. No.	274543
Contig ID	51657_1.R1011
5'-most EST	LIB148-060-Q1-E1-H6
Method	BLASTX
NCBI GI	g1076288
BLAST score	376
E value	4.0e-36
Match length	101
% identity	72
NCBI Description	amino acid permease AAP3 - Arabidopsis thaliana
Seq. No.	274544
Contig ID	51671_1.R1011
5'-most EST	LIB3066-009-Q1-K1-E5
Method	BLASTX
NCBI GI	g3790587
BLAST score	157

E value	4.0e-10
Match length	107
% identity	44
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	274545
Contig ID	51673_1.R1011
5'-most EST	LIB148-043-Q1-E1-A6
Method	BLASTX
NCBI GI	g4006888
BLAST score	215
E value	2.0e-17
Match length	89
% identity	48
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	274546
Contig ID	51685_1.R1011
5'-most EST	LIB148-043-Q1-E1-B6

Seq. No.	274547
Contig ID	51694_1.R1011
5'-most EST	LIB148-043-Q1-E1-C3
Method	BLASTX
NCBI GI	g4220514
BLAST score	271
E value	6.0e-24
Match length	115
% identity	51
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	274548
Contig ID	51698_1.R1011
5'-most EST	uwc700150879.h1
Method	BLASTX
NCBI GI	g1708421
BLAST score	712
E value	2.0e-75
Match length	147
% identity	99
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG IRL >gi_1205986 (U33318) sulfur starvation induced isoflavone reductase-like IRL [Zea mays]

Seq. No.	274549
Contig ID	51738_1.R1011
5'-most EST	LIB148-064-Q1-E1-H5

Seq. No.	274550
Contig ID	51752_1.R1011
5'-most EST	LIB3066-023-Q1-K1-A7

Seq. No.	274551
Contig ID	51756_1.R1011
5'-most EST	LIB148-043-Q1-E1-H8
Method	BLASTX

NCBI GI	g1653344
BLAST score	198
E value	9.0e-15
Match length	201
% identity	24
NCBI Description	(D90912) hypothetical protein [Synechocystis sp.]

Seq. No.	274552
Contig ID	51793_1.R1011
5'-most EST	LIB1488-047-Q1-E1-C8
Method	BLASTX
NCBI GI	g1354515
BLAST score	204
E value	9.0e-16
Match length	69
% identity	58
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	274553
Contig ID	51793_2.R1011
5'-most EST	LIB3069-041-Q1-K1-A7
Method	BLASTX
NCBI GI	g3549660
BLAST score	504
E value	1.0e-50
Match length	142
% identity	66
NCBI Description	(AL031394) carbonate dehydratase - like protein [Arabidopsis thaliana]

Seq. No.	274554
Contig ID	51846_1.R1011
5'-most EST	uC-zmflb73286e07b1
Method	BLASTX
NCBI GI	g2832683
BLAST score	904
E value	1.0e-97
Match length	230
% identity	72
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	274555
Contig ID	51849_1.R1011
5'-most EST	fxb700397432.h1
Method	BLASTX
NCBI GI	g2853072
BLAST score	661
E value	3.0e-69
Match length	207
% identity	63
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	274556
Contig ID	51856_1.R1011
5'-most EST	LIB1488-047-Q1-E1-A9
Method	BLASTX

NCBI GI	g4417291
BLAST score	224
E value	3.0e-18
Match length	153
% identity	40
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274557
Contig ID	51871_1.R1011
5'-most EST	xsy700213821.h1

Seq. No.	274558
Contig ID	51872_1.R1011
5'-most EST	uC-zmflb73119h05b1

Seq. No.	274559
Contig ID	51872_2.R1011
5'-most EST	LIB3066-053-Q1-K1-C8

Seq. No.	274560
Contig ID	51872_3.R1011
5'-most EST	LIB148-045-Q1-E1-C7

Seq. No.	274561
Contig ID	51886_1.R1011
5'-most EST	LIB148-045-Q1-E1-E11
Method	BLASTX
NCBI GI	g452357
BLAST score	334
E value	7.0e-31
Match length	74
% identity	88
NCBI Description	(Z29591) guanine nucleotide regulatory protein [Vicia faba] >gi_1098294_prf__2115367B small GTP-binding protein [Vicia faba]

Seq. No.	274562
Contig ID	51886_2.R1011
5'-most EST	zla700379905.h1
Method	BLASTX
NCBI GI	g452357
BLAST score	536
E value	5.0e-55
Match length	116
% identity	91
NCBI Description	(Z29591) guanine nucleotide regulatory protein [Vicia faba] >gi_1098294_prf__2115367B small GTP-binding protein [Vicia faba]

Seq. No.	274563
Contig ID	51888_1.R1011
5'-most EST	uC-zmflmo17021a08b1

Seq. No.	274564
Contig ID	51892_1.R1011
5'-most EST	LIB148-045-Q1-E1-E9

Seq. No.	274565
Contig ID	51925_1.R1011
5'-most EST	LIB3062-038-Q1-K1-G1
Method	BLASTX
NCBI GI	g2191152
BLAST score	302
E value	8.0e-43
Match length	192
% identity	45
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	274566
Contig ID	51939_1.R1011
5'-most EST	cyk700051619.f1

Seq. No.	274567
Contig ID	51949_1.R1011
5'-most EST	uC-zmflb73356e05a2

Seq. No.	274568
Contig ID	51956_1.R1011
5'-most EST	LIB148-046-Q1-E1-C9

Seq. No.	274569
Contig ID	51969_1.R1011
5'-most EST	LIB148-046-Q1-E1-E10
Method	BLASTX
NCBI GI	g4539351
BLAST score	260
E value	2.0e-26
Match length	166
% identity	44
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	274570
Contig ID	51982_1.R1011
5'-most EST	gwl700615037.h1

Seq. No.	274571
Contig ID	51987_1.R1011
5'-most EST	xsy700210829.h1

Seq. No.	274572
Contig ID	51988_1.R1011
5'-most EST	LIB3066-008-Q1-K1-C6
Method	BLASTX
NCBI GI	g3068704
BLAST score	556
E value	5.0e-57
Match length	143
% identity	40
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	274573
Contig ID	51990_1.R1011
5'-most EST	LIB148-046-Q1-E1-G2

Method	BLASTX
NCBI GI	g4455309
BLAST score	295
E value	1.0e-26
Match length	99
% identity	65
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274574
Contig ID	51992_1.R1011
5'-most EST	ntr700073332.h1

Seq. No.	274575
Contig ID	51992_2.R1011
5'-most EST	xsy700217366.h1

Seq. No.	274576
Contig ID	52004_1.R1011
5'-most EST	uC-zmflmo17197f11b1

Seq. No.	274577
Contig ID	52027_1.R1011
5'-most EST	LIB148-049-Q1-E1-F3

Seq. No.	274578
Contig ID	52062_2.R1011
5'-most EST	pmx700091985.h1
Method	BLASTX
NCBI GI	g1914685
BLAST score	472
E value	4.0e-47
Match length	177
% identity	56
NCBI Description	(Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No.	274579
Contig ID	52066_1.R1011
5'-most EST	LIB148-047-Q1-E1-F12
Method	BLASTX
NCBI GI	g2792238
BLAST score	416
E value	2.0e-40
Match length	274
% identity	35
NCBI Description	(AF032697) NBS-LRR type resistance protein [Oryza sativa]

Seq. No.	274580
Contig ID	52107_1.R1011
5'-most EST	LIB3060-046-Q1-K1-G8
Method	BLASTX
NCBI GI	g4432867
BLAST score	674
E value	2.0e-70
Match length	327
% identity	42
NCBI Description	(AC006300) putative dnaJ-like protein [Arabidopsis thaliana]

Seq. No. 274581
Contig ID 52137_1.R1011
5'-most EST LIB1488-048-Q1-E1-E12

Seq. No. 274582
Contig ID 52192_1.R1011
5'-most EST LIB1488-049-Q1-E1-B6
Method BLASTX
NCBI GI g4586058
BLAST score 158
E value 2.0e-10
Match length 57
% identity 54
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 274583
Contig ID 52206_1.R1011
5'-most EST LIB3066-026-Q1-K1-D11

Seq. No. 274584
Contig ID 52229_1.R1011
5'-most EST LIB3066-018-Q1-K1-B12
Method BLASTX
NCBI GI g4522009
BLAST score 372
E value 2.0e-35
Match length 200
% identity 41
NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 274585
Contig ID 52234_1.R1011
5'-most EST cat700017726.r1
Method BLASTX
NCBI GI g2459424
BLAST score 144
E value 8.0e-09
Match length 62
% identity 52
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 274586
Contig ID 52250_1.R1011
5'-most EST LIB1488-049-Q1-E1-H3
Method BLASTX
NCBI GI g2384758
BLAST score 303
E value 2.0e-27
Match length 69
% identity 80
NCBI Description (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No. 274587
Contig ID 52284_1.R1011
5'-most EST ymt700223447.h1

Method	BLASTX
NCBI GI	g2462749
BLAST score	464
E value	4.0e-46
Match length	142
% identity	67
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	274588
Contig ID	52296_1.R1011
5'-most EST	LIB148-050-Q1-E1-E11
Method	BLASTX
NCBI GI	g4006878
BLAST score	312
E value	6.0e-37
Match length	178
% identity	46
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	274589
Contig ID	52299_1.R1011
5'-most EST	xsy700208554.h1
Method	BLASTX
NCBI GI	g3329368
BLAST score	746
E value	5.0e-79
Match length	217
% identity	65
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	274590
Contig ID	52316_1.R1011
5'-most EST	rvl700456128.h1
Method	BLASTX
NCBI GI	g1931631
BLAST score	2117
E value	0.0e+00
Match length	411
% identity	99
NCBI Description	(U93561) glutamate dehydrogenase [Zea mays]

Seq. No.	274591
Contig ID	52316_2.R1011
5'-most EST	pmx700081993.h1
Method	BLASTX
NCBI GI	g695411
BLAST score	350
E value	3.0e-33
Match length	69
% identity	100
NCBI Description	(D49475) glutamate dehydrogenase [Zea mays]

Seq. No.	274592
Contig ID	52316_4.R1011
5'-most EST	xsy700217677.h1
Method	BLASTN

NCBI GI	g695410
BLAST score	178
E value	2.0e-95
Match length	249
% identity	93
NCBI Description	Corn mRNA for glutamate dehydrogenase, complete cds

Seq. No.	274593
Contig ID	52335_1.R1011
5'-most EST	uC-zmroB73017e02b1
Method	BLASTX
NCBI GI	g4406777
BLAST score	366
E value	6.0e-35
Match length	98
% identity	68
NCBI Description	(AC006532) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	274594
Contig ID	52367_1.R1011
5'-most EST	uC-zmroteosinte070c07b1
Method	BLASTX
NCBI GI	g3687230
BLAST score	396
E value	2.0e-38
Match length	112
% identity	69
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274595
Contig ID	52367_2.R1011
5'-most EST	xyt700347289.h1
Method	BLASTX
NCBI GI	g3687230
BLAST score	204
E value	7.0e-16
Match length	67
% identity	61
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274596
Contig ID	52373_1.R1011
5'-most EST	LIB3066-045-Q1-K1-C11

Seq. No.	274597
Contig ID	52374_1.R1011
5'-most EST	LIB148-061-Q1-E1-F9
Method	BLASTX
NCBI GI	g2494143
BLAST score	485
E value	6.0e-49
Match length	142
% identity	61
NCBI Description	(AC002329) Mlo-like protein [Arabidopsis thaliana]

Seq. No.	274598

Contig ID	52388_1.R1011
5'-most EST	LIB148-051-Q1-E1-F4

Seq. No.	274599
Contig ID	52389_1.R1011
5'-most EST	LIB3066-016-Q1-K1-F10
Method	BLASTX
NCBI GI	g4587519
BLAST score	572
E value	7.0e-59
Match length	174
% identity	67
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No.	274600
Contig ID	52395_1.R1011
5'-most EST	uC-zmflb73039b10b1
Method	BLASTX
NCBI GI	g4417304
BLAST score	1098
E value	1.0e-120
Match length	327
% identity	58
NCBI Description	(AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]

Seq. No.	274601
Contig ID	52396_1.R1011
5'-most EST	pmx700089290.h1
Method	BLASTX
NCBI GI	g3759177
BLAST score	565
E value	6.0e-58
Match length	152
% identity	74
NCBI Description	(AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807.1_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No.	274602
Contig ID	52396_2.R1011
5'-most EST	LIB3137-002-Q1-K1-G4
Method	BLASTX
NCBI GI	g3759177
BLAST score	421
E value	2.0e-41
Match length	114
% identity	73
NCBI Description	(AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807.1_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No.	274603

Contig ID	52418_1.R1011
5'-most EST	qmh700027869.f1
Method	BLASTX
NCBI GI	g4314401
BLAST score	356
E value	6.0e-34
Match length	117
% identity	61
NCBI Description	(AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	274604
Contig ID	52432_1.R1011
5'-most EST	fwa700097075.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	274605
Contig ID	52436_1.R1011
5'-most EST	LIB148-052-Q1-E1-B8
Method	BLASTX
NCBI GI	g3318613
BLAST score	296
E value	8.0e-27
Match length	113
% identity	54
NCBI Description	(AB016064) mitochondrial phosphate transporter [Zea mays]

Seq. No.	274606
Contig ID	52469_1.R1011
5'-most EST	uC-zmflmo17132d08a1

Seq. No.	274607
Contig ID	52469_2.R1011
5'-most EST	LIB148-052-Q1-E1-E7
Method	BLASTX
NCBI GI	g3395439
BLAST score	231
E value	5.0e-19
Match length	97
% identity	48
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274608
Contig ID	52472_1.R1011
5'-most EST	LIB3066-009-Q1-K1-H8
Method	BLASTX
NCBI GI	g2129774
BLAST score	316
E value	4.0e-29
Match length	86
% identity	69

NCBI Description	xyloglucan endotransglycosylase-related protein XTR4 - Arabidopsis thaliana (fragment) >gi_1244754 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]
Seq. No.	274609
Contig ID	52478_1.R1011
5'-most EST	LIB3066-054-Q1-K1-G7
Seq. No.	274610
Contig ID	52519_1.R1011
5'-most EST	LIB148-053-Q1-E1-B7
Method	BLASTX
NCBI GI	g3063691
BLAST score	282
E value	3.0e-25
Match length	97
% identity	54
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]
Seq. No.	274611
Contig ID	52538_1.R1011
5'-most EST	LIB148-053-Q1-E1-D5
Method	BLASTX
NCBI GI	g4406764
BLAST score	292
E value	2.0e-26
Match length	111
% identity	55
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]
Seq. No.	274612
Contig ID	52539_1.R1011
5'-most EST	wyr700238713.h1
Method	BLASTX
NCBI GI	g3273200
BLAST score	314
E value	3.0e-48
Match length	167
% identity	63
NCBI Description	(AB010917) responce reactor3 [Arabidopsis thaliana] >gi_3894192 (AC005662) response regulator 3 [Arabidopsis thaliana]
Seq. No.	274613
Contig ID	52553_1.R1011
5'-most EST	uC-zmf1b73137b12b1
Seq. No.	274614
Contig ID	52585_1.R1011
5'-most EST	LIB3066-010-Q1-K1-D9
Method	BLASTN
NCBI GI	g454880
BLAST score	51
E value	1.0e-19
Match length	121

% identity	93
NCBI Description	Rice mRNA for WSI724 protein induced by water stress, complete cds

Seq. No.	274615
Contig ID	52607_1.R1011
5'-most EST	ymt700222667.h1

Seq. No.	274616
Contig ID	52607_2.R1011
5'-most EST	uC-zmflmo17176d10b1

Seq. No.	274617
Contig ID	52622_1.R1011
5'-most EST	ymt700218617.h1
Method	BLASTX
NCBI GI	g4454484
BLAST score	312
E value	3.0e-28
Match length	167
% identity	61
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	274618
Contig ID	52670_1.R1011
5'-most EST	LIB1488-057-Q1-E1-A10

Seq. No.	274619
Contig ID	52672_1.R1011
5'-most EST	LIB1488-057-Q1-E1-A2
Method	BLASTN
NCBI GI	g576885
BLAST score	578
E value	0.0e+00
Match length	669
% identity	97
NCBI Description	Zea mays kaurene synthase A (An1) mRNA, complete cds

Seq. No.	274620
Contig ID	52703_1.R1011
5'-most EST	LIB1488-057-Q1-E1-D3

Seq. No.	274621
Contig ID	52730_1.R1011
5'-most EST	LIB1488-057-Q1-E1-G1
Method	BLASTX
NCBI GI	g4200165
BLAST score	759
E value	5.0e-81
Match length	164
% identity	84
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	274622
Contig ID	52744_1.R1011
5'-most EST	LIB3066-049-Q1-K1-E7

Seq. No.	274623
Contig ID	52782_1.R1011
5'-most EST	uC-zmroteosinte074d12b1
Method	BLASTX
NCBI GI	g4091117
BLAST score	832
E value	3.0e-89
Match length	230
% identity	67
NCBI Description	(AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No.	274624
Contig ID	52807_1.R1011
5'-most EST	gwl700617464.h1

Seq. No.	274625
Contig ID	52856_1.R1011
5'-most EST	xmt700264464.h1
Method	BLASTX
NCBI GI	g3043612
BLAST score	166
E value	2.0e-11
Match length	142
% identity	36
NCBI Description	(AB011116) KIAA0544 protein [Homo sapiens]

Seq. No.	274626
Contig ID	52880_1.R1011
5'-most EST	LIB148-059-Q1-E1-D3

Seq. No.	274627
Contig ID	52898_1.R1011
5'-most EST	LIB148-059-Q1-E1-F10
Method	BLASTX
NCBI GI	g2827649
BLAST score	214
E value	1.0e-16
Match length	133
% identity	41
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	274628
Contig ID	52913_1.R1011
5'-most EST	LIB148-059-Q1-E1-G3
Method	BLASTX
NCBI GI	g3850111
BLAST score	390
E value	8.0e-38
Match length	124
% identity	52
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	274629
Contig ID	52945_1.R1011
5'-most EST	LIB148-060-Q1-E1-B4

Method	BLASTX
NCBI GI	g4337196
BLAST score	399
E value	3.0e-41
Match length	124
% identity	73
NCBI Description	(AC006403) putative serine/threonine receptor kinase [Arabidopsis thaliana]

Seq. No.	274630
Contig ID	52959_1.R1011
5'-most EST	LIB148-060-Q1-E1-C6
Method	BLASTX
NCBI GI	g4337196
BLAST score	414
E value	2.0e-40
Match length	206
% identity	49
NCBI Description	(AC006403) putative serine/threonine receptor kinase [Arabidopsis thaliana]

Seq. No.	274631
Contig ID	52992_1.R1011
5'-most EST	LIB148-060-Q1-E1-F5
Method	BLASTX
NCBI GI	g2129774
BLAST score	476
E value	8.0e-48
Match length	157
% identity	57
NCBI Description	xyloglucan endotransglycosylase-related protein XTR4 - Arabidopsis thaliana (fragment) >gi_1244754 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	274632
Contig ID	53046_1.R1011
5'-most EST	LIB148-061-Q1-E1-C9
Method	BLASTX
NCBI GI	g3358091
BLAST score	175
E value	2.0e-12
Match length	115
% identity	41
NCBI Description	(AB015974) glycerol kinase [Pseudomonas tolaasii]

Seq. No.	274633
Contig ID	53051_1.R1011
5'-most EST	LIB3066-023-Q1-K1-B7

Seq. No.	274634
Contig ID	53051_2.R1011
5'-most EST	uC-zmflmo17287a06b1
Method	BLASTX
NCBI GI	g4239974
BLAST score	297
E value	2.0e-26

Match length	193
% identity	18
NCBI Description	(AB017112) mCAC [Mus musculus]

Seq. No.	274635
Contig ID	53101_1.R1011
5'-most EST	uC-zmflmo17278g10b1

Seq. No.	274636
Contig ID	53119_1.R1011
5'-most EST	LIB3066-022-Q1-K1-E11

Seq. No.	274637
Contig ID	53136_1.R1011
5'-most EST	uC-zmflmo17213b09a1

Seq. No.	274638
Contig ID	53148_1.R1011
5'-most EST	hvj700619889.h1
Method	BLASTX
NCBI GI	g2623295
BLAST score	393
E value	1.0e-37
Match length	129
% identity	58
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274639
Contig ID	53148_3.R1011
5'-most EST	uC-zmflb73161e05b2
Method	BLASTX
NCBI GI	g2623295
BLAST score	202
E value	1.0e-15
Match length	57
% identity	61
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274640
Contig ID	53213_1.R1011
5'-most EST	LIB148-064-Q1-E1-A1

Seq. No.	274641
Contig ID	53264_1.R1011
5'-most EST	uwc700153035.h1

Seq. No.	274642
Contig ID	53266_1.R1011
5'-most EST	uC-zmflmo17097h08b1

Seq. No.	274643
Contig ID	53378_1.R1011
5'-most EST	uC-zmflB73009c11b1
Method	BLASTX
NCBI GI	g2959767
BLAST score	903
E value	1.0e-97

Match length	219
% identity	80
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	274644
Contig ID	53378_2.R1011
5'-most EST	uC-zmromo17113b05a1

Seq. No.	274645
Contig ID	53380_1.R1011
5'-most EST	LIB3069-050-Q1-K1-H12

Seq. No.	274646
Contig ID	53380_2.R1011
5'-most EST	pmx700089223.h1

Seq. No.	274647
Contig ID	53480_1.R1011
5'-most EST	uC-zmflmo17299b01b1

Seq. No.	274648
Contig ID	53482_1.R1011
5'-most EST	uC-zmflmo17156d12b1
Method	BLASTX
NCBI GI	g2262105
BLAST score	725
E value	1.0e-76
Match length	271
% identity	48
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	274649
Contig ID	53496_1.R1011
5'-most EST	clt700041925.f1
Method	BLASTX
NCBI GI	g4508073
BLAST score	299
E value	5.0e-27
Match length	108
% identity	47
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	274650
Contig ID	53499_1.R1011
5'-most EST	LIB3136-054-Q1-K1-B2

Seq. No.	274651
Contig ID	53500_1.R1011
5'-most EST	LIB3060-036-Q1-K1-A5
Method	BLASTX
NCBI GI	g2695929
BLAST score	166
E value	2.0e-11
Match length	70
% identity	47

NCBI Description	(AJ222778) putative thiol protease [Hordeum vulgare]
Seq. No.	274652
Contig ID	53500_2.R1011
5'-most EST	uC-zmroteosinte104d07b2
Method	BLASTX
NCBI GI	g3377950
BLAST score	368
E value	5.0e-35
Match length	119
% identity	56
NCBI Description	(AJ009830) cysteine proteinase precursor, AN11 [Ananas comosus]
Seq. No.	274653
Contig ID	53503_1.R1011
5'-most EST	LIB189-001-Q1-E1-C7
Method	BLASTX
NCBI GI	g1174862
BLAST score	240
E value	8.0e-20
Match length	230
% identity	28
NCBI Description	PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) >gi_984225_emb_CAA90805_ (Z54096) unknown [Schizosaccharomyces pombe]
Seq. No.	274654
Contig ID	53513_1.R1011
5'-most EST	ceu700427194.h1
Method	BLASTX
NCBI GI	g1169544
BLAST score	514
E value	2.0e-52
Match length	145
% identity	71
NCBI Description	ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) ERD1 protein [Arabidopsis thaliana]
Seq. No.	274655
Contig ID	53518_1.R1011
5'-most EST	LIB189-029-Q1-E1-F11
Method	BLASTX
NCBI GI	g2130096
BLAST score	284
E value	7.0e-34
Match length	108
% identity	70
NCBI Description	cytochrome P450tyr - sorghum >gi_984543 (U32624) cytochrome P-450 [Sorghum bicolor]
Seq. No.	274656
Contig ID	53525_1.R1011
5'-most EST	fwa700097743.h1

Seq. No.	274657
Contig ID	53536_1.R1011
5'-most EST	uwc700151591.h1
Method	BLASTX
NCBI GI	g3582335
BLAST score	2086
E value	0.0e+00
Match length	422
% identity	91
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	274658
Contig ID	53536_2.R1011
5'-most EST	yyf700351747.h1

Seq. No.	274659
Contig ID	53538_1.R1011
5'-most EST	LIB189-001-Q1-E1-G11

Seq. No.	274660
Contig ID	53541_1.R1011
5'-most EST	dyk700105444.h1
Method	BLASTX
NCBI GI	g4454050
BLAST score	283
E value	7.0e-25
Match length	118
% identity	54
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	274661
Contig ID	53541_2.R1011
5'-most EST	uC-zmflmo17031b10b1
Method	BLASTX
NCBI GI	g4454050
BLAST score	232
E value	6.0e-19
Match length	57
% identity	70
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	274662
Contig ID	53543_1.R1011
5'-most EST	LIB3068-027-Q1-K1-A2
Method	BLASTX
NCBI GI	g170507
BLAST score	156
E value	4.0e-10
Match length	95
% identity	44
NCBI Description	(M59251) ORF [Lycopersicon esculentum] >gi_1172167 (U44386) heat shock protein [Solanum lycopersicum]

Seq. No.	274663
Contig ID	53545_1.R1011
5'-most EST	LIB189-001-Q1-E1-G7

Method	BLASTX
NCBI GI	g1771160
BLAST score	185
E value	1.0e-13
Match length	80
% identity	49
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	274664
Contig ID	53548_1.R1011
5'-most EST	uC-zmflmo17219f01b1

Seq. No.	274665
Contig ID	53553_1.R1011
5'-most EST	LIB189-001-Q1-E1-H3
Method	BLASTX
NCBI GI	g2792295
BLAST score	392
E value	7.0e-38
Match length	161
% identity	46
NCBI Description	(AF039182) unknown [Fragaria x ananassa]

Seq. No.	274666
Contig ID	53558_1.R1011
5'-most EST	LIB83-008-Q1-E1-E6
Method	BLASTX
NCBI GI	g2244765
BLAST score	172
E value	9.0e-12
Match length	71
% identity	48
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274667
Contig ID	53567_1.R1011
5'-most EST	fwa70098737.h1
Method	BLASTX
NCBI GI	g2911058
BLAST score	318
E value	4.0e-29
Match length	107
% identity	53
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	274668
Contig ID	53571_1.R1011
5'-most EST	xsy70207894.h1
Method	BLASTX
NCBI GI	g1854378
BLAST score	776
E value	6.0e-83
Match length	177
% identity	80
NCBI Description	(AB001338) Sucrose-Phosphate Synthase [Saccharum

officinarum]

Seq. No. 274669
Contig ID 53573_1.R1011
5'-most EST LIB189-002-Q1-E1-B6

Seq. No. 274670
Contig ID 53583_1.R1011
5'-most EST LIB189-002-Q1-E1-C6

Seq. No. 274671
Contig ID 53593_1.R1011
5'-most EST LIB189-002-Q1-E1-D5
Method BLASTX
NCBI GI g3395439
BLAST score 430
E value 3.0e-42
Match length 197
% identity 47
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 274672
Contig ID 53595_1.R1011
5'-most EST LIB189-002-Q1-E1-D7

Seq. No. 274673
Contig ID 53603_1.R1011
5'-most EST LIB189-002-Q1-E1-E4
Method BLASTX
NCBI GI g2462839
BLAST score 824
E value 3.0e-88
Match length 206
% identity 80
NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]

Seq. No. 274674
Contig ID 53605_1.R1011
5'-most EST LIB3137-059-Q1-K1-D6

Seq. No. 274675
Contig ID 53625_1.R1011
5'-most EST LIB3069-005-Q1-K1-G3
Method BLASTX
NCBI GI g1363325
BLAST score 233
E value 4.0e-19
Match length 124
% identity 42
NCBI Description RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No. 274676
Contig ID 53627_1.R1011
5'-most EST LIB189-002-Q1-E1-G5
Method BLASTX
NCBI GI g4468798

BLAST score	432
E value	1.0e-42
Match length	143
% identity	58
NCBI Description	(AJ010440) GST7 protein [Zea mays]

Seq. No.	274677
Contig ID	53628_1.R1011
5'-most EST	LIB189-002-Q1-E1-G6

Seq. No.	274678
Contig ID	53639_2.R1011
5'-most EST	pmx700084850.h1

Seq. No.	274679
Contig ID	53651_1.R1011
5'-most EST	cyk700047363.f1
Method	BLASTX
NCBI GI	g1167955
BLAST score	180
E value	5.0e-13
Match length	107
% identity	39
NCBI Description	(U43497) putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein [Hordeum vulgare]

Seq. No.	274680
Contig ID	53656_1.R1011
5'-most EST	LIB189-003-Q1-E1-B4
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	274681
Contig ID	53660_1.R1011
5'-most EST	LIB189-003-Q1-E1-C1
Method	BLASTX
NCBI GI	g2801699
BLAST score	142
E value	1.0e-08
Match length	118
% identity	31
NCBI Description	(AF042378) spindle pole body protein spc98 homolog GCP3 [Homo sapiens]

Seq. No.	274682
Contig ID	53665_1.R1011
5'-most EST	ntr700074184.h1
Method	BLASTX
NCBI GI	g4572677
BLAST score	203
E value	8.0e-16

Match length	130
% identity	40
NCBI Description	(AC006954) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274683
Contig ID	53668_1.R1011
5'-most EST	LIB189-003-Q1-E1-C6
Method	BLASTX
NCBI GI	g2459440
BLAST score	384
E value	6.0e-37
Match length	169
% identity	46
NCBI Description	(AC002332) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	274684
Contig ID	53669_1.R1011
5'-most EST	uC-zmroteosinte038a06b1
Method	BLASTX
NCBI GI	g3063471
BLAST score	402
E value	8.0e-39
Match length	137
% identity	57
NCBI Description	(AC003981) F22O13.33 [Arabidopsis thaliana]

Seq. No.	274685
Contig ID	53674_1.R1011
5'-most EST	xsy700209257.h1
Method	BLASTX
NCBI GI	g3702327
BLAST score	162
E value	7.0e-11
Match length	53
% identity	51
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	274686
Contig ID	53683_1.R1011
5'-most EST	LIB189-003-Q1-E1-E1

Seq. No.	274687
Contig ID	53684_1.R1011
5'-most EST	uC-zmflb73242c02b1
Method	BLASTX
NCBI GI	g2252866
BLAST score	214
E value	6.0e-17
Match length	79
% identity	59
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	274688
Contig ID	53686_1.R1011
5'-most EST	ntr700072447.h2
Method	BLASTX

NCBI GI	g1071913
BLAST score	1015
E value	1.0e-110
Match length	253
% identity	75
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	274689
Contig ID	53687_1.R1011
5'-most EST	LIB189-003-Q1-E1-E2
Method	BLASTX
NCBI GI	g3426048
BLAST score	777
E value	7.0e-83
Match length	221
% identity	69
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	274690
Contig ID	53688_1.R1011
5'-most EST	xjt700094468.h1
Method	BLASTX
NCBI GI	g4587517
BLAST score	515
E value	3.0e-58
Match length	230
% identity	49
NCBI Description	(AC007060) T5I8.6 [Arabidopsis thaliana]

Seq. No.	274691
Contig ID	53695_1.R1011
5'-most EST	dyk700106515.h1

Seq. No.	274692
Contig ID	53701_1.R1011
5'-most EST	fwa700097893.h1
Method	BLASTX
NCBI GI	g1652327
BLAST score	253
E value	2.0e-21
Match length	142
% identity	44
NCBI Description	(D90904) hypothetical protein [Synechocystis sp.]

Seq. No.	274693
Contig ID	53710_1.R1011
5'-most EST	LIB189-011-Q1-E1-B9
Method	BLASTX
NCBI GI	g3024871
BLAST score	500
E value	2.0e-50
Match length	185
% identity	52
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005

>gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	274694
Contig ID	53716_1.R1011
5'-most EST	LIB84-014-Q1-E1-G6
Method	BLASTX
NCBI GI	g2129698
BLAST score	917
E value	6.0e-99
Match length	280
% identity	62
NCBI Description	protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana >gi_1054633_emb_CAA63387_ (X92728) protein kinase [Arabidopsis thaliana]

Seq. No.	274695
Contig ID	53719_1.R1011
5'-most EST	vux700161205.h1
Method	BLASTX
NCBI GI	g3059129
BLAST score	369
E value	4.0e-35
Match length	123
% identity	53
NCBI Description	(AJ000477) cytochrome P450 [Helianthus tuberosus]

Seq. No.	274696
Contig ID	53719_2.R1011
5'-most EST	tfd700571051.h1
Method	BLASTX
NCBI GI	g3059129
BLAST score	191
E value	8.0e-15
Match length	70
% identity	51
NCBI Description	(AJ000477) cytochrome P450 [Helianthus tuberosus]

Seq. No.	274697
Contig ID	53719_3.R1011
5'-most EST	uwc700152777.h1

Seq. No.	274698
Contig ID	53729_1.R1011
5'-most EST	LIB3136-033-Q1-K1-G2

Seq. No.	274699
Contig ID	53734_1.R1011
5'-most EST	LIB189-004-Q1-E1-A9

Seq. No.	274700
Contig ID	53742_1.R1011
5'-most EST	qmh700029955.f1

Seq. No.	274701
Contig ID	53744_1.R1011
5'-most EST	uC-zmf1b73125g09b2

Seq. No.	274702
Contig ID	53751_1.R1011
5'-most EST	xsy700217506.h1
Method	BLASTX
NCBI GI	g2252634
BLAST score	341
E value	5.0e-32
Match length	125
% identity	46
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274703
Contig ID	53755_1.R1011
5'-most EST	LIB189-004-Q1-E1-D1
Method	BLASTX
NCBI GI	g2582822
BLAST score	209
E value	6.0e-21
Match length	102
% identity	61
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	274704
Contig ID	53763_1.R1011
5'-most EST	rvt700552433.h1
Method	BLASTX
NCBI GI	g4204276
BLAST score	832
E value	3.0e-89
Match length	275
% identity	62
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	274705
Contig ID	53772_1.R1011
5'-most EST	ntr700073945.h1
Method	BLASTX
NCBI GI	g4105794
BLAST score	250
E value	2.0e-21
Match length	87
% identity	55
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	274706
Contig ID	53776_1.R1011
5'-most EST	LIB189-004-Q1-E1-F1

Seq. No.	274707
Contig ID	53779_1.R1011
5'-most EST	xmt700264144.h1
Method	BLASTX
NCBI GI	g3021357
BLAST score	968
E value	1.0e-105

Match length	222
% identity	82
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	274708
Contig ID	53784_1.R1011
5'-most EST	gct701179537.h1

Seq. No.	274709
Contig ID	53786_1.R1011
5'-most EST	uC-zmflb73200g10b1
Method	BLASTX
NCBI GI	g120657
BLAST score	1113
E value	1.0e-122
Match length	218
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66024_pir__DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	274710
Contig ID	53792_1.R1011
5'-most EST	LIB189-017-Q1-E1-G2

Seq. No.	274711
Contig ID	53794_1.R1011
5'-most EST	qmh700027039.f1
Method	BLASTX
NCBI GI	g2944180
BLAST score	311
E value	2.0e-28
Match length	93
% identity	62
NCBI Description	(AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	274712
Contig ID	53798_1.R1011
5'-most EST	LIB189-004-Q1-E1-H12
Method	BLASTX
NCBI GI	g294845
BLAST score	149
E value	2.0e-09
Match length	38
% identity	61
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	274713
Contig ID	53801_1.R1011
5'-most EST	uC-zmflmo17044a05b1

Method	BLASTX
NCBI GI	g4455338
BLAST score	904
E value	3.0e-97
Match length	303
% identity	60
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	274714
Contig ID	53801_2.R1011
5'-most EST	LIB189-004-Q1-E1-H5
Method	BLASTX
NCBI GI	g4455338
BLAST score	336
E value	8.0e-57
Match length	209
% identity	57
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	274715
Contig ID	53801_3.R1011
5'-most EST	uC-zmf1mo17028g07a1

Seq. No.	274716
Contig ID	53813_1.R1011
5'-most EST	qmh700029093.f1

Seq. No.	274717
Contig ID	53819_1.R1011
5'-most EST	LIB189-005-Q1-E1-B5

Seq. No.	274718
Contig ID	53823_1.R1011
5'-most EST	LIB189-005-Q1-E1-C1

Seq. No.	274719
Contig ID	53824_1.R1011
5'-most EST	fwa700097371.h1
Method	BLASTX
NCBI GI	g3668091
BLAST score	761
E value	8.0e-81
Match length	237
% identity	18
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274720
Contig ID	53834_1.R1011
5'-most EST	uer700579592.h1
Method	BLASTX
NCBI GI	g3953471
BLAST score	777
E value	1.0e-82
Match length	254
% identity	53
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	274721
Contig ID	53839_1.R1011
5'-most EST	LIB189-005-Q1-E1-D4
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	274722
Contig ID	53853_1.R1011
5'-most EST	LIB189-005-Q1-E1-E8
Method	BLASTX
NCBI GI	g4539525
BLAST score	219
E value	9.0e-18
Match length	142
% identity	36
NCBI Description	(AJ012370) NAALADase II protein [Homo sapiens]

Seq. No.	274723
Contig ID	53856_1.R1011
5'-most EST	LIB189-005-Q1-E1-F10
Method	BLASTX
NCBI GI	g1653513
BLAST score	171
E value	5.0e-12
Match length	131
% identity	34
NCBI Description	(D90914) hypothetical protein [Synechocystis sp.]

Seq. No.	274724
Contig ID	53865_1.R1011
5'-most EST	tzu700203071.h1

Seq. No.	274725
Contig ID	53872_1.R1011
5'-most EST	uC-zmf1b73135b02b2
Method	BLASTX
NCBI GI	g4587615
BLAST score	882
E value	7.0e-95
Match length	353
% identity	50
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	274726
Contig ID	53876_1.R1011
5'-most EST	ceu700429727.h1
Method	BLASTN
NCBI GI	g4416300
BLAST score	97
E value	5.0e-47
Match length	214

% identity	43
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	274727
Contig ID	53881_1.R1011
5'-most EST	uC-zmrob73033g05b1
Method	BLASTX
NCBI GI	g3059131
BLAST score	260
E value	7.0e-41
Match length	255
% identity	38
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	274728
Contig ID	53888_1.R1011
5'-most EST	LIB189-006-Q1-E1-A10

Seq. No.	274729
Contig ID	53903_1.R1011
5'-most EST	pmx700085033.h1

Seq. No.	274730
Contig ID	53912_1.R1011
5'-most EST	pmx700085624.h1

Seq. No.	274731
Contig ID	53914_1.R1011
5'-most EST	uC-zmflmo17079f10b1

Seq. No.	274732
Contig ID	53917_1.R1011
5'-most EST	LIB3137-057-Q1-K1-A4

Seq. No.	274733
Contig ID	53917_2.R1011
5'-most EST	uC-zmrob73079b11b1

Seq. No.	274734
Contig ID	53920_1.R1011
5'-most EST	fwa700097466.h1
Method	BLASTX
NCBI GI	g1653103
BLAST score	159
E value	3.0e-10
Match length	187
% identity	26
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	274735
Contig ID	53925_1.R1011
5'-most EST	LIB189-006-Q1-E1-D7

Seq. No.	274736
Contig ID	53937_1.R1011
5'-most EST	uC-zmroteosinte098g01b2

Method	BLASTX
NCBI GI	g4586251
BLAST score	252
E value	3.0e-21
Match length	224
% identity	31
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	274737
Contig ID	53945_1.R1011
5'-most EST	ymt70̄221369.h1
Method	BLASTX
NCBI GI	g3885334
BLAST score	761
E value	4.0e-81
Match length	202
% identity	72
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	274738
Contig ID	53951_1.R1011
5'-most EST	LIB18̄9-006-Q1-E1-G11
Method	BLASTX
NCBI GI	g3822036
BLAST score	337
E value	2.0e-31
Match length	137
% identity	53
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	274739
Contig ID	53953_1.R1011
5'-most EST	uC-zmroteosinte022c09b1
Method	BLASTX
NCBI GI	g4336747
BLAST score	1213
E value	1.0e-158
Match length	309
% identity	94
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No.	274740
Contig ID	53958_1.R1011
5'-most EST	LIB18̄9-030-Q1-E1-E4
Method	BLASTX
NCBI GI	g602292
BLAST score	674
E value	2.0e-70
Match length	271
% identity	49
NCBI Description	(U17987) RCH2 protein [Brassica napus]

Seq. No.	274741
Contig ID	53959_1.R1011
5'-most EST	LIB18̄9-006-Q1-E1-G9

Seq. No.	274742
Contig ID	53966_1.R1011
5'-most EST	uC-zmroB73028g06b1

Seq. No.	274743
Contig ID	53968_1.R1011
5'-most EST	dyk700105536.h1

Seq. No.	274744
Contig ID	53970_1.R1011
5'-most EST	LIB189-007-Q1-E1-A11

Seq. No.	274745
Contig ID	53971_1.R1011
5'-most EST	LIB189-007-Q1-E1-A12
Method	BLASTX
NCBI GI	g3912918
BLAST score	674
E value	8.0e-71
Match length	145
% identity	84
NCBI Description	(AF001308) putative curlyleaf-like 1 homeotic protein [Arabidopsis thaliana]

Seq. No.	274746
Contig ID	53980_1.R1011
5'-most EST	uC-zmflb73067a05b1
Method	BLASTX
NCBI GI	g347853
BLAST score	933
E value	1.0e-101
Match length	193
% identity	95
NCBI Description	(L21752) glucose transporter [Saccharum hybrid cultivar H65-7052]

Seq. No.	274747
Contig ID	53989_1.R1011
5'-most EST	uC-zmflmo17259e02b1
Method	BLASTX
NCBI GI	g3249071
BLAST score	243
E value	2.0e-20
Match length	88
% identity	48
NCBI Description	(AC004473) Contains similarity to protein-tyrosine phosphatase 2 gb_L15420 from Dictyostelium discoideum. EST gb_N38718 comes from this g [Arabidopsis thaliana]

Seq. No.	274748
Contig ID	54002_1.R1011
5'-most EST	LIB189-007-Q1-E1-D11

Seq. No.	274749
Contig ID	54003_1.R1011
5'-most EST	LIB189-007-Q1-E1-D12
Method	BLASTX

NCBI GI	g1703200
BLAST score	218
E value	1.0e-17
Match length	49
% identity	84
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	274750
Contig ID	54005_1.R1011
5'-most EST	LIB189-007-Q1-E1-D4

Seq. No.	274751
Contig ID	54008_1.R1011
5'-most EST	LIB189-007-Q1-E1-D7

Seq. No.	274752
Contig ID	54013_1.R1011
5'-most EST	LIB3069-054-Q1-K1-C8
Method	BLASTX
NCBI GI	g3281846
BLAST score	476
E value	4.0e-47
Match length	376
% identity	35
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	274753
Contig ID	54013_2.R1011
5'-most EST	wty700164032.h1
Method	BLASTX
NCBI GI	g3281846
BLAST score	182
E value	4.0e-13
Match length	139
% identity	41
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	274754
Contig ID	54022_1.R1011
5'-most EST	LIB189-007-Q1-E1-F1
Method	BLASTX
NCBI GI	g531829
BLAST score	189
E value	2.0e-14
Match length	79
% identity	51
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No.	274755
Contig ID	54026_1.R1011
5'-most EST	LIB83-007-Q1-E1-G10

Seq. No.	274756
Contig ID	54029_1.R1011
5'-most EST	fdz701163985.h1
Method	BLASTX
NCBI GI	g3861294
BLAST score	152
E value	2.0e-09
Match length	126
% identity	29
NCBI Description	(AJ235273) GUANYLATE KINASE (gmk) [Rickettsia prowazekii]

Seq. No.	274757
Contig ID	54037_1.R1011
5'-most EST	hvj700619423.h1

Seq. No.	274758
Contig ID	54046_1.R1011
5'-most EST	LIB189-007-Q1-E1-H2

Seq. No.	274759
Contig ID	54048_1.R1011
5'-most EST	uC-zmrob73019h11b1

Seq. No.	274760
Contig ID	54050_1.R1011
5'-most EST	LIB189-007-Q1-E1-H7
Method	BLASTX
NCBI GI	g4585706
BLAST score	324
E value	2.0e-44
Match length	93
% identity	79
NCBI Description	(AJ238116) putative phospholipase A2 [Oryza sativa]

Seq. No.	274761
Contig ID	54053_1.R1011
5'-most EST	LIB189-008-Q1-E1-A10
Method	BLASTX
NCBI GI	g2388577
BLAST score	280
E value	5.0e-25
Match length	111
% identity	49
NCBI Description	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No.	274762
Contig ID	54054_1.R1011
5'-most EST	hbs701183032.h1

Seq. No.	274763
Contig ID	54057_1.R1011
5'-most EST	LIB3069-036-Q1-K1-B2
Method	BLASTX
NCBI GI	g114653
BLAST score	205
E value	1.0e-15

Match length	43
% identity	100
NCBI Description	ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III) >gi_67896_pir__LWSPA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - spinach chloroplast >gi_67897_pir__LWRZA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - rice chloroplast >gi_279576_pir__LWZMC H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - maize chloroplast >gi_11976_emb_CAA33991_ (X15901) ATPase III subunit [Oryza sativa] >gi_12251_emb_CAA27402_ (X03775) CFo subunit III (atpH) (aa 1-81) proteolipid [Spinacia oleracea] >gi_12258_emb_CAA29345_ (X05916) atpH protein (cf0III subunit) (AA 1-81) [Spinacia oleracea] >gi_12407_emb_CAA28875_ (X05254) CF(0) subunit III (AA 1-81) [Zea mays] >gi_342580 (M27557) phosphorylation coupling factor alpha subunit (atpA) [Zea mays] >gi_343673 (J01458) ATP synthase proton-translocating subunit [Triticum aestivum] >gi_902217_emb_CAA60281_ (X86563) ATPase III subunit [Zea mays] >gi_223270_prf__0702201A synthase proteolipid subunit,ATP [Spinacia sp.] >gi_226694_prf__1603356V ATPase III [Oryza sativa]

Seq. No.	274764
Contig ID	54062_1.R1011
5'-most EST	hbs70l183919.h1
Method	BLASTX
NCBI GI	g1532175
BLAST score	473
E value	4.0e-47
Match length	105
% identity	80
NCBI Description	(U63815) similar to protein disulfide isomerase [Arabidopsis thaliana]

Seq. No.	274765
Contig ID	54063_1.R1011
5'-most EST	uC-zmroteosinte012a02b1
Method	BLASTX
NCBI GI	g1504008
BLAST score	442
E value	9.0e-44
Match length	180
% identity	51
NCBI Description	(D86967) Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [Homo sapiens]

Seq. No.	274766
Contig ID	54067_1.R1011
5'-most EST	LIB189-008-Q1-E1-B3
Method	BLASTX
NCBI GI	g4335763
BLAST score	344
E value	4.0e-32
Match length	129
% identity	53

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 274767
Contig ID 54069_1.R1011
5'-most EST LIB189-008-Q1-E1-B6

Seq. No. 274768
Contig ID 54070_1.R1011
5'-most EST LIB3059-059-Q1-K1-B3

Seq. No. 274769
Contig ID 54074_1.R1011
5'-most EST clt700042928.f1
Method BLASTX
NCBI GI g1001311
BLAST score 191
E value 1.0e-16
Match length 156
% identity 34
NCBI Description (D64006) hypothetical protein [Synechocystis sp.]

Seq. No. 274770
Contig ID 54089_1.R1011
5'-most EST uC-zmf1b73274b02b1
Method BLASTX
NCBI GI g4160292
BLAST score 1026
E value 1.0e-112
Match length 314
% identity 63
NCBI Description (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]

Seq. No. 274771
Contig ID 54095_1.R1011
5'-most EST LIB189-008-Q1-E1-E2
Method BLASTX
NCBI GI g3983103
BLAST score 252
E value 2.0e-21
Match length 161
% identity 36
NCBI Description (AF097441) phenylalanine-tRNA synthetase [Homo sapiens]

Seq. No. 274772
Contig ID 54095_2.R1011
5'-most EST uC-zmrob73037b01a1

Seq. No. 274773
Contig ID 54097_1.R1011
5'-most EST wen700334139.h1
Method BLASTX
NCBI GI g4538935
BLAST score 246
E value 2.0e-20
Match length 76
% identity 55
NCBI Description (AL049483) putative protein [Arabidopsis thaliana]

Seq. No.	274774
Contig ID	54097_3.R1011
5'-most EST	LIB3137-004-Q1-K1-H8
Method	BLASTX
NCBI GI	g4538935
BLAST score	219
E value	1.0e-17
Match length	66
% identity	56
NCBI Description	(AL049483) putative protein [Arabidopsis thaliana]

Seq. No.	274775
Contig ID	54103_1.R1011
5'-most EST	fwa70097255.h1

Seq. No.	274776
Contig ID	54131_1.R1011
5'-most EST	cyk70050417.f1
Method	BLASTX
NCBI GI	g629669
BLAST score	252
E value	1.0e-21
Match length	104
% identity	51
NCBI Description	hypothetical protein - tomato

Seq. No.	274777
Contig ID	54132_1.R1011
5'-most EST	LIB189-009-Q1-E1-C5
Method	BLASTX
NCBI GI	g2118675
BLAST score	282
E value	4.0e-25
Match length	111
% identity	11
NCBI Description	vitellogenin receptor - African clawed frog >gi_2366773_dbj_BAA22145_ (AB006906) vitellogenin receptor [Xenopus laevis]

Seq. No.	274778
Contig ID	54136_1.R1011
5'-most EST	xjt70094943.h1
Method	BLASTX
NCBI GI	g4455367
BLAST score	415
E value	2.0e-40
Match length	138
% identity	62
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	274779
Contig ID	54142_1.R1011
5'-most EST	xsy70210471.h1

Seq. No.	274780
Contig ID	54150_1.R1011

5'-most EST	LIB189-009-Q1-E1-B6
Seq. No.	274781
Contig ID	54169_1.R1011
5'-most EST	uC-zmf1B73021d12b1
Method	BLASTX
NCBI GI	g2129730
BLAST score	220
E value	2.0e-29
Match length	102
% identity	66
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana (fragment)
Seq. No.	274782
Contig ID	54177_1.R1011
5'-most EST	uC-zmflb73154e12a1
Seq. No.	274783
Contig ID	54186_1.R1011
5'-most EST	xmt700264376.h1
Method	BLASTX
NCBI GI	g2160182
BLAST score	233
E value	5.0e-19
Match length	155
% identity	40
NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]
Seq. No.	274784
Contig ID	54186_2.R1011
5'-most EST	uC-zmroteosinte068d09b1
Method	BLASTX
NCBI GI	g2160182
BLAST score	145
E value	5.0e-09
Match length	57
% identity	51
NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]
Seq. No.	274785
Contig ID	54186_3.R1011
5'-most EST	hvj700624385.h1
Seq. No.	274786
Contig ID	54188_1.R1011
5'-most EST	uC-zmflb73210b11a1
Seq. No.	274787
Contig ID	54188_2.R1011
5'-most EST	uC-zmflb73074h05a1
Seq. No.	274788
Contig ID	54197_1.R1011
5'-most EST	wen700336954.h1

Method	BLASTX
NCBI GI	g2213626
BLAST score	353
E value	6.0e-33
Match length	212
% identity	36
NCBI Description	(AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No.	274789
Contig ID	54208_1.R1011
5'-most EST	LIB189-009-Q1-E1-H10

Seq. No.	274790
Contig ID	54216_1.R1011
5'-most EST	uC-zmroteosinte117b12b2
Method	BLASTX
NCBI GI	g3290004
BLAST score	487
E value	2.0e-52
Match length	147
% identity	73
NCBI Description	(U82200) pathogenesis related protein-1 [Zea mays]

Seq. No.	274791
Contig ID	54216_2.R1011
5'-most EST	LIB189-025-Q1-E1-C8
Method	BLASTX
NCBI GI	g3290004
BLAST score	444
E value	5.0e-44
Match length	110
% identity	75
NCBI Description	(U82200) pathogenesis related protein-1 [Zea mays]

Seq. No.	274792
Contig ID	54222_1.R1011
5'-most EST	uC-zmflb73015h10b1

Seq. No.	274793
Contig ID	54229_1.R1011
5'-most EST	LIB189-010-Q1-E1-B1
Method	BLASTX
NCBI GI	g3123286
BLAST score	327
E value	3.0e-30
Match length	148
% identity	43
NCBI Description	LEUCYL-TRNA SYNTHETASE (LEUCINE--TRNA LIGASE) (LEURS) >gi_2293181 (AF008220) leucine tRNA synthetase [Bacillus subtilis] >gi_2635516_emb_CAB15010_ (Z99119) leucyl-tRNA synthetase [Bacillus subtilis]

Seq. No.	274794
Contig ID	54230_1.R1011
5'-most EST	ntr700075363.h1

Seq. No.	274795

Contig ID	54237_1.R1011
5'-most EST	LIB189-010-Q1-E1-B6
Seq. No.	274796
Contig ID	54239_1.R1011
5'-most EST	ymt700223873.h1
Seq. No.	274797
Contig ID	54245_1.R1011
5'-most EST	uC-zmromo17113d10a1
Seq. No.	274798
Contig ID	54248_1.R1011
5'-most EST	LIB189-010-Q1-E1-C6
Method	BLASTX
NCBI GI	g417546
BLAST score	671
E value	9.0e-71
Match length	140
% identity	90
NCBI Description	PHOTOSYSTEM II D2 PROTEIN (PHOTOSYSTEM Q(A) PROTEIN) >gi_82444_pir__A31183 photosystem II protein D2 - barley chloroplast >gi_552472 (M38290) membrane polypeptide D2 [Hordeum vulgare]
Seq. No.	274799
Contig ID	54258_1.R1011
5'-most EST	LIB189-010-Q1-E1-D5
Method	BLASTX
NCBI GI	g3738302
BLAST score	800
E value	1.0e-85
Match length	226
% identity	68
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]
Seq. No.	274800
Contig ID	54262_1.R1011
5'-most EST	LIB189-010-Q1-E1-E1
Seq. No.	274801
Contig ID	54271_1.R1011
5'-most EST	LIB189-010-Q1-E1-F10
Seq. No.	274802
Contig ID	54276_1.R1011
5'-most EST	uC-zmflmo17158d12b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	274803
Contig ID	54290_1.R1011
5'-most EST	dyk700102561.h1

Seq. No.	274804
Contig ID	54295_1.R1011
5'-most EST	uC-zmflb73283c12b2
Method	BLASTX
NCBI GI	g1353135
BLAST score	227
E value	1.0e-18
Match length	105
% identity	47
NCBI Description	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR >gi_3874887_emb_CAA88100_ (Z48045) similar to serine/threonine kinase; cDNA EST EMBL:D26974 comes from this gene; cDNA EST EMBL:D26978 comes from this gene; cDNA EST EMBL:D26977 comes from this gene; cDNA EST EMBL:D26976 comes from this gene; cDNA EST E

Seq. No.	274805
Contig ID	54297_1.R1011
5'-most EST	wyr700237741.h1

Seq. No.	274806
Contig ID	54297_2.R1011
5'-most EST	LIB3137-028-Q1-K1-E4
Method	BLASTX
NCBI GI	g2739046
BLAST score	168
E value	3.0e-11
Match length	110
% identity	31
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	274807
Contig ID	54297_3.R1011
5'-most EST	LIB83-001-Q1-E1-A4

Seq. No.	274808
Contig ID	54301_1.R1011
5'-most EST	xdb700339369.h1
Method	BLASTN
NCBI GI	g2198852
BLAST score	41
E value	2.0e-13
Match length	77
% identity	88
NCBI Description	Zea mays cystathionine gamma-synthase (CGS1) gene, complete cds

Seq. No.	274809
Contig ID	54304_1.R1011
5'-most EST	xsy700209724.h1

Seq. No.	274810

Contig ID	54308_1.R1011
5'-most EST	nwy700448092.h1

Seq. No.	274811
Contig ID	54309_1.R1011
5'-most EST	LIB189-011-Q1-E1-A8
Method	BLASTX
NCBI GI	g2586083
BLAST score	225
E value	3.0e-18
Match length	128
% identity	40
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	274812
Contig ID	54309_3.R1011
5'-most EST	rvl700458826.h1

Seq. No.	274813
Contig ID	54313_1.R1011
5'-most EST	ymt700219264.h1

Seq. No.	274814
Contig ID	54320_1.R1011
5'-most EST	qmh700028717.f1
Method	BLASTX
NCBI GI	g2708307
BLAST score	228
E value	2.0e-18
Match length	149
% identity	35
NCBI Description	(AF016370) U4/U6 small nuclear ribonucleoprotein hPrp3 [Homo sapiens]

Seq. No.	274815
Contig ID	54321_1.R1011
5'-most EST	LIB189-011-Q1-E1-C2

Seq. No.	274816
Contig ID	54343_1.R1011
5'-most EST	LIB3067-036-Q1-K1-F6
Method	BLASTX
NCBI GI	g4454006
BLAST score	298
E value	2.0e-26
Match length	185
% identity	40
NCBI Description	(AL035396) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274817
Contig ID	54345_1.R1011
5'-most EST	pwr700451863.h1

Seq. No.	274818
Contig ID	54349_1.R1011
5'-most EST	uC-zmflb73061h11b1

Seq. No.	274819
Contig ID	54349_2.R1011
5'-most EST	uC-zmflb73280d09b2
Method	BLASTX
NCBI GI	g3152605
BLAST score	180
E value	6.0e-13
Match length	138
% identity	36
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274820
Contig ID	54349_3.R1011
5'-most EST	LIB189-011-Q1-E1-F4

Seq. No.	274821
Contig ID	54350_1.R1011
5'-most EST	wty700168616.h1
Method	BLASTX
NCBI GI	g4454484
BLAST score	1199
E value	1.0e-132
Match length	313
% identity	71
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	274822
Contig ID	54352_1.R1011
5'-most EST	uC-zmflb73117d06b2
Method	BLASTX
NCBI GI	g4544390
BLAST score	621
E value	2.0e-75
Match length	278
% identity	55
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274823
Contig ID	54358_1.R1011
5'-most EST	LIB189-011-Q1-E1-G2
Method	BLASTX
NCBI GI	g1168548
BLAST score	269
E value	2.0e-23
Match length	90
% identity	59
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN ATHB-7) >gi_629527_pir__S47137 homeotic protein Athb-7 - Arabidopsis thaliana >gi_499164_emb_CAA47425_ (X67032) orf [Arabidopsis thaliana]

Seq. No.	274824
Contig ID	54365_1.R1011
5'-most EST	LIB189-011-Q1-E1-G9

Seq. No.	274825
Contig ID	54377_1.R1011
5'-most EST	yyf700352440.h1
Method	BLASTX
NCBI GI	g3482979
BLAST score	198
E value	1.0e-14
Match length	179
% identity	30
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana] >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274826
Contig ID	54407_1.R1011
5'-most EST	LIB189-012-Q1-E1-D4

Seq. No.	274827
Contig ID	54419_1.R1011
5'-most EST	LIB189-012-Q1-E1-E6

Seq. No.	274828
Contig ID	54424_1.R1011
5'-most EST	uC-zmrob73080g07b1
Method	BLASTX
NCBI GI	g3193297
BLAST score	482
E value	2.0e-82
Match length	287
% identity	51
NCBI Description	(AF069298) similar to epoxide hydrolases [Arabidopsis thaliana]

Seq. No.	274829
Contig ID	54431_1.R1011
5'-most EST	nbm700466335.h1
Method	BLASTX
NCBI GI	g3738284
BLAST score	261
E value	2.0e-22
Match length	83
% identity	60
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	274830
Contig ID	54432_1.R1011
5'-most EST	LIB189-012-Q1-E1-G12

Seq. No.	274831
Contig ID	54434_1.R1011
5'-most EST	vux700160684.h1
Method	BLASTX
NCBI GI	g3894186
BLAST score	198
E value	3.0e-15
Match length	111
% identity	41

NCBI Description	(AC005662) putative embryo-abundant protein [Arabidopsis thaliana]

Seq. No.	274832
Contig ID	54435_1.R1011
5'-most EST	LIB3137-027-Q1-K1-G12

Seq. No.	274833
Contig ID	54444_1.R1011
5'-most EST	LIB189-012-Q1-E1-H4
Method	BLASTX
NCBI GI	g4115377
BLAST score	258
E value	2.0e-22
Match length	74
% identity	69
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	274834
Contig ID	54453_1.R1011
5'-most EST	LIB189-013-Q1-E1-A2
Method	BLASTX
NCBI GI	g3063448
BLAST score	303
E value	1.0e-27
Match length	97
% identity	55
NCBI Description	(AC003981) F22O13.10 [Arabidopsis thaliana]

Seq. No.	274835
Contig ID	54454_1.R1011
5'-most EST	LIB189-013-Q1-E1-A3

Seq. No.	274836
Contig ID	54458_1.R1011
5'-most EST	dhd700198081.h1
Method	BLASTX
NCBI GI	g3355480
BLAST score	433
E value	2.0e-42
Match length	142
% identity	55
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	274837
Contig ID	54471_1.R1011
5'-most EST	uC-zmroteosinte066h07b1
Method	BLASTX
NCBI GI	g1353193
BLAST score	771
E value	6.0e-82
Match length	256
% identity	61
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	274838
Contig ID	54471_2.R1011
5'-most EST	wty70$\bar{0}$167981.h1
Method	BLASTX
NCBI GI	g1353193
BLAST score	563
E value	9.0e-58
Match length	193
% identity	61
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	274839
Contig ID	54474_1.R1011
5'-most EST	LIB18$\bar{9}$-013-Q1-E1-C4

Seq. No.	274840
Contig ID	54478_1.R1011
5'-most EST	LIB18$\bar{9}$-013-Q1-E1-C9

Seq. No.	274841
Contig ID	54483_1.R1011
5'-most EST	LIB30$\bar{6}$6-047-Q1-K1-H12

Seq. No.	274842
Contig ID	54486_1.R1011
5'-most EST	LIB18$\bar{9}$-013-Q1-E1-D6
Method	BLASTX
NCBI GI	g1370182
BLAST score	615
E value	5.0e-64
Match length	132
% identity	88
NCBI Description	(Z73940) RAB7A [Lotus japonicus]

Seq. No.	274843
Contig ID	54513_1.R1011
5'-most EST	LIB18$\bar{9}$-013-Q1-E1-G11

Seq. No.	274844
Contig ID	54520_1.R1011
5'-most EST	LIB18$\bar{9}$-013-Q1-E1-H10

Seq. No.	274845
Contig ID	54540_1.R1011
5'-most EST	mwy70$\bar{0}$441919.h1
Method	BLASTX
NCBI GI	g4539301
BLAST score	303
E value	3.0e-27
Match length	174
% identity	43
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	274846
Contig ID	54548_1.R1011
5'-most EST	uC-zmflmo17220a11b1
Method	BLASTN
NCBI GI	g1042259
BLAST score	97
E value	5.0e-47
Match length	124
% identity	96
NCBI Description	{Mu1 element insertion site, clone 9} [maize, Transposon, 252 nt]

Seq. No.	274847
Contig ID	54549_1.R1011
5'-most EST	uC-zmroteosinte086f07b1
Method	BLASTX
NCBI GI	g3645899
BLAST score	1182
E value	1.0e-130
Match length	225
% identity	98
NCBI Description	(U68408) 5' end not determined experimentally [Zea mays]

Seq. No.	274848
Contig ID	54549_2.R1011
5'-most EST	uC-zmflm017084b12b1
Method	BLASTX
NCBI GI	g3645899
BLAST score	321
E value	2.0e-29
Match length	67
% identity	91
NCBI Description	(U68408) 5' end not determined experimentally [Zea mays]

Seq. No.	274849
Contig ID	54549_5.R1011
5'-most EST	uC-zmflm017025c09b1
Method	BLASTX
NCBI GI	g3645899
BLAST score	486
E value	4.0e-83
Match length	164
% identity	94
NCBI Description	(U68408) 5' end not determined experimentally [Zea mays]

Seq. No.	274850
Contig ID	54551_1.R1011
5'-most EST	LIB3136-010-Q1-K1-F1
Method	BLASTX
NCBI GI	g3367638
BLAST score	894
E value	1.0e-96
Match length	223
% identity	74
NCBI Description	(AJ000331) monogalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No.	274851
Contig ID	54554_1.R1011
5'-most EST	uC-zmflmo17155d11b1

Seq. No.	274852
Contig ID	54559_2.R1011
5'-most EST	uC-zmflMo17004h11b1
Method	BLASTX
NCBI GI	g3250693
BLAST score	145
E value	5.0e-09
Match length	51
% identity	53
NCBI Description	(AL024486) lectin like protein [Arabidopsis thaliana]

Seq. No.	274853
Contig ID	54561_1.R1011
5'-most EST	tzu700203323.h1

Seq. No.	274854
Contig ID	54571_1.R1011
5'-most EST	LIB3060-020-Q1-K1-A6
Method	BLASTX
NCBI GI	g3924613
BLAST score	309
E value	1.0e-27
Match length	146
% identity	44
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana] >gi_4263512_gb_AAD15338_ (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274855
Contig ID	54574_1.R1011
5'-most EST	LIB3069-043-Q1-K1-B3
Method	BLASTX
NCBI GI	g4263714
BLAST score	421
E value	4.0e-41
Match length	216
% identity	63
NCBI Description	(AC006223) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	274856
Contig ID	54575_1.R1011
5'-most EST	LIB189-014-Q1-E1-E3

Seq. No.	274857
Contig ID	54594_1.R1011
5'-most EST	LIB189-014-Q1-E1-G1
Method	BLASTX
NCBI GI	g3702323
BLAST score	285
E value	2.0e-25
Match length	83
% identity	67

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 274858
Contig ID 54621_1.R1011
5'-most EST LIB36-012-Q1-E1-A7
Method BLASTX
NCBI GI g3075402
BLAST score 190
E value 6.0e-14
Match length 104
% identity 42
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 274859
Contig ID 54622_1.R1011
5'-most EST pmx700088376.h1
Method BLASTX
NCBI GI g1946371
BLAST score 458
E value 2.0e-45
Match length 192
% identity 46
NCBI Description (U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]

Seq. No. 274860
Contig ID 54623_1.R1011
5'-most EST LIB84-004-Q1-E1-E6

Seq. No. 274861
Contig ID 54636_1.R1011
5'-most EST LIB3060-025-Q1-K1-E12
Method BLASTX
NCBI GI g3738303
BLAST score 570
E value 1.0e-58
Match length 177
% identity 62
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] >gi_4249399 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 274862
Contig ID 54653_1.R1011
5'-most EST xmt700258655.h1

Seq. No. 274863
Contig ID 54660_1.R1011
5'-most EST uC-zmflmo17017f08b1
Method BLASTX
NCBI GI g2501599
BLAST score 251
E value 2.0e-21
Match length 76
% identity 63
NCBI Description HYPOTHETICAL 29.1 KD PROTEIN W06E11.4 IN CHROMOSOME III >gi_669022 (U20862) W06E11.4 gene product [Caenorhabditis

elegans]

Seq. No.	274864
Contig ID	54673_1.R1011
5'-most EST	LIB3137-049-Q1-K1-F4
Method	BLASTX
NCBI GI	g3152568
BLAST score	909
E value	1.0e-101
Match length	355
% identity	58
NCBI Description	(AC002986) Similar to hypothetical protein product gb_Z97337 from A. thaliana. EST gb_H76597 comes from this gene. [Arabidopsis thaliana]

Seq. No.	274865
Contig ID	54680_1.R1011
5'-most EST	LIB189-016-Q1-E1-B5
Method	BLASTX
NCBI GI	g3668091
BLAST score	241
E value	4.0e-20
Match length	187
% identity	12
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274866
Contig ID	54681_1.R1011
5'-most EST	uC-zmflmo17040f12b1

Seq. No.	274867
Contig ID	54681_2.R1011
5'-most EST	uC-zmflMo17005f02b1

Seq. No.	274868
Contig ID	54691_1.R1011
5'-most EST	wyr700239986.h1

Seq. No.	274869
Contig ID	54693_1.R1011
5'-most EST	uC-zmroteosinte084d01b1
Method	BLASTX
NCBI GI	g4432844
BLAST score	543
E value	2.0e-93
Match length	237
% identity	74
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	274870
Contig ID	54703_1.R1011
5'-most EST	LIB189-016-Q1-E1-E6
Method	BLASTX
NCBI GI	g4455236
BLAST score	155
E value	4.0e-10
Match length	76

% identity	47
NCBI Description	(AL035523) hypothetical protein [Arabidopsis thaliana]
Seq. No.	274871
Contig ID	54721_1.R1011
5'-most EST	xyt700345456.h1
Method	BLASTX
NCBI GI	g421842
BLAST score	159
E value	1.0e-10
Match length	120
% identity	35
NCBI Description	potassium channel protein - Arabidopsis thaliana >gi_166774 (M86990) potassium channel protein [Arabidopsis thaliana] >gi_1065906 (U25088) potassium channel protein [Arabidopsis thaliana]
Seq. No.	274872
Contig ID	54722_1.R1011
5'-most EST	uC-zmflmo17031h04b1
Seq. No.	274873
Contig ID	54736_1.R1011
5'-most EST	LIB3060-029-Q1-K1-D9
Method	BLASTX
NCBI GI	g2262116
BLAST score	322
E value	2.0e-29
Match length	248
% identity	32
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.	274874
Contig ID	54745_2.R1011
5'-most EST	uC-zmflb73018f02b1
Seq. No.	274875
Contig ID	54751_1.R1011
5'-most EST	LIB3062-019-Q1-K1-D2
Method	BLASTX
NCBI GI	g4512678
BLAST score	881
E value	1.0e-94
Match length	292
% identity	61
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]
Seq. No.	274876
Contig ID	54751_2.R1011
5'-most EST	uer700582820.h1
Seq. No.	274877
Contig ID	54757_1.R1011
5'-most EST	tzu700201251.h1
Method	BLASTX
NCBI GI	g2589164
BLAST score	489

E value	7.0e-49
Match length	169
% identity	78
NCBI Description	(D88452) aldehyde oxidase-2 [Zea mays]

Seq. No.	274878
Contig ID	54757_3.R1011
5'-most EST	ntr70O073364.h1
Method	BLASTX
NCBI GI	g2589164
BLAST score	1672
E value	0.0e+00
Match length	361
% identity	89
NCBI Description	(D88452) aldehyde oxidase-2 [Zea mays]

Seq. No.	274879
Contig ID	54762_1.R1011
5'-most EST	LIB189-017-Q1-E1-D4

Seq. No.	274880
Contig ID	54763_1.R1011
5'-most EST	LIB189-017-Q1-E1-D6
Method	BLASTX
NCBI GI	g4512705
BLAST score	510
E value	6.0e-52
Match length	133
% identity	78
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	274881
Contig ID	54766_1.R1011
5'-most EST	LIB189-017-Q1-E1-D9

Seq. No.	274882
Contig ID	54769_1.R1011
5'-most EST	LIB3069-039-Q1-K1-E11
Method	BLASTX
NCBI GI	g1399265
BLAST score	399
E value	1.0e-38
Match length	133
% identity	59
NCBI Description	(U31751) calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana]

Seq. No.	274883
Contig ID	54772_1.R1011
5'-most EST	uC-zmflb73071d08b3

Seq. No.	274884
Contig ID	54775_1.R1011
5'-most EST	cyk70O051682.f1
Method	BLASTX
NCBI GI	g1762144

BLAST score 452
E value 8.0e-45
Match length 205
% identity 44
NCBI Description (U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No. 274885
Contig ID 54790_1.R1011
5'-most EST LIB189-017-Q1-E1-F9
Method BLASTX
NCBI GI g2331287
BLAST score 224
E value 4.0e-18
Match length 143
% identity 36
NCBI Description (AF013188) release factor 2 [Bacillus subtilis] >gi_2618874 (AF017113) putative peptide chain release factor RF-2 [Bacillus subtilis] >gi_2636055_emb_CAB15546.1_ (Z99122) peptide chain release factor 2 [Bacillus subtilis]

Seq. No. 274886
Contig ID 54799_1.R1011
5'-most EST wyr700237818.h1

Seq. No. 274887
Contig ID 54801_1.R1011
5'-most EST gct701179302.h1

Seq. No. 274888
Contig ID 54801_2.R1011
5'-most EST xdb700339129.h1

Seq. No. 274889
Contig ID 54820_1.R1011
5'-most EST dyk700105945.h1

Seq. No. 274890
Contig ID 54821_1.R1011
5'-most EST rvt700551289.h1
Method BLASTX
NCBI GI g132731
BLAST score 151
E value 2.0e-09
Match length 112
% identity 34
NCBI Description 50S RIBOSOMAL PROTEIN L18 >gi_71260_pir__R5YM18 ribosomal protein L18 - Mycoplasma capricolum (SGC3) >gi_44225_emb_CAA29720_ (X06414) ribosomal protein L18 (AA 1-116) [Mycoplasma capricolum]

Seq. No. 274891
Contig ID 54825_1.R1011
5'-most EST vux700160060.h1

Seq. No. 274892
Contig ID 54841_1.R1011
5'-most EST LIB189-018-Q1-E1-D1

Seq. No.	274893
Contig ID	54853_1.R1011
5'-most EST	nbm700472983.h1
Seq. No.	274894
Contig ID	54855_1.R1011
5'-most EST	gct701174014.h1
Seq. No.	274895
Contig ID	54858_1.R1011
5'-most EST	LIB189-018-Q1-E1-E6
Seq. No.	274896
Contig ID	54860_1.R1011
5'-most EST	uC-zmflb73116c01b2
Method	BLASTX
NCBI GI	g4455338
BLAST score	252
E value	2.0e-21
Match length	71
% identity	62
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]
Seq. No.	274897
Contig ID	54866_1.R1011
5'-most EST	clt700044863.f1
Seq. No.	274898
Contig ID	54874_2.R1011
5'-most EST	qmh700029735.f1
Seq. No.	274899
Contig ID	54874_4.R1011
5'-most EST	xsy700212989.h1
Seq. No.	274900
Contig ID	54891_1.R1011
5'-most EST	LIB189-018-Q1-E1-H7
Method	BLASTX
NCBI GI	g3540207
BLAST score	322
E value	8.0e-30
Match length	144
% identity	44
NCBI Description	(AC004260) Putative protein kinase [Arabidopsis thaliana]
Seq. No.	274901
Contig ID	54897_2.R1011
5'-most EST	LIB189-019-Q1-E1-A3
Seq. No.	274902
Contig ID	54897_3.R1011
5'-most EST	uwc700152133.h1
Seq. No.	274903
Contig ID	54905_1.R1011

5'-most EST	LIB83-002-Q1-E1-F9
Method	BLASTN
NCBI GI	g1245938
BLAST score	37
E value	5.0e-11
Match length	37
% identity	100
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	274904
Contig ID	54911_1.R1011
5'-most EST	fwa70099959.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	274905
Contig ID	54914_1.R1011
5'-most EST	LIB189-019-Q1-E1-C1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	274906
Contig ID	54916_1.R1011
5'-most EST	uC-zmroteosinte088h03b1
Method	BLASTX
NCBI GI	g3334193
BLAST score	1469
E value	1.0e-164
Match length	317
% identity	87
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (G6PD) >gi_2276344_emb_CAA03939_ (AJ000182) Glucose-6-phosphate dehydrogenase [Spinacia oleracea]

Seq. No.	274907
Contig ID	54918_1.R1011
5'-most EST	uC-zmflmo17100d03b1
Method	BLASTX
NCBI GI	g927575
BLAST score	666
E value	6.0e-70
Match length	196
% identity	60
NCBI Description	(U12926) alpha galactosidase [Glycine max]

Seq. No.	274908

Contig ID	54921_1.R1011
5'-most EST	nbm700477028.h1
Method	BLASTX
NCBI GI	g4204275
BLAST score	250
E value	5.0e-21
Match length	234
% identity	32
NCBI Description	(AC004146) Unknown protein [Arabidopsis thaliana]

Seq. No.	274909
Contig ID	54932_1.R1011
5'-most EST	LIB3062-050-Q1-K1-D3

Seq. No.	274910
Contig ID	54933_1.R1011
5'-most EST	LIB3066-004-Q1-K1-F9
Method	BLASTX
NCBI GI	g4455244
BLAST score	190
E value	3.0e-14
Match length	103
% identity	40
NCBI Description	(AL035523) MtN3-like protein [Arabidopsis thaliana]

Seq. No.	274911
Contig ID	54942_1.R1011
5'-most EST	LIB189-019-Q1-E1-E4
Method	BLASTX
NCBI GI	g2500543
BLAST score	243
E value	3.0e-22
Match length	173
% identity	35
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEED8.5 >gi_733602 (U23484) similar to S. cerevisiae pre-mRNA splicing factor RNA helicase PRP22 (SP:PR22_YEAST, P24384) and other DEAH subfamily members of the DEAD box family helicases [Caenorhabditis elegans]

Seq. No.	274912
Contig ID	54944_1.R1011
5'-most EST	gwl700615179.h1
Method	BLASTX
NCBI GI	g2880049
BLAST score	417
E value	1.0e-46
Match length	155
% identity	66
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274913
Contig ID	54950_1.R1011
5'-most EST	LIB189-019-Q1-E1-F2
Method	BLASTX
NCBI GI	g4417304
BLAST score	381

E value	1.0e-36
Match length	139
% identity	51
NCBI Description	(AC006446) putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis thaliana]

Seq. No.	274914
Contig ID	54953_1.R1011
5'-most EST	uC-zmflm017205g04b1
Method	BLASTX
NCBI GI	g3402690
BLAST score	165
E value	3.0e-16
Match length	129
% identity	45
NCBI Description	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	274915
Contig ID	54957_1.R1011
5'-most EST	LIB189-019-Q1-E1-G11

Seq. No.	274916
Contig ID	54958_1.R1011
5'-most EST	uC-zmromo17068h08a1

Seq. No.	274917
Contig ID	54964_1.R1011
5'-most EST	LIB189-019-Q1-E1-H1

Seq. No.	274918
Contig ID	54965_1.R1011
5'-most EST	LIB83-001-Q1-E1-D5
Method	BLASTX
NCBI GI	g3283057
BLAST score	173
E value	3.0e-12
Match length	48
% identity	71
NCBI Description	(AF054617) one helix protein [Arabidopsis thaliana]

Seq. No.	274919
Contig ID	54969_1.R1011
5'-most EST	LIB3136-009-Q1-K1-H12

Seq. No.	274920
Contig ID	54993_1.R1011
5'-most EST	LIB3136-036-Q1-K1-F1
Method	BLASTN
NCBI GI	g22245
BLAST score	34
E value	2.0e-09
Match length	82
% identity	85
NCBI Description	Zea mays DNA for cin4 element (showing homology to reverse transcriptase)

Seq. No. 274921
Contig ID 54993_2.R1011
5'-most EST uC-zmflmo17023g07b1

Seq. No. 274922
Contig ID 54999_1.R1011
5'-most EST fwa700100825.h1
Method BLASTX
NCBI GI g4101705
BLAST score 429
E value 3.0e-42
Match length 137
% identity 58
NCBI Description (AF006079) glucose acyltransferase [Solanum berthaultii]

Seq. No. 274923
Contig ID 55000_1.R1011
5'-most EST clt700046122.f1
Method BLASTX
NCBI GI g2760327
BLAST score 469
E value 6.0e-47
Match length 103
% identity 44
NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No. 274924
Contig ID 55005_2.R1011
5'-most EST wen700333615.h1
Method BLASTX
NCBI GI g1438883
BLAST score 304
E value 2.0e-27
Match length 85
% identity 62
NCBI Description (U43840) GmCK3p [Glycine max]

Seq. No. 274925
Contig ID 55011_1.R1011
5'-most EST uC-zmroteosinte057c09b1

Seq. No. 274926
Contig ID 55038_1.R1011
5'-most EST uC-zmflb73206d12b1
Method BLASTX
NCBI GI g3461836
BLAST score 287
E value 3.0e-25
Match length 167
% identity 43
NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927841 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No. 274927
Contig ID 55040_1.R1011

5'-most EST	uC-zmflmo17293g09b1
Method	BLASTX
NCBI GI	g4582451
BLAST score	186
E value	1.0e-13
Match length	47
% identity	77
NCBI Description	(AC007071) unknown protein [Arabidopsis thaliana]

Seq. No.	274928
Contig ID	55047_1.R1011
5'-most EST	pmx700082661.h1
Method	BLASTX
NCBI GI	g3831457
BLAST score	536
E value	8.0e-55
Match length	158
% identity	65
NCBI Description	(AC005700) putative ion channel protein [Arabidopsis thaliana]

Seq. No.	274929
Contig ID	55051_1.R1011
5'-most EST	zla700379734.h1
Method	BLASTX
NCBI GI	g3047106
BLAST score	184
E value	1.0e-13
Match length	73
% identity	55
NCBI Description	(AF058919) Arabidopsis thaliana homeodomain protein AHDP (SP:P93041) [Arabidopsis thaliana]

Seq. No.	274930
Contig ID	55055_1.R1011
5'-most EST	uC-zmflmo17179g02b1
Method	BLASTX
NCBI GI	g4539400
BLAST score	984
E value	1.0e-106
Match length	375
% identity	73
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	274931
Contig ID	55055_2.R1011
5'-most EST	LIB189-021-Q1-E1-B3
Method	BLASTX
NCBI GI	g4539400
BLAST score	535
E value	8.0e-55
Match length	144
% identity	77
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	274932
Contig ID	55060_1.R1011

5'-most EST	uC-zmflmo17266h10b1
Method	BLASTX
NCBI GI	g3393062
BLAST score	843
E value	2.0e-90
Match length	235
% identity	66
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	274933
Contig ID	55060_2.R1011
5'-most EST	uC-zmflb73030c06b1
Method	BLASTX
NCBI GI	g3393062
BLAST score	611
E value	3.0e-63
Match length	156
% identity	70
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	274934
Contig ID	55069_1.R1011
5'-most EST	uC-zmflmo17288a06b1
Method	BLASTX
NCBI GI	g3258570
BLAST score	782
E value	2.0e-83
Match length	195
% identity	79
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	274935
Contig ID	55072_1.R1011
5'-most EST	rvt700551684.h1
Method	BLASTX
NCBI GI	g4539665
BLAST score	509
E value	4.0e-72
Match length	198
% identity	70
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	274936
Contig ID	55079_1.R1011
5'-most EST	LIB189-021-Q1-E1-D9
Method	BLASTX
NCBI GI	g1616661
BLAST score	481
E value	1.0e-48
Match length	117
% identity	79
NCBI Description	(U49388) adenylosuccinate synthetase [Zea mays]

Seq. No.	274937
Contig ID	55096_1.R1011
5'-most EST	clt700046209.f1

Seq. No.	274938
Contig ID	55097_1.R1011
5'-most EST	uC-zmflb73296d04a1
Method	BLASTX
NCBI GI	g4263711
BLAST score	478
E value	4.0e-48
Match length	118
% identity	75
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	274939
Contig ID	55099_1.R1011
5'-most EST	uwc700152154.h1

Seq. No.	274940
Contig ID	55113_1.R1011
5'-most EST	uC-zmroteosinte032e01b1
Method	BLASTX
NCBI GI	g3549672
BLAST score	715
E value	3.0e-75
Match length	282
% identity	56
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	274941
Contig ID	55118_1.R1011
5'-most EST	uC-zmroteosinte093f06b2

Seq. No.	274942
Contig ID	55124_1.R1011
5'-most EST	LIB3136-057-Q1-K1-G9
Method	BLASTX
NCBI GI	g4544427
BLAST score	237
E value	2.0e-35
Match length	99
% identity	77
NCBI Description	(AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	274943
Contig ID	55124_2.R1011
5'-most EST	LIB189-024-Q1-E1-E11
Method	BLASTX
NCBI GI	g729535
BLAST score	446
E value	2.0e-44
Match length	111
% identity	92
NCBI Description	FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B) (FTR-B)

Seq. No.	274944

Contig ID	55124_3.R1011
5'-most EST	pmx700091005.h1
Method	BLASTX
NCBI GI	g729535
BLAST score	342
E value	5.0e-32
Match length	75
% identity	89
NCBI Description	FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B) (FTR-B)

Seq. No.	274945
Contig ID	55134_1.R1011
5'-most EST	LIB189-022-Q1-E1-B3
Method	BLASTX
NCBI GI	g2576255
BLAST score	574
E value	3.0e-59
Match length	186
% identity	60
NCBI Description	(AJ001729) TH65 protein [Arabidopsis thaliana]

Seq. No.	274946
Contig ID	55149_1.R1011
5'-most EST	LIB189-022-Q1-E1-C9

Seq. No.	274947
Contig ID	55164_1.R1011
5'-most EST	LIB189-022-Q1-E1-E4
Method	BLASTX
NCBI GI	g537404
BLAST score	1319
E value	1.0e-146
Match length	276
% identity	86
NCBI Description	(D26537) WSI76 protein induced by water stress [Oryza sativa]

Seq. No.	274948
Contig ID	55164_3.R1011
5'-most EST	xsy700208794.h1
Method	BLASTX
NCBI GI	g537404
BLAST score	181
E value	2.0e-13
Match length	38
% identity	92
NCBI Description	(D26537) WSI76 protein induced by water stress [Oryza sativa]

Seq. No.	274949
Contig ID	55166_2.R1011
5'-most EST	uC-zmroteosinte011f06b1
Method	BLASTX
NCBI GI	g3650036
BLAST score	201

E value 4.0e-15
Match length 71
% identity 52
NCBI Description (AC005396) putative transposase [Arabidopsis thaliana]

Seq. No. 274950
Contig ID 55167_1.R1011
5'-most EST xjt700096639.h1
Method BLASTX
NCBI GI g2288985
BLAST score 377
E value 5.0e-36
Match length 203
% identity 40
NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 274951
Contig ID 55184_1.R1011
5'-most EST LIB189-022-Q1-E1-G4

Seq. No. 274952
Contig ID 55185_1.R1011
5'-most EST LIB189-030-Q1-E1-F2

Seq. No. 274953
Contig ID 55199_1.R1011
5'-most EST ymt700218848.h1
Method BLASTX
NCBI GI g3880929
BLAST score 172
E value 4.0e-12
Match length 135
% identity 32
NCBI Description (AL021481) similar to WD domain, G-beta repeat (2 domains); cDNA EST yk258d4.3 comes from this gene; cDNA EST yk338d5.3 comes from this gene; cDNA EST yk338d5.5 comes from this gene; cDNA EST yk258d4.5 comes from this gene [Cae

Seq. No. 274954
Contig ID 55214_1.R1011
5'-most EST xsy700211173.h1

Seq. No. 274955
Contig ID 55227_1.R1011
5'-most EST LIB189-023-Q1-E1-D1

Seq. No. 274956
Contig ID 55230_1.R1011
5'-most EST uC-zmf1Mo17004g04b1
Method BLASTX
NCBI GI g4581111
BLAST score 167
E value 2.0e-11
Match length 153
% identity 27
NCBI Description (AC005825) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	274957
Contig ID	55238_1.R1011
5'-most EST	ceu700422753.h1
Method	BLASTX
NCBI GI	g3426048
BLAST score	313
E value	7.0e-29
Match length	78
% identity	78
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	274958
Contig ID	55243_1.R1011
5'-most EST	LIB189-023-Q1-E1-E4

Seq. No.	274959
Contig ID	55243_2.R1011
5'-most EST	fdz701165269.h1

Seq. No.	274960
Contig ID	55247_1.R1011
5'-most EST	LIB189-023-Q1-E1-E8
Method	BLASTX
NCBI GI	g3688191
BLAST score	151
E value	8.0e-10
Match length	79
% identity	47
NCBI Description	(AJ010090) MAP3K alpha protein kinase [Arabidopsis thaliana]

Seq. No.	274961
Contig ID	55256_1.R1011
5'-most EST	LIB3067-039-Q1-K1-B12
Method	BLASTX
NCBI GI	g4406764
BLAST score	486
E value	9.0e-49
Match length	234
% identity	44
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	274962
Contig ID	55258_1.R1011
5'-most EST	LIB189-023-Q1-E1-F8

Seq. No.	274963
Contig ID	55279_1.R1011
5'-most EST	tfd700576289.h1
Method	BLASTX
NCBI GI	g4539003
BLAST score	359
E value	9.0e-34
Match length	200

% identity 39
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 274964
Contig ID 55285_1.R1011
5'-most EST LIB189-024-Q1-E1-A4

Seq. No. 274965
Contig ID 55291_1.R1011
5'-most EST uC-zmflb73142h01b1

Seq. No. 274966
Contig ID 55307_1.R1011
5'-most EST pmx700086234.h1

Seq. No. 274967
Contig ID 55307_2.R1011
5'-most EST uC-zmflmo17057e02b1

Seq. No. 274968
Contig ID 55307_3.R1011
5'-most EST LIB189-024-Q1-E1-C5

Seq. No. 274969
Contig ID 55316_1.R1011
5'-most EST LIB189-024-Q1-E1-D4

Seq. No. 274970
Contig ID 55330_1.R1011
5'-most EST LIB189-024-Q1-E1-E8
Method BLASTX
NCBI GI g3738299
BLAST score 159
E value 5.0e-11
Match length 48
% identity 58
NCBI Description (AC005309) putative glutaredoxin [Arabidopsis thaliana] >gi_4249395 (AC006072) putative glutaredoxin [Arabidopsis thaliana]

Seq. No. 274971
Contig ID 55333_1.R1011
5'-most EST tfd700571009.h1
Method BLASTX
NCBI GI g2506470
BLAST score 578
E value 3.0e-66
Match length 179
% identity 70
NCBI Description ALPHA-1,4 GLUCAN PHOSPHORYLASE, L ISOFORM PRECURSOR (STARCH PHOSPHORYLASE L) >gi_1616637_emb_CAA85354_ (Z36880) alpha-1,4 Glucan Phosphorylase, L isoform precursor [Vicia faba]

Seq. No. 274972
Contig ID 55344_1.R1011
5'-most EST lhp700053424.r1

Method	BLASTX
NCBI GI	g2369690
BLAST score	207
E value	3.0e-16
Match length	109
% identity	42
NCBI Description	(Y11988) FPF1 protein [Arabidopsis thaliana]

Seq. No.	274973
Contig ID	55354_1.R1011
5'-most EST	LIB3137-030-Q1-K1-C1

Seq. No.	274974
Contig ID	55354_2.R1011
5'-most EST	LIB3136-011-Q1-K1-G5

Seq. No.	274975
Contig ID	55354_3.R1011
5'-most EST	uC-zmflmo17221f10b1

Seq. No.	274976
Contig ID	55354_4.R1011
5'-most EST	dyk700102046.h1

Seq. No.	274977
Contig ID	55355_1.R1011
5'-most EST	LIB189-024-Q1-E1-H11
Method	BLASTN
NCBI GI	g4185305
BLAST score	75
E value	2.0e-33
Match length	102
% identity	93
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	274978
Contig ID	55355_2.R1011
5'-most EST	wty700167950.h1
Method	BLASTN
NCBI GI	g4185305
BLAST score	68
E value	8.0e-30
Match length	72
% identity	99
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	274979
Contig ID	55355_3.R1011
5'-most EST	uC-zmflmo17163a08a1

Seq. No.	274980

Contig ID	55356_1.R1011
5'-most EST	uC-zmflmo17264a05a1
Seq. No.	274981
Contig ID	55356_2.R1011
5'-most EST	LIB189-024-Q1-E1-H12
Seq. No.	274982
Contig ID	55358_1.R1011
5'-most EST	LIB189-024-Q1-E1-H3
Seq. No.	274983
Contig ID	55363_1.R1011
5'-most EST	uC-zmflm017086d05b1
Method	BLASTX
NCBI GI	g4557445
BLAST score	208
E value	3.0e-16
Match length	153
% identity	14
NCBI Description	RCC1-like G exchanging factor RLG >gi_3789799 (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens]
Seq. No.	274984
Contig ID	55371_1.R1011
5'-most EST	uC-zmflMo17019b07b1
Method	BLASTX
NCBI GI	g461999
BLAST score	632
E value	4.0e-66
Match length	145
% identity	81
NCBI Description	ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)
Seq. No.	274985
Contig ID	55387_1.R1011
5'-most EST	xmt700263457.h1
Method	BLASTX
NCBI GI	g3025189
BLAST score	380
E value	2.0e-36
Match length	174
% identity	42
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]
Seq. No.	274986
Contig ID	55391_1.R1011
5'-most EST	wyr700240610.h1
Method	BLASTX
NCBI GI	g3142301
BLAST score	343
E value	7.0e-32
Match length	90
% identity	72
NCBI Description	(AC002411) Contains similarity to neural cell adhesion

molecule 2, large isoform precursor gb_M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101, gb_H3630

Seq. No.	274987
Contig ID	55397_1.R1011
5'-most EST	LIB189-025-Q1-E1-D12
Method	BLASTX
NCBI GI	g3292826
BLAST score	168
E value	1.0e-11
Match length	54
% identity	56
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274988
Contig ID	55403_1.R1011
5'-most EST	nbm700466410.h1
Method	BLASTX
NCBI GI	g3953458
BLAST score	948
E value	1.0e-111
Match length	264
% identity	78
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	274989
Contig ID	55404_1.R1011
5'-most EST	hbs701183884.h1
Method	BLASTX
NCBI GI	g1871176
BLAST score	378
E value	6.0e-36
Match length	221
% identity	40
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	274990
Contig ID	55408_1.R1011
5'-most EST	uC-zmflmo17180g01b1
Method	BLASTX
NCBI GI	g3927831
BLAST score	269
E value	5.0e-23
Match length	304
% identity	29
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	274991
Contig ID	55408_2.R1011
5'-most EST	LIB189-025-Q1-E1-E2

Seq. No.	274992
Contig ID	55418_1.R1011
5'-most EST	LIB189-025-Q1-E1-F3

Seq. No.	274993
Contig ID	55419_1.R1011
5'-most EST	LIB189-025-Q1-E1-F4

Seq. No.	274994
Contig ID	55421_1.R1011
5'-most EST	ymt700219052.h1
Method	BLASTX
NCBI GI	g4587549
BLAST score	920
E value	3.0e-99
Match length	271
% identity	66
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

Seq. No.	274995
Contig ID	55424_1.R1011
5'-most EST	LIB189-025-Q1-E1-G10
Method	BLASTX
NCBI GI	g2347195
BLAST score	270
E value	7.0e-24
Match length	84
% identity	61
NCBI Description	(AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	274996
Contig ID	55437_1.R1011
5'-most EST	uC-zmflmo17190d01b1
Method	BLASTN
NCBI GI	g5091496
BLAST score	41
E value	1.0e-13
Match length	89
% identity	87
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	274997
Contig ID	55444_1.R1011
5'-most EST	LIB189-026-Q1-E1-A1

Seq. No.	274998
Contig ID	55447_1.R1011
5'-most EST	LIB189-026-Q1-E1-A12
Method	BLASTX
NCBI GI	g3258576
BLAST score	598
E value	9.0e-62
Match length	218
% identity	55
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	274999
Contig ID	55457_1.R1011
5'-most EST	LIB189-026-Q1-E1-B4

Seq. No.	275000
Contig ID	55482_1.R1011
5'-most EST	LIB189-026-Q1-E1-E11

Seq. No.	275001
Contig ID	55484_1.R1011
5'-most EST	LIB189-028-Q1-E1-C10

Seq. No.	275002
Contig ID	55490_1.R1011
5'-most EST	LIB189-026-Q1-E1-F11
Method	BLASTX
NCBI GI	g1731023
BLAST score	239
E value	6.0e-20
Match length	104
% identity	45
NCBI Description	HYPOTHETICAL 56.4 KD PROTEIN IN SODA-COMGA INTERGENIC REGION >gi_1303863_dbj_BAA12519_ (D84432) YqgP [Bacillus subtilis] >gi_2634921_emb_CAB14418_ (Z99116) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	275003
Contig ID	55493_2.R1011
5'-most EST	dyk700103072.h1
Method	BLASTX
NCBI GI	g1946265
BLAST score	217
E value	1.0e-19
Match length	51
% identity	84
NCBI Description	(Y11414) myb [Oryza sativa]

Seq. No.	275004
Contig ID	55525_1.R1011
5'-most EST	LIB189-027-Q1-E1-A9

Seq. No.	275005
Contig ID	55562_1.R1011
5'-most EST	cjh700197567.h1

Seq. No.	275006
Contig ID	55568_1.R1011
5'-most EST	LIB189-027-Q1-E1-E8
Method	BLASTX
NCBI GI	g2632252
BLAST score	179
E value	1.0e-12
Match length	119
% identity	35
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 275007

Contig ID	55582_1.R1011
5'-most EST	LIB189-027-Q1-E1-G11
Seq. No.	275008
Contig ID	55591_1.R1011
5'-most EST	LIB3060-047-Q1-K1-A8
Seq. No.	275009
Contig ID	55594_1.R1011
5'-most EST	pmx700084123.h1
Seq. No.	275010
Contig ID	55596_1.R1011
5'-most EST	LIB189-029-Q1-E1-D5
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	275011
Contig ID	55599_1.R1011
5'-most EST	LIB189-028-Q1-E1-A11
Seq. No.	275012
Contig ID	55600_1.R1011
5'-most EST	uC-zmf1Mo17065g09b1
Seq. No.	275013
Contig ID	55604_1.R1011
5'-most EST	LIB189-028-Q1-E1-A6
Seq. No.	275014
Contig ID	55628_1.R1011
5'-most EST	wty700164450.h1
Method	BLASTX
NCBI GI	g3511223
BLAST score	759
E value	5.0e-81
Match length	157
% identity	89
NCBI Description	(AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]
Seq. No.	275015
Contig ID	55632_1.R1011
5'-most EST	dyk700105076.h1
Method	BLASTX
NCBI GI	g1514971
BLAST score	168
E value	2.0e-11
Match length	107
% identity	36
NCBI Description	(D83948) S1-1 protein [Rattus norvegicus]
Seq. No.	275016

Contig ID	55634_1.R1011
5'-most EST	uC-zmrob73057g11a1
Method	BLASTX
NCBI GI	g2088651
BLAST score	354
E value	2.0e-33
Match length	105
% identity	61
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	275017
Contig ID	55637_1.R1011
5'-most EST	arm700460715.h1
Method	BLASTX
NCBI GI	g2062168
BLAST score	226
E value	1.0e-18
Match length	78
% identity	51
NCBI Description	(AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275018
Contig ID	55645_1.R1011
5'-most EST	LIB189-028-Q1-E1-E5
Method	BLASTX
NCBI GI	g576886
BLAST score	866
E value	2.0e-93
Match length	170
% identity	94
NCBI Description	(L37750) kaurene synthase A [Zea mays]

Seq. No.	275019
Contig ID	55646_1.R1011
5'-most EST	ceu700429860.h1
Method	BLASTN
NCBI GI	g2286120
BLAST score	38
E value	7.0e-12
Match length	42
% identity	98
NCBI Description	Oryza sativa sec14 like protein mRNA, complete cds

Seq. No.	275020
Contig ID	55657_1.R1011
5'-most EST	xjt700094146.h1
Method	BLASTX
NCBI GI	g4519671
BLAST score	405
E value	2.0e-39
Match length	152
% identity	61
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	275021
Contig ID	55669_1.R1011

5'-most EST	LIB189-028-Q1-E1-G9
Seq. No.	275022
Contig ID	55677_1.R1011
5'-most EST	wen700335650.h1
Seq. No.	275023
Contig ID	55690_1.R1011
5'-most EST	xsy700214776.h1
Method	BLASTX
NCBI GI	g3721926
BLAST score	731
E value	1.0e-77
Match length	160
% identity	91
NCBI Description	(AB017480) chloroplast FtsH protease [Nicotiana tabacum]
Seq. No.	275024
Contig ID	55694_1.R1011
5'-most EST	LIB189-029-Q1-E1-B10
Seq. No.	275025
Contig ID	55696_1.R1011
5'-most EST	clt700043707.f1
Seq. No.	275026
Contig ID	55703_1.R1011
5'-most EST	cat700016784.r1
Method	BLASTX
NCBI GI	g3980397
BLAST score	192
E value	4.0e-14
Match length	123
% identity	41
NCBI Description	(AC004561) putative protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	275027
Contig ID	55703_2.R1011
5'-most EST	uC-zmflmo17139b05a1
Seq. No.	275028
Contig ID	55708_1.R1011
5'-most EST	LIB189-029-Q1-E1-C3
Seq. No.	275029
Contig ID	55708_2.R1011
5'-most EST	mwy700441505.h1
Seq. No.	275030
Contig ID	55711_1.R1011
5'-most EST	uC-zmflb73258h06a2
Seq. No.	275031
Contig ID	55711_2.R1011
5'-most EST	LIB189-029-Q1-E1-C6
Method	BLASTX

NCBI GI	g729842
BLAST score	270
E value	1.0e-23
Match length	86
% identity	66
NCBI Description	CHLOROPLAST MEMBRANE-ASSOCIATED 30 KD PROTEIN PRECURSOR (M30) >gi_1076532_pir__S47966 probable lipid transfer protein M30 precursor - garden pea >gi_169107 (M73744) IM30 [Pisum sativum]

Seq. No.	275032
Contig ID	55715_1.R1011
5'-most EST	LIB189-029-Q1-E1-D1
Method	BLASTX
NCBI GI	g586038
BLAST score	554
E value	5.0e-57
Match length	132
% identity	83
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN CHLOROPLAST PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC) >gi_480296_pir__S36637 signal recognition particle 54CP protein precursor - Arabidopsis thaliana >gi_396701_emb_CAA79981_ (Z21970) 54CP [Arabidopsis thaliana]

Seq. No.	275033
Contig ID	55724_1.R1011
5'-most EST	LIB3066-009-Q1-K1-C8
Method	BLASTX
NCBI GI	g3212865
BLAST score	741
E value	1.0e-78
Match length	225
% identity	64
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	275034
Contig ID	55726_1.R1011
5'-most EST	LIB189-029-Q1-E1-E1

Seq. No.	275035
Contig ID	55726_2.R1011
5'-most EST	uC-zmflb73048a12b1

Seq. No.	275036
Contig ID	55726_3.R1011
5'-most EST	LIB3136-021-Q1-K1-C1

Seq. No.	275037
Contig ID	55728_1.R1011
5'-most EST	LIB189-029-Q1-E1-E11

Seq. No.	275038
Contig ID	55729_1.R1011
5'-most EST	LIB3059-029-Q1-K1-F2
Method	BLASTX

NCBI GI	g1652434
BLAST score	445
E value	7.0e-44
Match length	184
% identity	52
NCBI Description	(D90905) N-acetylglutamate kinase [Synechocystis sp.]

Seq. No.	275039
Contig ID	55747_1.R1011
5'-most EST	LIB189-029-Q1-E1-G1

Seq. No.	275040
Contig ID	55751_1.R1011
5'-most EST	LIB3060-015-Q1-K1-D4

Seq. No.	275041
Contig ID	55755_1.R1011
5'-most EST	LIB83-013-Q1-E1-B7
Method	BLASTX
NCBI GI	g2980765
BLAST score	381
E value	1.0e-36
Match length	157
% identity	50
NCBI Description	(AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275042
Contig ID	55765_1.R1011
5'-most EST	uC-zmflmo17324c12a1

Seq. No.	275043
Contig ID	55773_1.R1011
5'-most EST	LIB189-030-Q1-E1-A5
Method	BLASTX
NCBI GI	g687677
BLAST score	312
E value	1.0e-28
Match length	93
% identity	57
NCBI Description	(U19925) unknown [Arabidopsis thaliana]

Seq. No.	275044
Contig ID	55776_1.R1011
5'-most EST	uC-zmflmo17238b08a1
Method	BLASTN
NCBI GI	g22651
BLAST score	39
E value	2.0e-12
Match length	51
% identity	94
NCBI Description	H.vulgare mRNA for GRP94 homologue

Seq. No.	275045
Contig ID	55782_1.R1011
5'-most EST	uC-zmflb73251d11b3
Method	BLASTX
NCBI GI	g585747

BLAST score	1172
E value	1.0e-129
Match length	277
% identity	81
NCBI Description	PHYTOENE SYNTHASE 2 PRECURSOR >gi_1076590_pir__A49558 phytoene synthase 2 precursor - tomato (fragment) >gi_437020 (L23424) phytoene synthase [Lycopersicon esculentum]

Seq. No.	275046
Contig ID	55786_1.R1011
5'-most EST	ceu70̄0427724.h1

Seq. No.	275047
Contig ID	55788_1.R1011
5'-most EST	LIB189̄-030-Q1-E1-C11
Method	BLASTX
NCBI GI	g4033424
BLAST score	980
E value	1.0e-106
Match length	203
% identity	91
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No.	275048
Contig ID	55819_1.R1011
5'-most EST	ntr70̄0071956.h1
Method	BLASTX
NCBI GI	g4263722
BLAST score	474
E value	2.0e-47
Match length	198
% identity	55
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	275049
Contig ID	55821_1.R1011
5'-most EST	uC-zmf̄lb73233b08b1
Method	BLASTX
NCBI GI	g1654140
BLAST score	649
E value	9.0e-68
Match length	276
% identity	52
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	275050
Contig ID	55822_1.R1011
5'-most EST	LIB306̄2-043-Q1-K1-H2
Method	BLASTX
NCBI GI	g2980776
BLAST score	504
E value	1.0e-50
Match length	109
% identity	79

NCBI Description (AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No. 275051
Contig ID 55823_1.R1011
5'-most EST LIB189-030-Q1-E1-F9

Seq. No. 275052
Contig ID 55840_2.R1011
5'-most EST LIB189-030-Q1-E1-H3

Seq. No. 275053
Contig ID 55842_1.R1011
5'-most EST uwc700152168.h1

Seq. No. 275054
Contig ID 55852_1.R1011
5'-most EST uC-zmflm017026a07b1
Method BLASTX
NCBI GI g2288982
BLAST score 1025
E value 1.0e-111
Match length 301
% identity 68
NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 275055
Contig ID 55861_1.R1011
5'-most EST cat700020190.r1

Seq. No. 275056
Contig ID 55863_1.R1011
5'-most EST wen700334874.h1

Seq. No. 275057
Contig ID 55869_1.R1011
5'-most EST LIB189-031-Q1-E1-C4
Method BLASTX
NCBI GI g4006873
BLAST score 284
E value 3.0e-25
Match length 151
% identity 44
NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No. 275058
Contig ID 55877_1.R1011
5'-most EST LIB189-031-Q1-E1-D2
Method BLASTX
NCBI GI g2708532
BLAST score 194
E value 7.0e-15
Match length 63
% identity 52
NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No. 275059
Contig ID 55879_1.R1011

5'-most EST	LIB189-031-Q1-E1-D4
Seq. No.	275060
Contig ID	55887_1.R1011
5'-most EST	LIB3136-016-Q1-K1-D6
Method	BLASTX
NCBI GI	g2827992
BLAST score	654
E value	2.0e-68
Match length	195
% identity	62
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]
Seq. No.	275061
Contig ID	55887_2.R1011
5'-most EST	LIB3069-018-Q1-K1-B5
Method	BLASTX
NCBI GI	g3928543
BLAST score	763
E value	5.0e-81
Match length	274
% identity	50
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]
Seq. No.	275062
Contig ID	55889_1.R1011
5'-most EST	ceu7000428977.h1
Seq. No.	275063
Contig ID	55891_1.R1011
5'-most EST	uC-zmflmo17039f12b1
Method	BLASTX
NCBI GI	g4220480
BLAST score	544
E value	2.0e-55
Match length	289
% identity	43
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.	275064
Contig ID	55892_1.R1011
5'-most EST	LIB189-031-Q1-E1-E9
Seq. No.	275065
Contig ID	55900_1.R1011
5'-most EST	LIB189-031-Q1-E1-F6
Method	BLASTX
NCBI GI	g3953463
BLAST score	493
E value	1.0e-49
Match length	174
% identity	53
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]
Seq. No.	275066
Contig ID	55900_2.R1011

5'-most EST	ceu700428719.h1
Method	BLASTX
NCBI GI	g3953463
BLAST score	280
E value	5.0e-25
Match length	113
% identity	47
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No.	275067
Contig ID	55902_1.R1011
5'-most EST	LIB189-031-Q1-E1-F8
Method	BLASTX
NCBI GI	g2655098
BLAST score	396
E value	2.0e-38
Match length	120
% identity	65
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	275068
Contig ID	55905_1.R1011
5'-most EST	LIB3060-018-Q1-K1-E8
Method	BLASTX
NCBI GI	g2244971
BLAST score	530
E value	6.0e-54
Match length	170
% identity	59
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275069
Contig ID	55905_2.R1011
5'-most EST	tzu700205492.h1
Method	BLASTX
NCBI GI	g2326372
BLAST score	435
E value	3.0e-43
Match length	120
% identity	69
NCBI Description	(Y14404) putative arabinose kinase [Arabidopsis thaliana]

Seq. No.	275070
Contig ID	55931_1.R1011
5'-most EST	wyr700241504.h1
Method	BLASTX
NCBI GI	g2443814
BLAST score	553
E value	7.0e-57
Match length	158
% identity	64
NCBI Description	(AF020500) myristoyl CoA:protein N-myristoyltransferase [Homo sapiens]

Seq. No.	275071
Contig ID	55932_1.R1011
5'-most EST	mwy700441426.h1

Seq. No.	275072
Contig ID	55940_1.R1011
5'-most EST	xsy700213488.h1
Method	BLASTX
NCBI GI	g2773249
BLAST score	165
E value	2.0e-11
Match length	115
% identity	33
NCBI Description	(AF039707) glutamate carboxypeptidase II [Rattus norvegicus]

Seq. No.	275073
Contig ID	55949_1.R1011
5'-most EST	wty700168602.h1
Method	BLASTX
NCBI GI	g4006910
BLAST score	381
E value	1.0e-36
Match length	124
% identity	58
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	275074
Contig ID	55950_1.R1011
5'-most EST	LIB189-032-Q1-E1-C5
Method	BLASTX
NCBI GI	g2688094
BLAST score	255
E value	1.0e-21
Match length	181
% identity	35
NCBI Description	(AE001130) guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (spoT) [Borrelia burgdorferi]

Seq. No.	275075
Contig ID	55955_1.R1011
5'-most EST	LIB3060-003-Q1-K1-G8

Seq. No.	275076
Contig ID	55962_1.R1011
5'-most EST	fwa700097461.h1
Method	BLASTX
NCBI GI	g1652303
BLAST score	189
E value	7.0e-14
Match length	168
% identity	32
NCBI Description	(D90904) hypothetical protein [Synechocystis sp.]

Seq. No.	275077
Contig ID	55973_1.R1011
5'-most EST	LIB189-032-Q1-E1-E6
Method	BLASTX
NCBI GI	g4204267
BLAST score	172

E value	3.0e-12
Match length	45
% identity	71
NCBI Description	(AC005223) 55585 [Arabidopsis thaliana]

Seq. No.	275078
Contig ID	55979_1.R1011
5'-most EST	LIB189-032-Q1-E1-F11

Seq. No.	275079
Contig ID	55987_2.R1011
5'-most EST	LIB189-032-Q1-E1-F8

Seq. No.	275080
Contig ID	55992_1.R1011
5'-most EST	fC-zmle700580708a2
Method	BLASTX
NCBI GI	g4115381
BLAST score	507
E value	9.0e-64
Match length	354
% identity	38
NCBI Description	(AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No.	275081
Contig ID	56014_1.R1011
5'-most EST	LIB189-033-Q1-E1-A2

Seq. No.	275082
Contig ID	56018_1.R1011
5'-most EST	zuv700356487.h1
Method	BLASTX
NCBI GI	g401114
BLAST score	1085
E value	1.0e-119
Match length	225
% identity	94
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE) >gi_82726_pir__JQ1329 sucrose-phosphate synthase (EC 2.4.1.14) - maize >gi_168626 (M97550) sucrose phosphate synthase [Zea mays]

Seq. No.	275083
Contig ID	56027_1.R1011
5'-most EST	wen700332593.h1
Method	BLASTX
NCBI GI	g4056486
BLAST score	477
E value	8.0e-48
Match length	174
% identity	53
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275084
Contig ID	56029_1.R1011
5'-most EST	uC-zmflmo17287g07b1
Method	BLASTX

NCBI GI	g1519701
BLAST score	184
E value	4.0e-13
Match length	69
% identity	51
NCBI Description	(U67957) K02H8.1 gene product [Caenorhabditis elegans]

Seq. No.	275085
Contig ID	56035_1.R1011
5'-most EST	gwl700615349.h1
Method	BLASTX
NCBI GI	g2117303
BLAST score	295
E value	3.0e-34
Match length	158
% identity	53
NCBI Description	(Z95620) n-acetylglucosaminyl-phosphatidylinositol [Schizosaccharomyces pombe]

Seq. No.	275086
Contig ID	56045_1.R1011
5'-most EST	uC-zmflmo17067d11b1
Method	BLASTX
NCBI GI	g3152587
BLAST score	720
E value	3.0e-76
Match length	223
% identity	61
NCBI Description	(AC002986) Similar to CREB-binding protein homolog gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No.	275087
Contig ID	56059_1.R1011
5'-most EST	uC-zmroteosinte092f12b2
Method	BLASTX
NCBI GI	g3880563
BLAST score	195
E value	2.0e-14
Match length	194
% identity	34
NCBI Description	(Z78018) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	275088
Contig ID	56067_1.R1011
5'-most EST	uC-zmflb73053c07b2
Method	BLASTX
NCBI GI	g4432844
BLAST score	458
E value	2.0e-45
Match length	200
% identity	45
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	275089
Contig ID	56068_1.R1011
5'-most EST	dyk700102786.h1
Method	BLASTX
NCBI GI	g4164473
BLAST score	148
E value	4.0e-09
Match length	71
% identity	51
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	275090
Contig ID	56073_1.R1011
5'-most EST	LIB189-034-Q1-E1-A2

Seq. No.	275091
Contig ID	56079_1.R1011
5'-most EST	ntr700076772.h1

Seq. No.	275092
Contig ID	56088_1.R1011
5'-most EST	uC-zmroteosinte031c03b1

Seq. No.	275093
Contig ID	56105_1.R1011
5'-most EST	fC-zmle700443661g2
Method	BLASTX
NCBI GI	g3287691
BLAST score	463
E value	9.0e-46
Match length	290
% identity	40
NCBI Description	(AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No.	275094
Contig ID	56105_2.R1011
5'-most EST	fC-zmle700443661d5

Seq. No.	275095
Contig ID	56119_1.R1011
5'-most EST	LIB189-034-Q1-E1-F11
Method	BLASTX
NCBI GI	g1352187
BLAST score	209
E value	1.0e-16
Match length	46
% identity	89
NCBI Description	CYTOCHROME P450 78 (CYPLXXVIII) >gi_1084477_pir__S51475 cytochrome P450 - maize >gi_349718 (L23209) cytochrome P-450 [Zea mays]

Seq. No.	275096
Contig ID	56136_1.R1011
5'-most EST	uC-zmflm017089h10b1
Method	BLASTX

NCBI GI	g3249068
BLAST score	269
E value	3.0e-23
Match length	239
% identity	30
NCBI Description	(AC004473) Contains similarity to zinc-binding protein (PWA33) gb_L04190 from Pleurodeles waltlii. [Arabidopsis thaliana]

Seq. No.	275097
Contig ID	56138_1.R1011
5'-most EST	pmx700087440.h1

Seq. No.	275098
Contig ID	56143_1.R1011
5'-most EST	LIB189-034-Q1-E1-H7

Seq. No.	275099
Contig ID	56146_1.R1011
5'-most EST	LIB3059-001-Q1-K2-A1
Method	BLASTX
NCBI GI	g1091678
BLAST score	477
E value	5.0e-48
Match length	137
% identity	66
NCBI Description	activator-like transposable element [Pennisetum glaucum]

Seq. No.	275100
Contig ID	56194_1.R1011
5'-most EST	xsy700213806.h1
Method	BLASTX
NCBI GI	g4456823
BLAST score	153
E value	7.0e-10
Match length	138
% identity	32
NCBI Description	(AL035548) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	275101
Contig ID	56210_1.R1011
5'-most EST	LIB3059-001-Q1-K2-E10
Method	BLASTX
NCBI GI	g4056490
BLAST score	208
E value	2.0e-16
Match length	99
% identity	40
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275102
Contig ID	56225_1.R1011
5'-most EST	LIB3059-001-Q1-K2-F9
Method	BLASTX
NCBI GI	g2459443
BLAST score	546
E value	9.0e-56

Match length	157
% identity	62
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana]

Seq. No.	275103
Contig ID	56230_1.R1011
5'-most EST	xmt70o264538.h1
Method	BLASTX
NCBI GI	g283044
BLAST score	332
E value	2.0e-43
Match length	91
% identity	95
NCBI Description	hybrid proline-rich protein - maize >gi_433707_emb_CAA42959_ (X60432) prolin rich protein [Zea mays]

Seq. No.	275104
Contig ID	56275_1.R1011
5'-most EST	uC-zmflmo17263f01b1
Method	BLASTX
NCBI GI	g4512659
BLAST score	354
E value	3.0e-33
Match length	110
% identity	61
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	275105
Contig ID	56299_1.R1011
5'-most EST	LIB3059-002-Q1-K2-G6

Seq. No.	275106
Contig ID	56317_1.R1011
5'-most EST	LIB3059-003-Q1-K1-A2
Method	BLASTX
NCBI GI	g3386607
BLAST score	199
E value	2.0e-15
Match length	79
% identity	53
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275107
Contig ID	56320_1.R1011
5'-most EST	LIB3059-003-Q1-K1-A7

Seq. No.	275108
Contig ID	56323_1.R1011
5'-most EST	LIB3059-003-Q1-K1-B10
Method	BLASTX
NCBI GI	g1079063
BLAST score	357
E value	2.0e-33

Match length	229
% identity	34
NCBI Description	deep orange protein - fruit fly (Drosophila melanogaster) >gi_798832_emb_CAA60382_ (X86683) deep orange (dor) [Drosophila melanogaster]

Seq. No.	275109
Contig ID	56334_1.R1011
5'-most EST	LIB3059-003-Q1-K1-C11
Method	BLASTX
NCBI GI	g1747310
BLAST score	201
E value	9.0e-16
Match length	97
% identity	46
NCBI Description	(D58424) Myb-like DNA binding protein [Arabidopsis thaliana]

Seq. No.	275110
Contig ID	56335_1.R1011
5'-most EST	uC-zmflb73019b06a1

Seq. No.	275111
Contig ID	56336_1.R1011
5'-most EST	LIB3059-003-Q1-K1-C3

Seq. No.	275112
Contig ID	56359_1.R1011
5'-most EST	LIB3066-047-Q1-K1-D8
Method	BLASTN
NCBI GI	g168436
BLAST score	51
E value	2.0e-19
Match length	91
% identity	89
NCBI Description	Zea mays catalase (Cat3) gene, complete cds

Seq. No.	275113
Contig ID	56375_1.R1011
5'-most EST	LIB3059-003-Q1-K1-G3

Seq. No.	275114
Contig ID	56386_1.R1011
5'-most EST	LIB3070-016-Q1-N1-D7

Seq. No.	275115
Contig ID	56397_1.R1011
5'-most EST	LIB36-007-Q1-E1-A6

Seq. No.	275116
Contig ID	56411_1.R1011
5'-most EST	LIB3059-004-Q1-K1-D5
Method	BLASTX
NCBI GI	g114200
BLAST score	683
E value	2.0e-71
Match length	259

% identity	56
NCBI Description	SHIKIMATE KINASE PRECURSOR >gi_100253_pir__S21584 shikimate kinase precursor - tomato >gi_19349_emb_CAA45121_ (X63560) shikimate kinase precursor [Lycopersicon esculentum]

Seq. No.	275117
Contig ID	56411_2.R1011
5'-most EST	cyk700050913.f1
Method	BLASTX
NCBI GI	g114200
BLAST score	211
E value	4.0e-35
Match length	119
% identity	66
NCBI Description	SHIKIMATE KINASE PRECURSOR >gi_100253_pir__S21584 shikimate kinase precursor - tomato >gi_19349_emb_CAA45121_ (X63560) shikimate kinase precursor [Lycopersicon esculentum]

Seq. No.	275118
Contig ID	56418_1.R1011
5'-most EST	LIB3059-004-Q1-K1-E2

Seq. No.	275119
Contig ID	56444_1.R1011
5'-most EST	LIB3059-004-Q1-K1-H11

Seq. No.	275120
Contig ID	56447_1.R1011
5'-most EST	LIB3136-042-P1-K1-B2
Method	BLASTX
NCBI GI	g4580398
BLAST score	953
E value	1.0e-103
Match length	305
% identity	59
NCBI Description	(AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No.	275121
Contig ID	56461_1.R1011
5'-most EST	LIB3059-005-Q1-K1-B9
Method	BLASTX
NCBI GI	g2583123
BLAST score	216
E value	3.0e-17
Match length	50
% identity	74
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	275122
Contig ID	56468_1.R1011
5'-most EST	LIB3059-005-Q1-K1-C5
Method	BLASTX
NCBI GI	g2130121
BLAST score	572
E value	8.0e-59

Match length	134
% identity	82
NCBI Description	cyclin II - maize >gi_516550 (U10077) cyclin IIZm [Zea mays]

Seq. No.	275123
Contig ID	56476_1.R1011
5'-most EST	hbs701180706.h1
Method	BLASTX
NCBI GI	g2651302
BLAST score	459
E value	8.0e-46
Match length	155
% identity	58
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275124
Contig ID	56485_1.R1011
5'-most EST	LIB3059-022-Q1-K1-A11
Method	BLASTX
NCBI GI	g168701
BLAST score	477
E value	6.0e-48
Match length	129
% identity	79
NCBI Description	(M60837) zein [Zea mays]

Seq. No.	275125
Contig ID	56495_1.R1011
5'-most EST	LIB3059-005-Q1-K1-F6

Seq. No.	275126
Contig ID	56499_1.R1011
5'-most EST	LIB3059-005-Q1-K1-G1

Seq. No.	275127
Contig ID	56512_1.R1011
5'-most EST	uC-zmrob73078c07b1

Seq. No.	275128
Contig ID	56516_1.R1011
5'-most EST	LIB3059-006-Q1-K1-A12
Method	BLASTX
NCBI GI	g4557495
BLAST score	242
E value	2.0e-20
Match length	121
% identity	45
NCBI Description	cleavage stimulation factor subunit 3 >gi_1082704_pir__S50852 cleavage stimulation factor 77K chain - human >gi_632498 (U15782) cleavage stimulation factor 77kDa subunit [Homo sapiens] >gi_1092656_prf__2024339A cleavage stimulation factor [Homo sapiens]

Seq. No.	275129
Contig ID	56533_1.R1011

5'-most EST	LIB3059-007-Q1-K1-C11
Method	BLASTX
NCBI GI	g232031
BLAST score	235
E value	1.0e-19
Match length	46
% identity	96
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	275130
Contig ID	56537_1.R1011
5'-most EST	LIB3059-006-Q1-K1-C4

Seq. No.	275131
Contig ID	56554_1.R1011
5'-most EST	uC-zmflmo17297a08b1
Method	BLASTX
NCBI GI	g1438883
BLAST score	346
E value	2.0e-32
Match length	130
% identity	58
NCBI Description	(U43840) GmCK3p [Glycine max]

Seq. No.	275132
Contig ID	56600_1.R1011
5'-most EST	uC-zmrob73061e03a1

Seq. No.	275133
Contig ID	56627_1.R1011
5'-most EST	LIB3059-053-Q1-K1-F1

Seq. No.	275134
Contig ID	56632_1.R1011
5'-most EST	uC-zmflmo17017f05b1
Method	BLASTX
NCBI GI	g732189
BLAST score	169
E value	8.0e-19
Match length	114
% identity	49
NCBI Description	HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION >gi_2131922_pir__S50724 hypothetical protein YNL207w - yeast (Saccharomyces cerevisiae) >gi_600058_emb_CAA55501_ (X78898) N1342 [Saccharomyces cerevisiae] >gi_1302211_emb_CAA96109_ (Z71483) ORF YNL207w [Saccharomyces cerevisiae]

Seq. No.	275135
Contig ID	56632_2.R1011
5'-most EST	gct701177157.h1
Method	BLASTX
NCBI GI	g732189
BLAST score	207

E value	3.0e-16
Match length	85
% identity	52
NCBI Description	HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION >gi_2131922_pir__S50724 hypothetical protein YNL207w - yeast (Saccharomyces cerevisiae) >gi_600058_emb_CAA55501_ (X78898) N1342 [Saccharomyces cerevisiae] >gi_1302211_emb_CAA96109_ (Z71483) ORF YNL207w [Saccharomyces cerevisiae]

Seq. No.	275136
Contig ID	56648_1.R1011
5'-most EST	LIB3059-007-Q1-K1-H12
Method	BLASTX
NCBI GI	g4588002
BLAST score	283
E value	4.0e-25
Match length	85
% identity	59
NCBI Description	(AF085279) hypothetical ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	275137
Contig ID	56691_1.R1011
5'-most EST	nbm700473568.h1

Seq. No.	275138
Contig ID	56691_2.R1011
5'-most EST	tfd700576379.h1

Seq. No.	275139
Contig ID	56695_1.R1011
5'-most EST	LIB3061-003-Q1-K1-D6
Method	BLASTX
NCBI GI	g322598
BLAST score	288
E value	1.0e-25
Match length	137
% identity	45
NCBI Description	St12p protein - Arabidopsis thaliana

Seq. No.	275140
Contig ID	56700_1.R1011
5'-most EST	LIB3059-008-Q1-K1-H10

Seq. No.	275141
Contig ID	56712_1.R1011
5'-most EST	LIB3059-041-Q1-K1-E3
Method	BLASTX
NCBI GI	g2522534
BLAST score	432
E value	2.0e-42
Match length	199
% identity	26
NCBI Description	(AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]

Seq. No.	275142

Contig ID	56719_1.R1011
5'-most EST	LIB3059-009-Q1-K1-B3
Method	BLASTX
NCBI GI	g2262172
BLAST score	410
E value	1.0e-39
Match length	97
% identity	77
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	275143
Contig ID	56726_1.R1011
5'-most EST	LIB3059-009-Q1-K1-C9

Seq. No.	275144
Contig ID	56740_1.R1011
5'-most EST	xdb700337256.h1
Method	BLASTN
NCBI GI	g949979
BLAST score	75
E value	9.0e-34
Match length	154
% identity	93
NCBI Description	Z.mays Glossy2 locus DNA

Seq. No.	275145
Contig ID	56740_2.R1011
5'-most EST	uC-zmflmo17130a09b1

Seq. No.	275146
Contig ID	56744_1.R1011
5'-most EST	ceu700430673.h1

Seq. No.	275147
Contig ID	56744_2.R1011
5'-most EST	tfd700574288.h1

Seq. No.	275148
Contig ID	56753_1.R1011
5'-most EST	uC-zmflm017018e11b1
Method	BLASTX
NCBI GI	g3023947
BLAST score	1739
E value	0.0e+00
Match length	398
% identity	92
NCBI Description	PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi_2665840 (AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No.	275149
Contig ID	56756_1.R1011
5'-most EST	pmx700086964.h1
Method	BLASTX
NCBI GI	g3193330
BLAST score	223
E value	6.0e-18

Match length	100
% identity	49
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	275150
Contig ID	56757_1.R1011
5'-most EST	ypc700804596.h1
Method	BLASTX
NCBI GI	g1055161
BLAST score	159
E value	1.0e-10
Match length	114
% identity	34
NCBI Description	(U40029) similar to human 100 kDa coactivator (U22055) [Caenorhabditis elegans]

Seq. No.	275151
Contig ID	56767_1.R1011
5'-most EST	pmx700089621.h1
Method	BLASTX
NCBI GI	g3776027
BLAST score	1313
E value	0.0e+00
Match length	514
% identity	70
NCBI Description	(AJ010475) RNA helicase [Arabidopsis thaliana]

Seq. No.	275152
Contig ID	56778_1.R1011
5'-most EST	LIB3059-010-Q1-K1-A2

Seq. No.	275153
Contig ID	56781_1.R1011
5'-most EST	LIB3059-010-Q1-K1-B1

Seq. No.	275154
Contig ID	56804_1.R1011
5'-most EST	LIB3059-010-Q1-K1-D11

Seq. No.	275155
Contig ID	56805_1.R1011
5'-most EST	hvj700623257.h1
Method	BLASTX
NCBI GI	g3928083
BLAST score	1217
E value	1.0e-134
Match length	309
% identity	72
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	275156
Contig ID	56807_1.R1011
5'-most EST	uC-zmflb73301f09b2
Method	BLASTX
NCBI GI	g4586107
BLAST score	441

E value	4.0e-45
Match length	135
% identity	22
NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	275157
Contig ID	56811_1.R1011
5'-most EST	LIB3059-010-Q1-K1-E1

Seq. No.	275158
Contig ID	56821_1.R1011
5'-most EST	ymt700220496.h1

Seq. No.	275159
Contig ID	56829_1.R1011
5'-most EST	LIB3059-010-Q1-K1-G1
Method	BLASTX
NCBI GI	g4587577
BLAST score	343
E value	5.0e-32
Match length	185
% identity	44
NCBI Description	(AC006550) F10O3.17 [Arabidopsis thaliana]

Seq. No.	275160
Contig ID	56832_1.R1011
5'-most EST	LIB3059-010-Q1-K1-G12

Seq. No.	275161
Contig ID	56832_2.R1011
5'-most EST	xmt700265563.h1

Seq. No.	275162
Contig ID	56837_1.R1011
5'-most EST	uC-zmflmo17289h09b1

Seq. No.	275163
Contig ID	56845_1.R1011
5'-most EST	ntr700077196.h1
Method	BLASTX
NCBI GI	g2950472
BLAST score	189
E value	6.0e-14
Match length	140
% identity	37
NCBI Description	(AL022070) putative autophagocytosis protein [Schizosaccharomyces pombe]

Seq. No.	275164
Contig ID	56862_1.R1011
5'-most EST	uC-zmrob73076c02b1
Method	BLASTX
NCBI GI	g3688162
BLAST score	218
E value	1.0e-17
Match length	110

% identity	51
NCBI Description	(AJ009672) centrin [Arabidopsis thaliana]

Seq. No.	275165
Contig ID	56869_1.R1011
5'-most EST	LIB3059-011-Q1-K1-C2

Seq. No.	275166
Contig ID	56872_1.R1011
5'-most EST	uC-zmflmo17266g09b1

Seq. No.	275167
Contig ID	56872_2.R1011
5'-most EST	ypc700799503.h1
Method	BLASTX
NCBI GI	g4584527
BLAST score	214
E value	1.0e-16
Match length	236
% identity	25
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	275168
Contig ID	56872_3.R1011
5'-most EST	LIB36-015-Q1-E1-A10

Seq. No.	275169
Contig ID	56874_1.R1011
5'-most EST	LIB3069-034-Q1-K1-H8
Method	BLASTX
NCBI GI	g4263048
BLAST score	456
E value	4.0e-45
Match length	158
% identity	58
NCBI Description	(AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No.	275170
Contig ID	56886_1.R1011
5'-most EST	uC-zmroteosinte021a05b1

Seq. No.	275171
Contig ID	56892_1.R1011
5'-most EST	LIB3059-011-Q1-K1-F11
Method	BLASTX
NCBI GI	g4572673
BLAST score	659
E value	5.0e-69
Match length	248
% identity	49
NCBI Description	(AC006954) putative sarcosine oxidase [Arabidopsis thaliana]

Seq. No.	275172
Contig ID	56906_1.R1011
5'-most EST	uC-zmflb73295g10b2

Seq. No.	275173
Contig ID	56913_1.R1011
5'-most EST	tbg700930466.h1
Method	BLASTX
NCBI GI	g4519673
BLAST score	296
E value	1.0e-26
Match length	164
% identity	44
NCBI Description	(AB017694) WREBP-2 [Nicotiana tabacum]

Seq. No.	275174
Contig ID	56935_1.R1011
5'-most EST	uC-zmflmo17289a04b1
Method	BLASTX
NCBI GI	g3135269
BLAST score	146
E value	4.0e-09
Match length	85
% identity	38
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	275175
Contig ID	56935_2.R1011
5'-most EST	LIB3059-012-Q1-K1-B9
Method	BLASTX
NCBI GI	g3135269
BLAST score	160
E value	2.0e-10
Match length	111
% identity	32
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	275176
Contig ID	56939_1.R1011
5'-most EST	LIB3059-012-Q1-K1-C7
Method	BLASTX
NCBI GI	g3540182
BLAST score	252
E value	3.0e-21
Match length	128
% identity	48
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	275177
Contig ID	56943_1.R1011
5'-most EST	uC-zmflb73257g03b3
Method	BLASTX
NCBI GI	g4586253
BLAST score	613
E value	2.0e-63
Match length	217
% identity	63
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	275178
Contig ID	56943_2.R1011

5'-most EST	uwc700154629.h1
Seq. No.	275179
Contig ID	56973_1.R1011
5'-most EST	afb700381024.h1
Seq. No.	275180
Contig ID	56975_1.R1011
5'-most EST	uC-zmflmo17040b10b1
Method	BLASTX
NCBI GI	g3298502
BLAST score	966
E value	1.0e-104
Match length	420
% identity	49
NCBI Description	(AB015046) xylulokinase [Homo sapiens]
Seq. No.	275181
Contig ID	56982_1.R1011
5'-most EST	xdb700337725.h1
Method	BLASTX
NCBI GI	g3540219
BLAST score	149
E value	2.0e-09
Match length	45
% identity	60
NCBI Description	(D87686) KIAA0017 protein [Homo sapiens]
Seq. No.	275182
Contig ID	57006_1.R1011
5'-most EST	LIB3059-013-Q1-K1-C9
Seq. No.	275183
Contig ID	57026_1.R1011
5'-most EST	rvt700553147.h1
Method	BLASTX
NCBI GI	g3688173
BLAST score	343
E value	6.0e-32
Match length	184
% identity	42
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]
Seq. No.	275184
Contig ID	57039_1.R1011
5'-most EST	uC-zmflmo17155a10b1
Seq. No.	275185
Contig ID	57048_1.R1011
5'-most EST	tzu700204883.h1
Seq. No.	275186
Contig ID	57057_1.R1011
5'-most EST	LIB3067-060-Q1-K1-A6
Method	BLASTN
NCBI GI	g3892651
BLAST score	267

E value	1.0e-148
Match length	351
% identity	93
NCBI Description	Z.mays mRNA for putative MADS-domain transcription factor, ZMM8

Seq. No.	275187
Contig ID	57078_1.R1011
5'-most EST	uC-zmflb73028g12b1
Method	BLASTX
NCBI GI	g4588012
BLAST score	957
E value	1.0e-104
Match length	254
% identity	71
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	275188
Contig ID	57078_2.R1011
5'-most EST	tfd700572778.h1
Method	BLASTX
NCBI GI	g4588012
BLAST score	891
E value	3.0e-96
Match length	215
% identity	79
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	275189
Contig ID	57086_1.R1011
5'-most EST	yyf700350531.h1
Method	BLASTX
NCBI GI	g2674203
BLAST score	1571
E value	1.0e-177
Match length	411
% identity	79
NCBI Description	(AF036328) CLP protease regulatory subunit CLPX [Arabidopsis thaliana]

Seq. No.	275190
Contig ID	57089_1.R1011
5'-most EST	uC-zmroteosinte104c08b2
Method	BLASTX
NCBI GI	g1362051
BLAST score	753
E value	6.0e-80
Match length	187
% identity	78
NCBI Description	protein kinase 3 - soybean >gi_310582 (L19361) protein kinase 3 [Glycine max]

Seq. No.	275191
Contig ID	57092_1.R1011
5'-most EST	LIB3059-014-Q1-K1-G2

Seq. No.	275192
Contig ID	57095_1.R1011
5'-most EST	ntr700072647.h1
Method	BLASTX
NCBI GI	g3406742
BLAST score	334
E value	8.0e-31
Match length	178
% identity	40
NCBI Description	(AF017990) Fkbp39p [Schizosaccharomyces pombe] >gi_4456817_emb_CAB37433.1_ (AL035548) Peptidyl Prolyl cis-trans isomerase [Schizosaccharomyces pombe]

Seq. No.	275193
Contig ID	57104_1.R1011
5'-most EST	LIB3059-015-Q1-K1-A1

Seq. No.	275194
Contig ID	57117_1.R1011
5'-most EST	uC-zmflb73177e06b1

Seq. No.	275195
Contig ID	57117_2.R1011
5'-most EST	LIB3059-015-Q1-K1-B11

Seq. No.	275196
Contig ID	57120_1.R1011
5'-most EST	pwr700450713.h1
Method	BLASTX
NCBI GI	g4371292
BLAST score	165
E value	1.0e-11
Match length	51
% identity	61
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	275197
Contig ID	57133_1.R1011
5'-most EST	gwl700616005.h1
Method	BLASTX
NCBI GI	g4559388
BLAST score	728
E value	5.0e-77
Match length	287
% identity	47
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275198
Contig ID	57160_1.R1011
5'-most EST	xyt700343658.h1

Seq. No.	275199
Contig ID	57160_3.R1011
5'-most EST	uC-zmflmo17243c05a1

Seq. No. 275200

Contig ID	57168_1.R1011
5'-most EST	ntr700072709.h1
Method	BLASTX
NCBI GI	g2323410
BLAST score	158
E value	1.0e-10
Match length	63
% identity	52
NCBI Description	(AF015913) Skb1Hs [Homo sapiens]

Seq. No.	275201
Contig ID	57181_1.R1011
5'-most EST	LIB3059-016-Q1-K1-A3

Seq. No.	275202
Contig ID	57195_1.R1011
5'-most EST	LIB3059-016-Q1-K1-C6
Method	BLASTX
NCBI GI	g4191791
BLAST score	406
E value	1.0e-39
Match length	124
% identity	60
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	275203
Contig ID	57219_1.R1011
5'-most EST	xsy700212261.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	275204
Contig ID	57222_1.R1011
5'-most EST	uC-zmflmo17185f09b1

Seq. No.	275205
Contig ID	57226_1.R1011
5'-most EST	mwy700439360.h1
Method	BLASTX
NCBI GI	g4006872
BLAST score	1197
E value	1.0e-132
Match length	290
% identity	77
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	275206
Contig ID	57229_1.R1011
5'-most EST	uC-zmflmo17039b03b1

Seq. No.	275207
Contig ID	57232_1.R1011
5'-most EST	uC-zmflb73003c02b1
Method	BLASTX
NCBI GI	g2344890
BLAST score	241
E value	4.0e-20
Match length	55
% identity	80
NCBI Description	(AC002388) TINY transcription factor isolog [Arabidopsis thaliana]

Seq. No.	275208
Contig ID	57235_1.R1011
5'-most EST	LIB3059-017-Q1-K1-A9
Method	BLASTX
NCBI GI	g2244986
BLAST score	148
E value	5.0e-09
Match length	32
% identity	75
NCBI Description	(Z97340) FCA gamma [Arabidopsis thaliana]

Seq. No.	275209
Contig ID	57249_1.R1011
5'-most EST	uC-zmflb73021d03a2

Seq. No.	275210
Contig ID	57250_1.R1011
5'-most EST	ymt700221017.h1

Seq. No.	275211
Contig ID	57263_1.R1011
5'-most EST	uC-zmflb73149e12a1
Method	BLASTX
NCBI GI	g4160298
BLAST score	684
E value	9.0e-72
Match length	286
% identity	52
NCBI Description	(AJ011892) cyclin D2.1 protein [Nicotiana tabacum]

Seq. No.	275212
Contig ID	57265_1.R1011
5'-most EST	uer700582055.h1

Seq. No.	275213
Contig ID	57268_1.R1011
5'-most EST	LIB3059-038-Q1-K1-A3
Method	BLASTX
NCBI GI	g2190544
BLAST score	567
E value	2.0e-58
Match length	152
% identity	75
NCBI Description	(AC001229) Similar to Saccharomyces hypothetical protein P9642.2 (gb_U40828). [Arabidopsis thaliana]

Seq. No.	275214
Contig ID	57270_1.R1011
5'-most EST	uC-zmflmo17328f03a1

Seq. No.	275215
Contig ID	57273_1.R1011
5'-most EST	uC-zmflmo17425f07a1
Method	BLASTX
NCBI GI	g3004565
BLAST score	269
E value	2.0e-23
Match length	66
% identity	71
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	275216
Contig ID	57307_1.R1011
5'-most EST	pmx700090827.h1
Method	BLASTX
NCBI GI	g2190547
BLAST score	1346
E value	1.0e-149
Match length	319
% identity	76
NCBI Description	(AC001229) ESTs gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come from this gene. [Arabidopsis thaliana]

Seq. No.	275217
Contig ID	57308_1.R1011
5'-most EST	uC-zmflb73032f12b1
Method	BLASTX
NCBI GI	g1911774
BLAST score	183
E value	2.0e-13
Match length	63
% identity	46
NCBI Description	(S83364) putative Rab5-interacting protein {clone L1-57} [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]

Seq. No.	275218
Contig ID	57319_1.R1011
5'-most EST	LIB3059-018-Q1-K1-B9

Seq. No.	275219
Contig ID	57324_2.R1011
5'-most EST	pmx700088226.h1

Seq. No.	275220
Contig ID	57368_1.R1011
5'-most EST	LIB3059-018-Q1-K1-H4

Seq. No.	275221
Contig ID	57391_1.R1011
5'-most EST	uC-zmflB73047c02b1

Seq. No.	275222
Contig ID	57391_2.R1011
5'-most EST	uC-zmroB73030b03b1

Seq. No.	275223
Contig ID	57405_1.R1011
5'-most EST	LIB3059-019-Q1-K1-D8
Method	BLASTX
NCBI GI	g465898
BLAST score	271
E value	1.0e-23
Match length	152
% identity	43
NCBI Description	HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III >gi_630692_pir__S44849 K12H4.8 protein - Caenorhabditis elegans >gi_289703 (L14331) homology with eukaryotic initiation factor-4A (eIF-4A) and E. coli Ribonuclease III; coded for by C. elegans cDNA GenBank:T02268; putative [Caenorhabditis elegans]

Seq. No.	275224
Contig ID	57435_1.R1011
5'-most EST	uC-zmflb73056d12b1
Method	BLASTX
NCBI GI	g2262113
BLAST score	458
E value	4.0e-45
Match length	369
% identity	34
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	275225
Contig ID	57435_2.R1011
5'-most EST	LIB3136-007-Q1-K1-G8
Method	BLASTX
NCBI GI	g2288997
BLAST score	253
E value	3.0e-21
Match length	87
% identity	57
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275226
Contig ID	57435_3.R1011
5'-most EST	uC-zmflmo17417a12a1

Seq. No.	275227
Contig ID	57439_1.R1011
5'-most EST	cjh700196278.h1

Seq. No.	275228
Contig ID	57446_1.R1011
5'-most EST	uC-zmflmo17246d08b1
Method	BLASTX
NCBI GI	g3122275
BLAST score	496
E value	2.0e-49

Match length	288
% identity	39
NCBI Description	PUTATIVE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (TRANSAMINASE B) (BCAT) >gi_2649663 (AE001039) branched-chain amino acid aminotransferase (ilvE) [Archaeoglobus fulgidus]

Seq. No.	275229
Contig ID	57455_1.R1011
5'-most EST	LIB3059-020-Q1-K1-A6

Seq. No.	275230
Contig ID	57459_1.R1011
5'-most EST	LIB3059-020-Q1-K1-B11
Method	BLASTX
NCBI GI	g464707
BLAST score	271
E value	2.0e-23
Match length	191
% identity	57
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	275231
Contig ID	57476_1.R1011
5'-most EST	cat700021550.r1
Method	BLASTX
NCBI GI	g2267597
BLAST score	411
E value	3.0e-40
Match length	95
% identity	87
NCBI Description	(AF009413) 10 kDa chaperonin [Oryza sativa]

Seq. No.	275232
Contig ID	57487_1.R1011
5'-most EST	xjt700092403.h1
Method	BLASTX
NCBI GI	g2827702
BLAST score	677
E value	3.0e-71
Match length	152
% identity	76
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	275233
Contig ID	57490_1.R1011
5'-most EST	LIB3059-020-Q1-K1-E4

Seq. No.	275234
Contig ID	57491_1.R1011
5'-most EST	xdb700341617.h1

Seq. No.	275235
Contig ID	57503_1.R1011
5'-most EST	uC-zmflmo17161c02b1

Seq. No.	275236
Contig ID	57518_1.R1011
5'-most EST	LIB3059-021-Q1-K1-A3
Method	BLASTX
NCBI GI	g4455356
BLAST score	175
E value	3.0e-12
Match length	87
% identity	44
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	275237
Contig ID	57526_1.R1011
5'-most EST	LIB3059-021-Q1-K1-B11

Seq. No.	275238
Contig ID	57535_1.R1011
5'-most EST	uwc700150656.h1

Seq. No.	275239
Contig ID	57550_1.R1011
5'-most EST	uC-zmroteosinte035a09b2
Method	BLASTX
NCBI GI	g627570
BLAST score	277
E value	6.0e-24
Match length	178
% identity	37
NCBI Description	phosphorylation regulatory protein HP-10 - human

Seq. No.	275240
Contig ID	57550_3.R1011
5'-most EST	uC-zmflmo17238f06b1

Seq. No.	275241
Contig ID	57557_1.R1011
5'-most EST	cjh700195318.h1
Method	BLASTX
NCBI GI	g1730557
BLAST score	493
E value	1.0e-49
Match length	105
% identity	85
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME 2 PRECURSOR (STARCH

PHOSPHORYLASE L-2) >gi_421957_pir__S34189 starch phosphorylase (EC 2.4.1.1) - potato >gi_1084437_pir__S53489 starch phosphorylase (EC 2.4.1.1) - potato >gi_313349_emb_CAA52036_ (X73684) starch phosphorylase [Solanum tuberosum]

Seq. No.	275242
Contig ID	57558_1.R1011
5'-most EST	LIB3059-021-Q1-K1-E8
Method	BLASTX
NCBI GI	g3913437
BLAST score	425
E value	9.0e-42
Match length	95
% identity	79
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970) RNA helicase [Arabidopsis thaliana]

Seq. No.	275243
Contig ID	57582_1.R1011
5'-most EST	LIB3059-021-Q1-K1-H5
Method	BLASTX
NCBI GI	g3892709
BLAST score	432
E value	9.0e-43
Match length	132
% identity	60
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	275244
Contig ID	57587_1.R1011
5'-most EST	xsy700211101.h1
Method	BLASTX
NCBI GI	g3249070
BLAST score	323
E value	3.0e-54
Match length	259
% identity	53
NCBI Description	(AC004473) Contains similarity to siah binding protein 1 (SiahBP1) gb_U51586 from Homo sapiens. ESTs gb_T43314, gb_T43315 and gb_R90521, gb_T75905 [Arabidopsis thaliana]

Seq. No.	275245
Contig ID	57587_2.R1011
5'-most EST	uC-zmflmo17116f06b1
Method	BLASTX
NCBI GI	g3249070
BLAST score	236
E value	2.0e-19
Match length	250
% identity	30
NCBI Description	(AC004473) Contains similarity to siah binding protein 1 (SiahBP1) gb_U51586 from Homo sapiens. ESTs gb_T43314, gb_T43315 and gb_R90521, gb_T75905 [Arabidopsis thaliana]

Seq. No.	275246
Contig ID	57587_3.R1011
5'-most EST	uC-zmflmo17212g02a1
Method	BLASTX
NCBI GI	g3249070
BLAST score	263
E value	9.0e-23
Match length	71
% identity	73
NCBI Description	(AC004473) Contains similarity to siah binding protein 1 (SiahBP1) gb_U51586 from Homo sapiens. ESTs gb_T43314, gb_T43315 and gb_R90521, gb_T75905 [Arabidopsis thaliana]

Seq. No.	275247
Contig ID	57613_1.R1011
5'-most EST	LIB3059-022-Q1-K1-C8

Seq. No.	275248
Contig ID	57631_1.R1011
5'-most EST	LIB3059-022-Q1-K1-E6
Method	BLASTX
NCBI GI	g4406815
BLAST score	480
E value	3.0e-48
Match length	113
% identity	79
NCBI Description	(AC006201) putative peptide methionine sulfoxide reductase [Arabidopsis thaliana]

Seq. No.	275249
Contig ID	57636_1.R1011
5'-most EST	LIB3059-022-Q1-K1-F3

Seq. No.	275250
Contig ID	57637_1.R1011
5'-most EST	uC-zmflb73160a09a1
Method	BLASTX
NCBI GI	g2809259
BLAST score	306
E value	8.0e-28
Match length	98
% identity	58
NCBI Description	(AC002560) F21B7.28 [Arabidopsis thaliana]

Seq. No.	275251
Contig ID	57649_1.R1011
5'-most EST	LIB3137-043-Q1-K1-F7
Method	BLASTX
NCBI GI	g407942
BLAST score	451
E value	1.0e-48
Match length	157
% identity	61
NCBI Description	(U02496) epoxide hydrolase [Solanum tuberosum]

Seq. No.	275252
Contig ID	57652_1.R1011

5'-most EST	LIB3059-022-Q1-K1-H4
Method	BLASTX
NCBI GI	g2467272
BLAST score	525
E value	2.0e-53
Match length	193
% identity	28
NCBI Description	(Z99759) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	275253
Contig ID	57661_1.R1011
5'-most EST	LIB3136-014-Q1-K2-D11

Seq. No.	275254
Contig ID	57670_1.R1011
5'-most EST	LIB3059-023-Q1-K1-B6
Method	BLASTX
NCBI GI	g2190552
BLAST score	249
E value	3.0e-21
Match length	89
% identity	54
NCBI Description	(AC001229) Similar to Holcus major pollen allergen (gb_Z27084). [Arabidopsis thaliana]

Seq. No.	275255
Contig ID	57691_1.R1011
5'-most EST	uC-zmflb73062b03b1

Seq. No.	275256
Contig ID	57739_1.R1011
5'-most EST	pwr700448606.h1
Method	BLASTX
NCBI GI	g1345978
BLAST score	1776
E value	0.0e+00
Match length	417
% identity	75
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_457631 (L29214) omega-6 desaturase [Brassica napus]

Seq. No.	275257
Contig ID	57739_2.R1011
5'-most EST	uC-zmflmo17046a04b1

Seq. No.	275258
Contig ID	57758_1.R1011
5'-most EST	uC-zmflmo17058b08b1
Method	BLASTX
NCBI GI	g4115925
BLAST score	657
E value	2.0e-68
Match length	186
% identity	45
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein

[Arabidopsis thaliana]

Seq. No.	275259
Contig ID	57762_1.R1011
5'-most EST	uC-zmflmo17198c08b1
Method	BLASTX
NCBI GI	g3367522
BLAST score	323
E value	1.0e-31
Match length	154
% identity	46
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	275260
Contig ID	57766_1.R1011
5'-most EST	LIB3059-024-Q1-K1-E8

Seq. No.	275261
Contig ID	57771_1.R1011
5'-most EST	LIB3068-047-Q1-K1-B6
Method	BLASTX
NCBI GI	g2285792
BLAST score	452
E value	6.0e-45
Match length	122
% identity	75
NCBI Description	(AB004568) cyanase [Arabidopsis thaliana] >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]

Seq. No.	275262
Contig ID	57772_1.R1011
5'-most EST	LIB3059-024-Q1-K1-F3
Method	BLASTX
NCBI GI	g2760333
BLAST score	286
E value	2.0e-25
Match length	178
% identity	34
NCBI Description	(AC002130) F1N21.18 [Arabidopsis thaliana]

Seq. No.	275263
Contig ID	57789_1.R1011
5'-most EST	tfd700574022.h1
Method	BLASTX
NCBI GI	g4455338
BLAST score	1009
E value	1.0e-110
Match length	229
% identity	84
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	275264
Contig ID	57802_1.R1011
5'-most EST	uC-zmroteosinte087a07b2

Seq. No.	275265
Contig ID	57803_1.R1011
5'-most EST	uC-zmflmo17399h08a1
Method	BLASTX
NCBI GI	g2160156
BLAST score	2137
E value	0.0e+00
Match length	615
% identity	64
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No.	275266
Contig ID	57843_1.R1011
5'-most EST	uC-zmflmo17135e05a1
Method	BLASTN
NCBI GI	g1151133
BLAST score	414
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Zea mays leaf permease 1 mRNA, complete cds

Seq. No.	275267
Contig ID	57852_1.R1011
5'-most EST	LIB3068-043-Q1-K1-E3
Method	BLASTX
NCBI GI	g3914800
BLAST score	287
E value	1.0e-25
Match length	79
% identity	70
NCBI Description	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 >gi_1877025_dbj_BAA11350_ (D78336) ribosomal protein L2 [Oryza sativa]

Seq. No.	275268
Contig ID	57858_1.R1011
5'-most EST	ceu700428901.h1
Method	BLASTX
NCBI GI	g1086586
BLAST score	197
E value	1.0e-14
Match length	182
% identity	26
NCBI Description	(U41007) similar to G beta repeats (PROSITE:PS00670) [Caenorhabditis elegans]

Seq. No.	275269
Contig ID	57877_1.R1011
5'-most EST	uC-zmflb73163b10b2
Method	BLASTX
NCBI GI	g3025188
BLAST score	229
E value	1.0e-18
Match length	73
% identity	49

NCBI Description	HYPOTHETICAL 11.9 KD PROTEIN SLR1846 >gi_1652154_dbj_BAA17078_ (D90903) hypothetical protein [Synechocystis sp.]
Seq. No.	275270
Contig ID	57888_1.R1011
5'-most EST	uC-zmflmo17109f07b1
Seq. No.	275271
Contig ID	57893_1.R1011
5'-most EST	xdg700405216.h1
Seq. No.	275272
Contig ID	57937_1.R1011
5'-most EST	wen700336186.h1
Seq. No.	275273
Contig ID	57940_1.R1011
5'-most EST	LIB3059-026-Q1-K1-H2
Seq. No.	275274
Contig ID	57940_2.R1011
5'-most EST	pwr700450082.h2
Seq. No.	275275
Contig ID	57943_1.R1011
5'-most EST	uC-zmf1B73002b07b1
Method	BLASTX
NCBI GI	g4510381
BLAST score	489
E value	8.0e-49
Match length	271
% identity	47
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.	275276
Contig ID	57948_1.R1011
5'-most EST	uC-zmflmo17333c12b1
Method	BLASTX
NCBI GI	g136125
BLAST score	445
E value	8.0e-44
Match length	221
% identity	43
NCBI Description	PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_ (X05424) ORFa [Zea mays]
Seq. No.	275277
Contig ID	57949_1.R1011
5'-most EST	LIB3059-027-Q1-K1-A3
Method	BLASTX
NCBI GI	g2344887
BLAST score	356
E value	1.0e-33
Match length	122
% identity	62
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	275278
Contig ID	57959_1.R1011
5'-most EST	LIB3059-027-Q1-K1-B8

Seq. No.	275279
Contig ID	57967_1.R1011
5'-most EST	LIB3059-027-Q1-K1-C6

Seq. No.	275280
Contig ID	57967_2.R1011
5'-most EST	rvt700548922.h1

Seq. No.	275281
Contig ID	57975_1.R1011
5'-most EST	LIB3059-027-Q1-K1-D4
Method	BLASTX
NCBI GI	g141617
BLAST score	254
E value	7.0e-22
Match length	65
% identity	74
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir__S12140 zein Zc1 - maize >gi_100945_pir__B29017 zein 2 - maize >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays] >gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No.	275282
Contig ID	57979_1.R1011
5'-most EST	LIB3059-027-Q1-K1-D9
Method	BLASTX
NCBI GI	g224513
BLAST score	215
E value	2.0e-18
Match length	117
% identity	52
NCBI Description	zein M6 [Zea mays]

Seq. No.	275283
Contig ID	57991_1.R1011
5'-most EST	LIB3061-049-Q1-K1-B2

Seq. No.	275284
Contig ID	58000_1.R1011
5'-most EST	fC-zmro700449739a1
Method	BLASTX
NCBI GI	g1362091
BLAST score	512
E value	2.0e-51
Match length	249
% identity	43
NCBI Description	cellulase (EC 3.2.1.4) precursor - tomato >gi_924622 (U20590) endo-1,4-beta-glucanase precursor [Solanum lycopersicum]

Seq. No. 275285

Contig ID	58001_1.R1011
5'-most EST	cyk700049378.f1

Seq. No.	275286
Contig ID	58002_1.R1011
5'-most EST	uC-zmflmo17156c09b1
Method	BLASTX
NCBI GI	g1362152
BLAST score	1734
E value	0.0e+00
Match length	384
% identity	86
NCBI Description	ribosomal protein S6 kinase homolog (clone Aspk11) - oat >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]

Seq. No.	275287
Contig ID	58007_1.R1011
5'-most EST	gct701179351.h1
Method	BLASTX
NCBI GI	g1076288
BLAST score	863
E value	9.0e-93
Match length	276
% identity	56
NCBI Description	amino acid permease AAP3 - Arabidopsis thaliana

Seq. No.	275288
Contig ID	58010_1.R1011
5'-most EST	nbm700466218.h1
Method	BLASTX
NCBI GI	g3193300
BLAST score	308
E value	3.0e-38
Match length	225
% identity	42
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	275289
Contig ID	58031_1.R1011
5'-most EST	LIB3067-045-Q1-K1-D5

Seq. No.	275290
Contig ID	58042_1.R1011
5'-most EST	LIB3059-028-Q1-K1-E7
Method	BLASTX
NCBI GI	g3413700
BLAST score	446
E value	5.0e-44
Match length	143
% identity	66
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	275291
Contig ID	58043_1.R1011
5'-most EST	LIB3059-028-Q1-K1-E8

Seq. No.	275292
Contig ID	58048_1.R1011
5'-most EST	tzu700206513.h1
Method	BLASTX
NCBI GI	g3128207
BLAST score	154
E value	4.0e-10
Match length	47
% identity	55
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275293
Contig ID	58067_1.R1011
5'-most EST	xdb700338234.h1

Seq. No.	275294
Contig ID	58087_1.R1011
5'-most EST	uC-zmflmo17031f08b1

Seq. No.	275295
Contig ID	58088_1.R1011
5'-most EST	LIB3059-029-Q1-K1-B7

Seq. No.	275296
Contig ID	58104_1.R1011
5'-most EST	xsy700208713.h1
Method	BLASTX
NCBI GI	g4510373
BLAST score	307
E value	9.0e-28
Match length	130
% identity	45
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	275297
Contig ID	58109_1.R1011
5'-most EST	uC-zmflmo17046g09b1
Method	BLASTN
NCBI GI	g22274
BLAST score	498
E value	0.0e+00
Match length	534
% identity	99
NCBI Description	Maize 26S - 17S rDNA spacer region from Black Mexican Sweet (BMS) suspension cells

Seq. No.	275298
Contig ID	58113_1.R1011
5'-most EST	LIB3059-029-Q1-K1-F11
Method	BLASTX
NCBI GI	g117291
BLAST score	448
E value	3.0e-44
Match length	104
% identity	83
NCBI Description	CHLOROPLAST PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) (P36)

(E29) >gi_81464_pir__S03638 triose phosphate/3-phosphoglycerate/phosphate translocator precursor - spinach >gi_21274_emb_CAA32016_ (X13754) phosphate translocator protein (AA 1 - 404) [Spinacia oleracea]

Seq. No.	275299
Contig ID	58116_1.R1011
5'-most EST	LIB3059-029-Q1-K1-F3
Method	BLASTN
NCBI GI	g4204371
BLAST score	107
E value	2.0e-53
Match length	119
% identity	97
NCBI Description	Zea mays acidic ribosomal protein P2a-2 (rpp2a-2) mRNA, complete cds

Seq. No.	275300
Contig ID	58120_2.R1011
5'-most EST	uC-zmflmo17326h04a1
Method	BLASTX
NCBI GI	g4432825
BLAST score	156
E value	4.0e-10
Match length	45
% identity	62
NCBI Description	(AC006593) putative SOP2p protein [Arabidopsis thaliana]

Seq. No.	275301
Contig ID	58120_3.R1011
5'-most EST	uC-zmflmo17290b05a1

Seq. No.	275302
Contig ID	58129_1.R1011
5'-most EST	xyt700345290.h1
Method	BLASTX
NCBI GI	g4469025
BLAST score	217
E value	3.0e-17
Match length	72
% identity	51
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	275303
Contig ID	58137_1.R1011
5'-most EST	LIB3059-029-Q1-K1-H8

Seq. No.	275304
Contig ID	58145_1.R1011
5'-most EST	LIB3059-030-Q1-K1-B1
Method	BLASTX
NCBI GI	g1665817
BLAST score	152
E value	1.0e-09
Match length	91
% identity	37

NCBI Description	(D87466) Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]

Seq. No.	275305
Contig ID	58158_1.R1011
5'-most EST	ceu700433549.h1

Seq. No.	275306
Contig ID	58163_1.R1011
5'-most EST	xyt700342579.h1
Method	BLASTX
NCBI GI	g1532168
BLAST score	238
E value	1.0e-19
Match length	65
% identity	68
NCBI Description	(U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis thaliana]

Seq. No.	275307
Contig ID	58166_1.R1011
5'-most EST	uC-zmflb73061a04b1
Method	BLASTX
NCBI GI	g3096949
BLAST score	1076
E value	1.0e-118
Match length	298
% identity	68
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	275308
Contig ID	58176_1.R1011
5'-most EST	uC-zmflb73349g05a2
Method	BLASTX
NCBI GI	g2766448
BLAST score	1905
E value	0.0e+00
Match length	469
% identity	95
NCBI Description	(AF029856) cytochrome P450 CYP98A1 [Sorghum bicolor]

Seq. No.	275309
Contig ID	58176_2.R1011
5'-most EST	tzu700202463.h1
Method	BLASTX
NCBI GI	g2766448
BLAST score	977
E value	1.0e-116
Match length	286
% identity	73
NCBI Description	(AF029856) cytochrome P450 CYP98A1 [Sorghum bicolor]

Seq. No.	275310
Contig ID	58177_1.R1011
5'-most EST	cyk700049568.f1

Seq. No.	275311
Contig ID	58184_1.R1011
5'-most EST	LIB3061-030-Q1-K1-H4
Method	BLASTX
NCBI GI	g4220532
BLAST score	591
E value	9.0e-61
Match length	379
% identity	43
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	275312
Contig ID	58191_1.R1011
5'-most EST	LIB3059-032-Q1-K1-G5

Seq. No.	275313
Contig ID	58199_1.R1011
5'-most EST	LIB83-002-Q1-E1-H3
Method	BLASTX
NCBI GI	g1907270
BLAST score	539
E value	4.0e-55
Match length	156
% identity	73
NCBI Description	(X96761) sulphate transporter protein [Sporobolus stapfianus]

Seq. No.	275314
Contig ID	58215_1.R1011
5'-most EST	LIB3059-031-Q1-K1-B11

Seq. No.	275315
Contig ID	58217_1.R1011
5'-most EST	uC-zmflmo17295a12b1
Method	BLASTX
NCBI GI	g3122326
BLAST score	636
E value	2.0e-66
Match length	178
% identity	67
NCBI Description	LEC14B PROTEIN >gi_1181604_dbj_BAA11768_ (D83074) LEC14B protein [Lithospermum erythrorhizon]

Seq. No.	275316
Contig ID	58249_1.R1011
5'-most EST	uC-zmflMo17005d02b1

Seq. No.	275317
Contig ID	58250_1.R1011
5'-most EST	pmx700087549.h1

Seq. No.	275318
Contig ID	58272_1.R1011

5'-most EST	LIB3059-032-Q1-K1-A7
Method	BLASTN
NCBI GI	g998429
BLAST score	52
E value	3.0e-20
Match length	71
% identity	94
NCBI Description	GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]

Seq. No.	275319
Contig ID	58277_1.R1011
5'-most EST	LIB3059-032-Q1-K1-B11
Method	BLASTX
NCBI GI	g2194123
BLAST score	178
E value	6.0e-13
Match length	70
% identity	47
NCBI Description	(AC002062) Similar to Secale chloroplast ribosomal protein L12 (gb_SCL121A). EST gb_H36579 comes from this gene. [Arabidopsis thaliana]

Seq. No.	275320
Contig ID	58278_1.R1011
5'-most EST	rvl700453730.h1
Method	BLASTX
NCBI GI	g29733
BLAST score	203
E value	1.0e-15
Match length	126
% identity	37
NCBI Description	(X07024) CCG1 protein (AA 1 - 1554) [Homo sapiens] >gi_742875_prf__2011225A CCG1 gene [Homo sapiens]

Seq. No.	275321
Contig ID	58291_1.R1011
5'-most EST	LIB3137-039-Q1-K1-F2
Method	BLASTX
NCBI GI	g3986470
BLAST score	382
E value	2.0e-36
Match length	209
% identity	40
NCBI Description	(AF083497) phospholipase D1 [Mus musculus]

Seq. No.	275322
Contig ID	58298_1.R1011
5'-most EST	LIB3136-038-P1-K1-G5
Method	BLASTX
NCBI GI	g3738208
BLAST score	578
E value	2.0e-59
Match length	175
% identity	63
NCBI Description	(AL031853) strong similarity to human Rev interacting protein Rip-1 [Schizosaccharomyces pombe]

Seq. No.	275323
Contig ID	58302_2.R1011
5'-most EST	nbm700472513.h1
Method	BLASTX
NCBI GI	g3881873
BLAST score	458
E value	2.0e-45
Match length	150
% identity	61
NCBI Description	(Z83246) predicted using Genefinder; cDNA EST EMBL:M79771 comes from this gene [Caenorhabditis elegans]

Seq. No.	275324
Contig ID	58313_1.R1011
5'-most EST	uC-zmf1b73256d03b1
Method	BLASTX
NCBI GI	g1352681
BLAST score	186
E value	9.0e-14
Match length	65
% identity	54
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	275325
Contig ID	58334_1.R1011
5'-most EST	uC-zmroteosinte091a11b2
Method	BLASTX
NCBI GI	g1174740
BLAST score	1151
E value	1.0e-134
Match length	436
% identity	58
NCBI Description	DNA TOPOISOMERASE II >gi_2129576_pir__S53599 DNA topoisomerase II - Arabidopsis thaliana >gi_474890 (L21015) topoisomerase II [Arabidopsis thaliana]

Seq. No.	275326
Contig ID	58334_2.R1011
5'-most EST	uC-zmf1B73006c04b1
Method	BLASTX
NCBI GI	g1174740
BLAST score	317
E value	5.0e-29
Match length	179
% identity	39
NCBI Description	DNA TOPOISOMERASE II >gi_2129576_pir__S53599 DNA topoisomerase II - Arabidopsis thaliana >gi_474890 (L21015) topoisomerase II [Arabidopsis thaliana]

Seq. No.	275327
Contig ID	58345_1.R1011
5'-most EST	LIB3059-033-Q1-K1-B1

Seq. No.	275328
Contig ID	58352_1.R1011
5'-most EST	uC-zmrob73019d02b1
Method	BLASTX
NCBI GI	g4220480
BLAST score	789
E value	7.0e-84
Match length	444
% identity	41
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	275329
Contig ID	58368_1.R1011
5'-most EST	LIB3059-033-Q1-K1-D4
Method	BLASTX
NCBI GI	g4102600
BLAST score	466
E value	1.0e-46
Match length	145
% identity	63
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	275330
Contig ID	58393_1.R1011
5'-most EST	uC-zmflb73019f07a1

Seq. No.	275331
Contig ID	58404_1.R1011
5'-most EST	LIB3061-005-Q1-K1-F6

Seq. No.	275332
Contig ID	58420_1.R1011
5'-most EST	nbm700475478.h1

Seq. No.	275333
Contig ID	58424_1.R1011
5'-most EST	hbs701185927.h1

Seq. No.	275334
Contig ID	58453_1.R1011
5'-most EST	wyr700235340.h1
Method	BLASTX
NCBI GI	g3687245
BLAST score	386
E value	3.0e-37
Match length	104
% identity	71
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	275335
Contig ID	58461_1.R1011
5'-most EST	yyf700349407.h1
Method	BLASTX
NCBI GI	g3021512
BLAST score	1654
E value	0.0e+00

Match length	360
% identity	86
NCBI Description	(X96728) isocitrate dehydrogenase (NADP+) [Nicotiana tabacum]

Seq. No.	275336
Contig ID	58471_1.R1011
5'-most EST	LIB3059-034-Q1-K1-H10
Method	BLASTX
NCBI GI	g112785
BLAST score	370
E value	4.0e-35
Match length	170
% identity	40
NCBI Description	DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1 3-methyladenine DNA glycosylase (EC 3.2.2.-) I - Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa 1-187) [Escherichia coli] >gi_147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432) 3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

Seq. No.	275337
Contig ID	58478_1.R1011
5'-most EST	LIB3059-034-Q1-K1-H8
Method	BLASTX
NCBI GI	g3183991
BLAST score	301
E value	7.0e-48
Match length	202
% identity	55
NCBI Description	(AJ005173) P69F protein [Lycopersicon esculentum]

Seq. No.	275338
Contig ID	58491_1.R1011
5'-most EST	uC-zmflmo17340a07b1

Seq. No.	275339
Contig ID	58491_2.R1011
5'-most EST	uC-zmflb73239g09b2

Seq. No.	275340
Contig ID	58497_1.R1011
5'-most EST	yyf70352546.h1
Method	BLASTX
NCBI GI	g2827529
BLAST score	599
E value	3.0e-76
Match length	351
% identity	44
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]

Seq. No.	275341
Contig ID	58499_1.R1011

5'-most EST	cat700018479.r1
Seq. No.	275342
Contig ID	58501_1.R1011
5'-most EST	rvl700457272.h1
Seq. No.	275343
Contig ID	58523_1.R1011
5'-most EST	uC-zmroB73017a06b1
Method	BLASTX
NCBI GI	g3176690
BLAST score	347
E value	1.0e-32
Match length	166
% identity	47
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]
Seq. No.	275344
Contig ID	58536_1.R1011
5'-most EST	LIB3059-035-Q1-K1-F8
Method	BLASTX
NCBI GI	g1076486
BLAST score	368
E value	3.0e-35
Match length	116
% identity	59
NCBI Description	cim1 protein - soybean >gi_555616 (U03860) cytokinin induced message [Glycine max]
Seq. No.	275345
Contig ID	58542_1.R1011
5'-most EST	uC-zmflb73221h10b1
Method	BLASTN
NCBI GI	g2995254
BLAST score	88
E value	1.0e-41
Match length	291
% identity	88
NCBI Description	Hordeum vulgare mRNA for hypothetical protein
Seq. No.	275346
Contig ID	58556_1.R1011
5'-most EST	LIB3059-036-Q1-K1-A12
Method	BLASTX
NCBI GI	g3600033
BLAST score	417
E value	6.0e-41
Match length	141
% identity	59
NCBI Description	(AF080119) contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana]
Seq. No.	275347
Contig ID	58581_1.R1011

5'-most EST	xmt700260882.h1
Seq. No.	275348
Contig ID	58594_1.R1011
5'-most EST	LIB3059-036-Q1-K1-E8
Seq. No.	275349
Contig ID	58613_1.R1011
5'-most EST	LIB3059-036-Q1-K1-G8
Seq. No.	275350
Contig ID	58627_1.R1011
5'-most EST	LIB3059-037-Q1-K1-A11
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	275351
Contig ID	58647_1.R1011
5'-most EST	uC-zmflmo17158d02b1
Method	BLASTX
NCBI GI	g3183991
BLAST score	858
E value	4.0e-92
Match length	412
% identity	45
NCBI Description	(AJ005173) P69F protein [Lycopersicon esculentum]
Seq. No.	275352
Contig ID	58649_1.R1011
5'-most EST	wen700336171.h1
Method	BLASTX
NCBI GI	g3860008
BLAST score	566
E value	7.0e-58
Match length	164
% identity	59
NCBI Description	(AF091085) unknown [Homo sapiens]
Seq. No.	275353
Contig ID	58662_1.R1011
5'-most EST	wyr700239186.h1
Seq. No.	275354
Contig ID	58663_1.R1011
5'-most EST	uer700583183.h1
Seq. No.	275355
Contig ID	58665_1.R1011
5'-most EST	LIB3059-037-Q1-K1-E11
Method	BLASTX
NCBI GI	g4493897
BLAST score	359

E value	8.0e-34
Match length	236
% identity	39
NCBI Description	(AL034558) predicted using hexExon; MAL3P2.19 (PFC0250c), AP endonuclease, len: 639 aa; Similarity to nucleases. B.subtilus exodeoxyribonuclease (SW:EXOA_BACSU) BLAST Score: 200, sum P(3) = 1.8e-25; 32% identity in 186 aa ove

Seq. No.	275356
Contig ID	58666_1.R1011
5'-most EST	LIB3059-037-Q1-K1-E12
Method	BLASTX
NCBI GI	g4220489
BLAST score	424
E value	9.0e-42
Match length	120
% identity	64
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275357
Contig ID	58671_1.R1011
5'-most EST	LIB3137-001-Q1-K1-A12
Method	BLASTX
NCBI GI	g2245020
BLAST score	666
E value	2.0e-69
Match length	389
% identity	39
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	275358
Contig ID	58674_1.R1011
5'-most EST	rvt700548926.h1

Seq. No.	275359
Contig ID	58677_1.R1011
5'-most EST	vux700157834.h1
Method	BLASTX
NCBI GI	g3282239
BLAST score	251
E value	5.0e-21
Match length	162
% identity	36
NCBI Description	(U88966) rapamycin associated protein FRAP2 [Homo sapiens]

Seq. No.	275360
Contig ID	58692_1.R1011
5'-most EST	LIB3059-037-Q1-K1-H12

Seq. No.	275361
Contig ID	58701_1.R1011
5'-most EST	LIB3066-052-Q1-K1-D12
Method	BLASTX
NCBI GI	g1076498
BLAST score	200
E value	9.0e-15
Match length	108

% identity	44
NCBI Description	zinc-finger protein (C-terminal) - soybean >gi_558543_emb_CAA85320_ (Z36749) C-terminal zinc-finger [Glycine max]

Seq. No.	275362
Contig ID	58716_1.R1011
5'-most EST	LIB3059-038-Q1-K1-C1
Method	BLASTX
NCBI GI	g4336606
BLAST score	782
E value	2.0e-83
Match length	185
% identity	84
NCBI Description	(AF099110) sigma factor; Sig1 [Zea mays]

Seq. No.	275363
Contig ID	58730_1.R1011
5'-most EST	cyk700048007.f1
Method	BLASTX
NCBI GI	g2649424
BLAST score	168
E value	9.0e-12
Match length	99
% identity	37
NCBI Description	(AE001023) A. fulgidus predicted coding region AF1178 [Archaeoglobus fulgidus]

Seq. No.	275364
Contig ID	58767_1.R1011
5'-most EST	xsy700209355.h1

Seq. No.	275365
Contig ID	58791_1.R1011
5'-most EST	LIB3059-039-Q1-K1-C4
Method	BLASTX
NCBI GI	g2129580
BLAST score	266
E value	3.0e-23
Match length	91
% identity	55
NCBI Description	envelope Ca2+-ATPase precursor - Arabidopsis thaliana >gi_493622_dbj_BAA03090_ (D13983) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana] >gi_4176435_emb_CAA49559_ (X69941) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	275366
Contig ID	58801_1.R1011
5'-most EST	xmt700265629.h1
Method	BLASTX
NCBI GI	g3776007
BLAST score	494
E value	1.0e-49
Match length	194
% identity	54
NCBI Description	(AJ010467) RNA helicase [Arabidopsis thaliana]

Seq. No.	275367
Contig ID	58811_1.R1011
5'-most EST	LIB3061-049-Q1-K1-B4
Method	BLASTX
NCBI GI	g2244899
BLAST score	1034
E value	1.0e-113
Match length	308
% identity	60
NCBI Description	(Z97338) similar to UFD1 protein [Arabidopsis thaliana]

Seq. No.	275368
Contig ID	58813_1.R1011
5'-most EST	nwy700445630.h1

Seq. No.	275369
Contig ID	58828_1.R1011
5'-most EST	LIB3059-039-Q1-K1-H12

Seq. No.	275370
Contig ID	58829_1.R1011
5'-most EST	LIB3067-052-Q1-K1-F6
Method	BLASTX
NCBI GI	g2129550
BLAST score	266
E value	1.0e-22
Match length	85
% identity	58
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	275371
Contig ID	58836_1.R1011
5'-most EST	uC-zmflb73294c07b1
Method	BLASTX
NCBI GI	g3876473
BLAST score	176
E value	3.0e-12
Match length	133
% identity	29
NCBI Description	(Z72508) F28H7.4 [Caenorhabditis elegans]

Seq. No.	275372
Contig ID	58863_1.R1011
5'-most EST	uC-zmflb73276e11b1
Method	BLASTX
NCBI GI	g1170471
BLAST score	145
E value	1.0e-08
Match length	66

% identity	38
NCBI Description	APOPTOSIS INHIBITOR 3 (IAP-3) >gi_625582_pir__A53989 apoptosis-inhibiting protein - Orgyia pseudotsugata nuclear polyhedrosis virus OpMNPV >gi_456114 (L22564) iap gene product [Orgyia pseudotsugata nuclear polyhedrosis virus] >gi_1911281 (U75930) inhibitor of apoptosis protein 3 [Orgyia pseudotsugata nuclear polyhedrosis virus]

Seq. No.	275373
Contig ID	58867_1.R1011
5'-most EST	LIB3059-040-Q1-K1-E12
Method	BLASTX
NCBI GI	g4587567
BLAST score	184
E value	2.0e-13
Match length	83
% identity	43
NCBI Description	(AC006550) F10O3.7 [Arabidopsis thaliana]

Seq. No.	275374
Contig ID	58874_2.R1011
5'-most EST	xmt700267465.h1
Method	BLASTX
NCBI GI	g2809251
BLAST score	457
E value	2.0e-45
Match length	170
% identity	48
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No.	275375
Contig ID	58930_1.R1011
5'-most EST	uC-zmflm017207h11b1
Method	BLASTX
NCBI GI	g3193285
BLAST score	146
E value	8.0e-09
Match length	96
% identity	32
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	275376
Contig ID	58930_2.R1011
5'-most EST	LIB3060-029-Q1-K1-H2

Seq. No.	275377
Contig ID	58949_1.R1011
5'-most EST	fwa700097396.h1

Seq. No.	275378
Contig ID	58957_1.R1011
5'-most EST	uC-zmflb73208b02a2
Method	BLASTX
NCBI GI	g2224913
BLAST score	540
E value	6.0e-55
Match length	141

% identity	66
NCBI Description	(U95967) beta-expansin [Arabidopsis thaliana]

Seq. No.	275379
Contig ID	58989_1.R1011
5'-most EST	uC-zmflmo17129b06b1
Method	BLASTX
NCBI GI	g4559388
BLAST score	425
E value	8.0e-42
Match length	162
% identity	52
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275380
Contig ID	59001_1.R1011
5'-most EST	gct701178965.h1

Seq. No.	275381
Contig ID	59002_1.R1011
5'-most EST	ceu700433248.h1
Method	BLASTX
NCBI GI	g2335100
BLAST score	393
E value	4.0e-38
Match length	152
% identity	49
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	275382
Contig ID	59011_1.R1011
5'-most EST	uwc700153481.h1
Method	BLASTX
NCBI GI	g4467128
BLAST score	1080
E value	1.0e-118
Match length	422
% identity	51
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	275383
Contig ID	59011_2.R1011
5'-most EST	rvl700457253.h1
Method	BLASTX
NCBI GI	g4501901
BLAST score	196
E value	7.0e-15
Match length	60
% identity	57
NCBI Description	aminoacylase 1 >gi_461466_sp_Q03154_ACY1_HUMAN AMINOACYLASE-1 (N-ACYL-L-AMINO-ACID AMIDOHYDROLASE) (ACY-1) >gi_1082202_pir__A47488 aminoacylase (EC 3.5.1.14) - human >gi_178071 (L07548) aminoacylase-1 [Homo sapiens] >gi_285903_dbj_BAA03397_ (D14524) aminoacylase-1 [Homo sapiens] >gi_303595_dbj_BAA03814_ (D16307) 45kDa protein [Homo sapiens]

Seq. No.	275384
Contig ID	59014_1.R1011
5'-most EST	LIB3059-042-Q1-K1-F11
Method	BLASTX
NCBI GI	g3551249
BLAST score	201
E value	2.0e-15
Match length	180
% identity	32
NCBI Description	(AB012704) 184 [Daucus carota]

Seq. No.	275385
Contig ID	59020_1.R1011
5'-most EST	ntr700076005.h1
Method	BLASTX
NCBI GI	g4587516
BLAST score	586
E value	2.0e-60
Match length	191
% identity	57
NCBI Description	(AC007060) Strong similarity to gb_U80583 proteinase TMP from Lycopersicon esculentum and is a member of the PF_00082 subtilase family. [Arabidopsis thaliana]

Seq. No.	275386
Contig ID	59026_1.R1011
5'-most EST	LIB3059-042-Q1-K1-G5
Method	BLASTX
NCBI GI	g2344901
BLAST score	258
E value	4.0e-36
Match length	190
% identity	50
NCBI Description	(AC002388) serine/threonine protein kinase isolog [Arabidopsis thaliana]

Seq. No.	275387
Contig ID	59028_1.R1011
5'-most EST	uC-zmrob73004d12b1

Seq. No.	275388
Contig ID	59028_2.R1011
5'-most EST	LIB3059-042-Q1-K1-G9

Seq. No.	275389
Contig ID	59029_1.R1011
5'-most EST	LIB3059-042-Q1-K1-H1

Seq. No.	275390
Contig ID	59035_1.R1011
5'-most EST	LIB3067-026-Q1-K1-D7

Seq. No.	275391
Contig ID	59060_1.R1011
5'-most EST	hvj700622456.h1

Seq. No.	275392

Contig ID	59063_1.R1011
5'-most EST	uC-zmflB73047h08b1
Method	BLASTX
NCBI GI	g4505727
BLAST score	231
E value	1.0e-18
Match length	274
% identity	30
NCBI Description	peroxisomal biogenesis factor 3 >gi_3914303_sp_P56589_PEX3_HUMAN PEROXISOMAL ASSEMBLY PROTEIN PEX3 (PEROXIN-3) >gi_3336882_emb_CAA04879_ (AJ001625) Pex3 protein [Homo sapiens] >gi_4092648_emb_CAA10362_ (AJ131389) PEX3 protein [Homo sapiens] >gi_4218426_emb_CAA08904_ (AJ009866) Pex3p [Homo sapiens]

Seq. No.	275393
Contig ID	59072_1.R1011
5'-most EST	LIB3059-043-Q1-K1-D12

Seq. No.	275394
Contig ID	59078_1.R1011
5'-most EST	wty700169885.h1

Seq. No.	275395
Contig ID	59112_1.R1011
5'-most EST	nbm700472369.h1

Seq. No.	275396
Contig ID	59124_1.R1011
5'-most EST	yyf700350973.h1

Seq. No.	275397
Contig ID	59129_1.R1011
5'-most EST	tzu700204922.h1
Method	BLASTX
NCBI GI	g3023535
BLAST score	1326
E value	1.0e-147
Match length	335
% identity	73
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX2 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX2) >gi_662871_emb_CAA88107_ (Z48047) Cnx2 [Arabidopsis thaliana]

Seq. No.	275398
Contig ID	59133_1.R1011
5'-most EST	tfd700572566.h1

Seq. No.	275399
Contig ID	59176_1.R1011
5'-most EST	uC-zmroteosinte040d08b1
Method	BLASTX
NCBI GI	g4585981
BLAST score	503
E value	4.0e-54
Match length	226

% identity	54
NCBI Description	(AC005287) similar to Na+/H+-exchanging proteins [Arabidopsis thaliana]

Seq. No.	275400
Contig ID	59188_1.R1011
5'-most EST	LIB36-020-Q1-E1-A12
Method	BLASTX
NCBI GI	g3025188
BLAST score	365
E value	1.0e-34
Match length	107
% identity	62
NCBI Description	HYPOTHETICAL 11.9 KD PROTEIN SLR1846 >gi_1652154_dbj_BAA17078_ (D90903) hypothetical protein [Synechocystis sp.]

Seq. No.	275401
Contig ID	59188_2.R1011
5'-most EST	gct701168678.h1

Seq. No.	275402
Contig ID	59198_1.R1011
5'-most EST	LIB3059-045-Q1-K1-B1

Seq. No.	275403
Contig ID	59203_1.R1011
5'-most EST	uC-zmflm017207c06b1
Method	BLASTX
NCBI GI	g1495768
BLAST score	887
E value	3.0e-95
Match length	298
% identity	59
NCBI Description	(Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No.	275404
Contig ID	59205_1.R1011
5'-most EST	LIB3059-045-Q1-K1-B8

Seq. No.	275405
Contig ID	59229_1.R1011
5'-most EST	uC-zmflMo17016c09b1

Seq. No.	275406
Contig ID	59231_1.R1011
5'-most EST	LIB3059-045-Q1-K1-E5

Seq. No.	275407
Contig ID	59234_1.R1011
5'-most EST	LIB3059-045-Q1-K1-E8
Method	BLASTX
NCBI GI	g3157950
BLAST score	293
E value	3.0e-26
Match length	175

% identity	45
NCBI Description	(AC002131) Contains similarity to hypothetical protein C18b11.05 gb_Z50728 from S. pombe. EST gb_H76601 comes from this gene. [Arabidopsis thaliana]

Seq. No.	275408
Contig ID	59241_1.R1011
5'-most EST	LIB3059-045-Q1-K1-F3
Method	BLASTX
NCBI GI	g4586030
BLAST score	173
E value	3.0e-12
Match length	62
% identity	56
NCBI Description	(AC007109) unknown protein [Arabidopsis thaliana]

Seq. No.	275409
Contig ID	59271_1.R1011
5'-most EST	LIB3059-046-Q1-K1-A8
Method	BLASTX
NCBI GI	g4262186
BLAST score	413
E value	2.0e-40
Match length	94
% identity	87
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	275410
Contig ID	59272_1.R1011
5'-most EST	LIB36-015-Q1-E1-H10
Method	BLASTX
NCBI GI	g2244765
BLAST score	168
E value	2.0e-11
Match length	64
% identity	53
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275411
Contig ID	59299_1.R1011
5'-most EST	LIB3059-046-Q1-K1-D5

Seq. No.	275412
Contig ID	59313_1.R1011
5'-most EST	uC-zmflmo17180e03a1

Seq. No.	275413
Contig ID	59323_1.R1011
5'-most EST	xsy700211381.h1
Method	BLASTX
NCBI GI	g4206122
BLAST score	1527
E value	1.0e-170
Match length	398
% identity	72
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No.	275414
Contig ID	59323_2.R1011
5'-most EST	uC-zmflb73264d12b1

Seq. No.	275415
Contig ID	59323_3.R1011
5'-most EST	LIB3062-020-Q1-K1-D7
Method	BLASTX
NCBI GI	g4206122
BLAST score	295
E value	2.0e-26
Match length	87
% identity	67
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	275416
Contig ID	59323_4.R1011
5'-most EST	uC-zmflb73236g02b1

Seq. No.	275417
Contig ID	59323_5.R1011
5'-most EST	LIB3061-038-Q1-K1-E2

Seq. No.	275418
Contig ID	59323_6.R1011
5'-most EST	uC-zmflmo17122c08b1
Method	BLASTX
NCBI GI	g4206122
BLAST score	244
E value	2.0e-20
Match length	72
% identity	68
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	275419
Contig ID	59323_7.R1011
5'-most EST	LIB84-024-Q1-E1-F9

Seq. No.	275420
Contig ID	59325_1.R1011
5'-most EST	LIB3059-046-Q1-K1-G3
Method	BLASTX
NCBI GI	g3047114
BLAST score	360
E value	6.0e-34
Match length	228
% identity	39
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	275421
Contig ID	59327_1.R1011
5'-most EST	LIB3059-046-Q1-K1-G6

Seq. No.	275422
Contig ID	59345_1.R1011
5'-most EST	ypc700802379.h1
Method	BLASTX
NCBI GI	g3377850
BLAST score	296
E value	2.0e-26
Match length	78
% identity	73
NCBI Description	(AF076274) contains simlarity to Canis familiaris signal peptidase complex 25 kDa subunit (GB:U12687) [Arabidopsis thaliana]

Seq. No.	275423
Contig ID	59354_1.R1011
5'-most EST	LIB3059-047-Q1-K1-B6
Method	BLASTX
NCBI GI	g2443329
BLAST score	494
E value	1.0e-49
Match length	119
% identity	76
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	275424
Contig ID	59357_1.R1011
5'-most EST	LIB3059-047-Q1-K1-C1

Seq. No.	275425
Contig ID	59366_1.R1011
5'-most EST	LIB3059-047-Q1-K1-C8
Method	BLASTX
NCBI GI	g3080443
BLAST score	374
E value	1.0e-35
Match length	191
% identity	45
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	275426
Contig ID	59368_1.R1011
5'-most EST	fwa700100640.h1
Method	BLASTX
NCBI GI	g4455800
BLAST score	369
E value	8.0e-35
Match length	218
% identity	41
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	275427
Contig ID	59383_1.R1011
5'-most EST	LIB3059-047-Q1-K1-E5
Method	BLASTX
NCBI GI	g4567251
BLAST score	393
E value	7.0e-38

Match length	196
% identity	48
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	275428
Contig ID	59405_1.R1011
5'-most EST	ntr700071986.h1

Seq. No.	275429
Contig ID	59406_2.R1011
5'-most EST	cat700017145.r1
Method	BLASTX
NCBI GI	g2245378
BLAST score	164
E value	3.0e-11
Match length	45
% identity	64
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	275430
Contig ID	59419_1.R1011
5'-most EST	LIB3069-002-Q1-K1-D9

Seq. No.	275431
Contig ID	59429_1.R1011
5'-most EST	zuv700355329.h1

Seq. No.	275432
Contig ID	59439_1.R1011
5'-most EST	pmx700086836.h1

Seq. No.	275433
Contig ID	59486_1.R1011
5'-most EST	ymt700222775.h1
Method	BLASTX
NCBI GI	g3776003
BLAST score	396
E value	5.0e-38
Match length	166
% identity	51
NCBI Description	(AJ010465) RNA helicase [Arabidopsis thaliana]

Seq. No.	275434
Contig ID	59494_1.R1011
5'-most EST	LIB3059-048-Q1-K1-H6
Method	BLASTX
NCBI GI	g4164408
BLAST score	617
E value	4.0e-64
Match length	227
% identity	51
NCBI Description	(AJ132228) amino acid carrier [Ricinus communis]

Seq. No.	275435
Contig ID	59497_1.R1011
5'-most EST	LIB3137-033-Q1-K1-H6
Method	BLASTX

NCBI GI	g1723513
BLAST score	165
E value	7.0e-11
Match length	238
% identity	27
NCBI Description	HYPOTHETICAL 63.9 KD PROTEIN C1F12.09 IN CHROMOSOME I >gi_2130242_pir__S67452 hypothetical protein - fission yeast (Schizosaccharomyces pombe) >gi_1217983_emb_CAA93813_ (Z69944) unknown [Schizosaccharomyces pombe]

Seq. No.	275436
Contig ID	59509_1.R1011
5'-most EST	zuv700357139.h1

Seq. No.	275437
Contig ID	59526_1.R1011
5'-most EST	uC-zmroteosinte057e10b1
Method	BLASTN
NCBI GI	g3046847
BLAST score	38
E value	1.0e-11
Match length	78
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	275438
Contig ID	59528_1.R1011
5'-most EST	LIB3059-049-Q1-K1-D12

Seq. No.	275439
Contig ID	59532_1.R1011
5'-most EST	LIB3059-049-Q1-K1-D5

Seq. No.	275440
Contig ID	59534_1.R1011
5'-most EST	tzu700205625.h1
Method	BLASTX
NCBI GI	g1731078
BLAST score	323
E value	2.0e-29
Match length	195
% identity	38
NCBI Description	HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION >gi_1303968_dbj_BAA12623_ (D84432) YqjQ [Bacillus subtilis] >gi_2634813_emb_CAB14310_ (Z99116) similar to ketoacyl reductase [Bacillus subtilis]

Seq. No.	275441
Contig ID	59549_1.R1011
5'-most EST	LIB84-029-Q1-E1-E12

Seq. No.	275442
Contig ID	59549_2.R1011
5'-most EST	LIB36-013-Q1-E1-E5

Seq. No.	275443

Contig ID	59555_1.R1011
5'-most EST	LIB3059-049-Q1-K1-G3
Method	BLASTX
NCBI GI	g1360090
BLAST score	400
E value	6.0e-39
Match length	144
% identity	52
NCBI Description	(X95576) C1C-Nt1 [Nicotiana tabacum]

Seq. No.	275444
Contig ID	59563_1.R1011
5'-most EST	qmh700026647.f1

Seq. No.	275445
Contig ID	59569_1.R1011
5'-most EST	gct701169216.h1

Seq. No.	275446
Contig ID	59569_2.R1011
5'-most EST	uC-zmflmo17174c12a1

Seq. No.	275447
Contig ID	59596_1.R1011
5'-most EST	LIB3137-023-Q1-K1-D6

Seq. No.	275448
Contig ID	59598_1.R1011
5'-most EST	gct701177976.h1

Seq. No.	275449
Contig ID	59605_1.R1011
5'-most EST	LIB3059-052-Q1-K1-D9

Seq. No.	275450
Contig ID	59629_1.R1011
5'-most EST	wen700332674.h1
Method	BLASTX
NCBI GI	g479413
BLAST score	319
E value	3.0e-29
Match length	182
% identity	40
NCBI Description	myosin-like protein - Arabidopsis thaliana

Seq. No.	275451
Contig ID	59629_2.R1011
5'-most EST	LIB3059-052-Q1-K1-G4
Method	BLASTX
NCBI GI	g2129651
BLAST score	195
E value	5.0e-15
Match length	94
% identity	50
NCBI Description	myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis thaliana]

Seq. No.	275452
Contig ID	59635_1.R1011
5'-most EST	LIB3059-052-Q1-K1-H1
Method	BLASTX
NCBI GI	g4335745
BLAST score	220
E value	1.0e-17
Match length	132
% identity	39
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	275453
Contig ID	59641_1.R1011
5'-most EST	uC-zmflmo17050e09b2

Seq. No.	275454
Contig ID	59656_1.R1011
5'-most EST	uC-zmflb73193c02a1

Seq. No.	275455
Contig ID	59661_1.R1011
5'-most EST	LIB3059-053-Q1-K1-C10
Method	BLASTX
NCBI GI	g2130033
BLAST score	166
E value	1.0e-11
Match length	112
% identity	33
NCBI Description	D-hordein precursor - barley

Seq. No.	275456
Contig ID	59664_1.R1011
5'-most EST	ymt700222803.h1

Seq. No.	275457
Contig ID	59675_1.R1011
5'-most EST	LIB3068-013-Q1-K1-D12

Seq. No.	275458
Contig ID	59675_2.R1011
5'-most EST	xyt700346944.h1
Method	BLASTX
NCBI GI	g4567278
BLAST score	1337
E value	1.0e-148
Match length	420
% identity	73
NCBI Description	(AC006841) putative anthracycline associated resistance ARX protein [Arabidopsis thaliana]

Seq. No.	275459
Contig ID	59681_1.R1011
5'-most EST	vux700159922.h1

Seq. No.	275460
Contig ID	59683_1.R1011
5'-most EST	LIB3067-017-Q1-K1-E1
Method	BLASTX
NCBI GI	g4455213
BLAST score	555
E value	6.0e-57
Match length	134
% identity	78
NCBI Description	(AL035440) glutamine amidotransferase/cyclase [Arabidopsis thaliana]

Seq. No.	275461
Contig ID	59683_2.R1011
5'-most EST	qmh700028907.f1
Method	BLASTX
NCBI GI	g4455213
BLAST score	816
E value	1.0e-87
Match length	191
% identity	82
NCBI Description	(AL035440) glutamine amidotransferase/cyclase [Arabidopsis thaliana]

Seq. No.	275462
Contig ID	59686_1.R1011
5'-most EST	LIB83-013-Q1-E1-C6
Method	BLASTX
NCBI GI	g3668091
BLAST score	227
E value	1.0e-18
Match length	148
% identity	5
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275463
Contig ID	59689_1.R1011
5'-most EST	LIB3062-053-Q1-K1-A12

Seq. No.	275464
Contig ID	59697_1.R1011
5'-most EST	LIB3059-053-Q1-K1-F7

Seq. No.	275465
Contig ID	59713_1.R1011
5'-most EST	hbs701185202.h1
Method	BLASTX
NCBI GI	g4519671
BLAST score	188
E value	4.0e-14
Match length	66
% identity	59
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	275466
Contig ID	59716_1.R1011
5'-most EST	LIB3059-054-Q1-K1-A7

Seq. No.	275467
Contig ID	59731_1.R1011
5'-most EST	uC-zmflb73196e02b1
Method	BLASTX
NCBI GI	g3560143
BLAST score	263
E value	1.0e-22
Match length	163
% identity	39
NCBI Description	(AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces pombe]

Seq. No.	275468
Contig ID	59731_2.R1011
5'-most EST	nwy700445945.h1

Seq. No.	275469
Contig ID	59731_3.R1011
5'-most EST	LIB3059-054-Q1-K1-C6

Seq. No.	275470
Contig ID	59735_1.R1011
5'-most EST	xjt700092633.h1
Method	BLASTX
NCBI GI	g4510341
BLAST score	485
E value	1.0e-48
Match length	251
% identity	33
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	275471
Contig ID	59737_1.R1011
5'-most EST	wyr700236914.h1
Method	BLASTX
NCBI GI	g122085
BLAST score	458
E value	6.0e-46
Match length	93
% identity	100
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3

homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	275472
Contig ID	59742_1.R1011
5'-most EST	uC-zmflmo17097h04b1
Method	BLASTX
NCBI GI	g3335336
BLAST score	297
E value	1.0e-26
Match length	121
% identity	51
NCBI Description	(AC004512) Contains similarity to DnaJ gene YM8520.10 gb_825566 from from S. cerevisiae cosmid gb_Z49705. ESTs gb_Z47720 and gb_Z29879 come from this gene. [Arabidopsis thaliana]

Seq. No.	275473
Contig ID	59745_1.R1011
5'-most EST	uC-zmroteosinte018e12b1
Method	BLASTX
NCBI GI	g4586056
BLAST score	384
E value	1.0e-36
Match length	227
% identity	40
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	275474
Contig ID	59768_1.R1011
5'-most EST	LIB3136-052-Q1-K1-A8

Seq. No.	275475
Contig ID	59776_1.R1011
5'-most EST	ypc700805464.h1
Method	BLASTX
NCBI GI	g3738331
BLAST score	145
E value	6.0e-09
Match length	45
% identity	56
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	275476
Contig ID	59776_3.R1011
5'-most EST	uC-zmflmo17428c03a1

Seq. No.	275477
Contig ID	59789_1.R1011
5'-most EST	pmx700091624.h1
Method	BLASTX

NCBI GI	g3176664
BLAST score	229
E value	1.0e-18
Match length	168
% identity	37
NCBI Description	(AC004393) Contains similarity to beta scruin gb_Z47541 from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955 come from this gene. [Arabidopsis thaliana]

Seq. No.	275478
Contig ID	59792_1.R1011
5'-most EST	vux700158922.h1

Seq. No.	275479
Contig ID	59806_1.R1011
5'-most EST	vvh700281866.h2

Seq. No.	275480
Contig ID	59807_1.R1011
5'-most EST	rvl700454405.h1

Seq. No.	275481
Contig ID	59838_1.R1011
5'-most EST	uer700580330.h1
Method	BLASTX
NCBI GI	g3128208
BLAST score	190
E value	2.0e-16
Match length	142
% identity	41
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275482
Contig ID	59865_1.R1011
5'-most EST	pmx700086342.h1
Method	BLASTX
NCBI GI	g3875280
BLAST score	173
E value	7.0e-12
Match length	249
% identity	27
NCBI Description	(Z81051) cDNA EST yk500a3.3 comes from this gene; cDNA EST yk500a3.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	275483
Contig ID	59869_1.R1011
5'-most EST	LIB3062-031-Q1-K1-D11
Method	BLASTX
NCBI GI	g2914703
BLAST score	1326
E value	1.0e-147
Match length	403
% identity	62
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	275484
Contig ID	59880_1.R1011

5'-most EST	uC-zmflb73249d11b3
Method	BLASTX
NCBI GI	g4586114
BLAST score	262
E value	2.0e-22
Match length	108
% identity	46
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	275485
Contig ID	59894_1.R1011
5'-most EST	LIB3069-005-Q1-K1-C2
Method	BLASTX
NCBI GI	g3236247
BLAST score	1005
E value	1.0e-109
Match length	306
% identity	60
NCBI Description	(AC004684) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No.	275486
Contig ID	59897_1.R1011
5'-most EST	pmx700091581.h1
Method	BLASTX
NCBI GI	g3367591
BLAST score	623
E value	7.0e-65
Match length	163
% identity	73
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	275487
Contig ID	59898_1.R1011
5'-most EST	LIB3060-039-Q1-K1-G9
Method	BLASTX
NCBI GI	g4090884
BLAST score	602
E value	4.0e-64
Match length	237
% identity	53
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

Seq. No.	275488
Contig ID	59898_2.R1011
5'-most EST	xyt700346843.h1

Seq. No.	275489
Contig ID	59910_1.R1011
5'-most EST	LIB3059-057-Q1-K1-C1
Method	BLASTX
NCBI GI	g3335376
BLAST score	299
E value	8.0e-27
Match length	133
% identity	47
NCBI Description	(AC003028) putative ammonium transporter [Arabidopsis

thaliana]

Seq. No.	275490
Contig ID	59910_3.R1011
5'-most EST	cat700020050.r1

Seq. No.	275491
Contig ID	59931_1.R1011
5'-most EST	uC-zmromo17045e02a1

Seq. No.	275492
Contig ID	59944_1.R1011
5'-most EST	LIB3059-057-Q1-K1-F7
Method	BLASTX
NCBI GI	g2832898
BLAST score	706
E value	1.0e-74
Match length	185
% identity	71
NCBI Description	(AJ000886) Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]

Seq. No.	275493
Contig ID	59958_1.R1011
5'-most EST	pmx700088563.h1
Method	BLASTX
NCBI GI	g960291
BLAST score	696
E value	2.0e-73
Match length	165
% identity	81
NCBI Description	(L34344) anthranilate synthase alpha subunit [Ruta graveolens]

Seq. No.	275494
Contig ID	59971_1.R1011
5'-most EST	LIB3059-058-Q1-K1-B1

Seq. No.	275495
Contig ID	59979_1.R1011
5'-most EST	nbm700471307.h1
Method	BLASTX
NCBI GI	g2826786
BLAST score	391
E value	2.0e-37
Match length	195
% identity	48
NCBI Description	(Y10905) RAPB protein [Oryza sativa]

Seq. No.	275496
Contig ID	59979_2.R1011
5'-most EST	uC-zmflmo17246e12b1

Seq. No.	275497
Contig ID	59979_3.R1011
5'-most EST	uC-zmflm017233b08b1

Seq. No.	275498
Contig ID	59979_4.R1011
5'-most EST	uC-zmf1b73052h04b1

Seq. No.	275499
Contig ID	59994_1.R1011
5'-most EST	LIB3059-058-Q1-K1-D3

Seq. No.	275500
Contig ID	60015_1.R1011
5'-most EST	gw1700615039.h1
Method	BLASTX
NCBI GI	g4467124
BLAST score	177
E value	1.0e-12
Match length	205
% identity	23
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275501
Contig ID	60017_1.R1011
5'-most EST	LIB3059-058-Q1-K1-G11

Seq. No.	275502
Contig ID	60020_1.R1011
5'-most EST	LIB3059-058-Q1-K1-G3

Seq. No.	275503
Contig ID	60021_1.R1011
5'-most EST	ceu700422572.h1
Method	BLASTX
NCBI GI	g549638
BLAST score	375
E value	2.0e-35
Match length	289
% identity	35
NCBI Description	HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION >gi_539279_pir__S38159 hypothetical protein YKR081c - yeast (Saccharomyces cerevisiae) >gi_415901_emb_CAA81632_ (Z27116) ORF YKR401 [Saccharomyces cerevisiae] >gi_486561_emb_CAA82160_ (Z28306) ORF YKR081c [Saccharomyces cerevisiae]

Seq. No.	275504
Contig ID	60031_1.R1011
5'-most EST	LIB3068-050-Q1-K1-G4
Method	BLASTX
NCBI GI	g4115377
BLAST score	923
E value	1.0e-99
Match length	275
% identity	68
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	275505
Contig ID	60033_1.R1011
5'-most EST	dyk700102649.h1

Seq. No.	275506
Contig ID	60052_1.R1011
5'-most EST	LIB3059-059-Q1-K1-B9

Seq. No.	275507
Contig ID	60052_2.R1011
5'-most EST	uC-zmrob73054a12a1

Seq. No.	275508
Contig ID	60081_1.R1011
5'-most EST	uC-zmflmo17113b04b1
Method	BLASTX
NCBI GI	g2947062
BLAST score	412
E value	2.0e-39
Match length	552
% identity	30
NCBI Description	(AC002521) unknown protein [Arabidopsis thaliana]

Seq. No.	275509
Contig ID	60084_1.R1011
5'-most EST	uer700582983.h1
Method	BLASTX
NCBI GI	g1362112
BLAST score	585
E value	2.0e-60
Match length	181
% identity	59
NCBI Description	protein kinase NPK2 (EC 2.7.1.-) - common tobacco >gi_862342_dbj_BAA06731_ (D31964) NPK2 [Nicotiana tabacum]

Seq. No.	275510
Contig ID	60086_1.R1011
5'-most EST	ceu700431113.h1
Method	BLASTX
NCBI GI	g1350548
BLAST score	224
E value	3.0e-18
Match length	78
% identity	60
NCBI Description	(L47609) heat shock-like protein [Picea glauca]

Seq. No.	275511
Contig ID	60098_1.R1011
5'-most EST	xjt700092817.h1
Method	BLASTX
NCBI GI	g3063453
BLAST score	576
E value	3.0e-59
Match length	136
% identity	85
NCBI Description	(AC003981) F22O13.15 [Arabidopsis thaliana]

Seq. No.	275512
Contig ID	60098_2.R1011
5'-most EST	LIB3059-059-Q1-K1-G7

Method	BLASTX
NCBI GI	g3063453
BLAST score	535
E value	1.0e-54
Match length	177
% identity	67
NCBI Description	(AC003981) F22O13.15 [Arabidopsis thaliana]

Seq. No.	275513
Contig ID	60114_1.R1011
5'-most EST	cjh700193873.h1

Seq. No.	275514
Contig ID	60121_1.R1011
5'-most EST	hvj700621532.h1

Seq. No.	275515
Contig ID	60133_1.R1011
5'-most EST	nwy700444226.h1
Method	BLASTX
NCBI GI	g4510377
BLAST score	664
E value	1.0e-69
Match length	162
% identity	78
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	275516
Contig ID	60138_1.R1011
5'-most EST	fwa700101522.h1
Method	BLASTX
NCBI GI	g4335739
BLAST score	175
E value	9.0e-13
Match length	42
% identity	71
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275517
Contig ID	60150_1.R1011
5'-most EST	LIB3059-060-Q1-K1-E12

Seq. No.	275518
Contig ID	60157_1.R1011
5'-most EST	uC-zmflb73285f09a1
Method	BLASTX
NCBI GI	g4490341
BLAST score	272
E value	7.0e-24
Match length	54
% identity	91
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	275519
Contig ID	60158_1.R1011
5'-most EST	LIB83-007-Q1-E1-F7
Method	BLASTX

NCBI GI	g4262402
BLAST score	357
E value	6.0e-34
Match length	135
% identity	53
NCBI Description	(AF098976) E1-like protein [Pichia pastoris]

Seq. No.	275520
Contig ID	60180_1.R1011
5'-most EST	gct701176146.h1

Seq. No.	275521
Contig ID	60181_1.R1011
5'-most EST	uC-zmflb73028c10a1

Seq. No.	275522
Contig ID	60184_1.R1011
5'-most EST	ymt700220145.h1
Method	BLASTX
NCBI GI	g3941543
BLAST score	1419
E value	1.0e-158
Match length	368
% identity	73
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1) [Arabidopsis thaliana]

Seq. No.	275523
Contig ID	60200_1.R1011
5'-most EST	gct701178145.h1

Seq. No.	275524
Contig ID	60209_1.R1011
5'-most EST	LIB36-013-Q1-E1-B1
Method	BLASTX
NCBI GI	g2921304
BLAST score	167
E value	1.0e-11
Match length	85
% identity	47
NCBI Description	(AF033496) herbicide safener binding protein [Zea mays]

Seq. No.	275525
Contig ID	60219_1.R1011
5'-most EST	LIB3060-001-Q1-K2-C5
Method	BLASTX
NCBI GI	g2262111
BLAST score	274
E value	4.0e-24
Match length	98
% identity	59
NCBI Description	(AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]

Seq. No.	275526
Contig ID	60221_1.R1011

5'-most EST	uC-zmflb73225f09b1
Method	BLASTX
NCBI GI	g4558665
BLAST score	222
E value	6.0e-18
Match length	124
% identity	47
NCBI Description	(AC007063) putative white protein [Arabidopsis thaliana]

Seq. No.	275527
Contig ID	60225_1.R1011
5'-most EST	LIB3060-001-Q1-K2-D2
Method	BLASTX
NCBI GI	g2245136
BLAST score	2053
E value	0.0e+00
Match length	556
% identity	71
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	275528
Contig ID	60226_1.R1011
5'-most EST	LIB3060-001-Q1-K2-D3

Seq. No.	275529
Contig ID	60227_1.R1011
5'-most EST	xsy700217331.h1

Seq. No.	275530
Contig ID	60227_2.R1011
5'-most EST	LIB84-021-Q1-E1-C12

Seq. No.	275531
Contig ID	60231_1.R1011
5'-most EST	LIB3060-001-Q1-K2-D9
Method	BLASTX
NCBI GI	g2702273
BLAST score	312
E value	1.0e-28
Match length	117
% identity	50
NCBI Description	(AC003033) carrot B2 protein-like [Arabidopsis thaliana]

Seq. No.	275532
Contig ID	60234_1.R1011
5'-most EST	wyr700240001.h1
Method	BLASTX
NCBI GI	g3236237
BLAST score	743
E value	1.0e-78
Match length	262
% identity	56
NCBI Description	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]

Seq. No.	275533

Contig ID	60234_2.R1011
5'-most EST	cyk700051501.f1
Method	BLASTX
NCBI GI	g629592
BLAST score	192
E value	2.0e-14
Match length	65
% identity	60
NCBI Description	hypothetical protein - rape

Seq. No.	275534
Contig ID	60238_1.R1011
5'-most EST	uC-zmflb73174a05b1

Seq. No.	275535
Contig ID	60250_1.R1011
5'-most EST	uwc700151017.h1

Seq. No.	275536
Contig ID	60252_1.R1011
5'-most EST	LIB3060-001-Q1-K2-G3
Method	BLASTX
NCBI GI	g4263787
BLAST score	442
E value	6.0e-71
Match length	287
% identity	55
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	275537
Contig ID	60252_2.R1011
5'-most EST	uC-zmflMo17085g08b1
Method	BLASTX
NCBI GI	g4263787
BLAST score	160
E value	3.0e-10
Match length	43
% identity	74
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	275538
Contig ID	60252_3.R1011
5'-most EST	uC-zmflmo17031d04b1
Method	BLASTX
NCBI GI	g2245074
BLAST score	197
E value	1.0e-14
Match length	191
% identity	36
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275539
Contig ID	60257_1.R1011
5'-most EST	LIB3060-001-Q1-K2-G8
Method	BLASTX
NCBI GI	g82798
BLAST score	178

E value	6.0e-13
Match length	122
% identity	35
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) I 189K chain - fission yeast (Schizosaccharomyces pombe) >gi_4995_emb_CAA32887_ (X14783) nuc1 product, RNA polymerase I largest subunit (AA 1-1689) [Schizosaccharomyces pombe]

Seq. No.	275540
Contig ID	60260_1.R1011
5'-most EST	ntr700076531.h1

Seq. No.	275541
Contig ID	60260_2.R1011
5'-most EST	pwr700448637.h1

Seq. No.	275542
Contig ID	60275_1.R1011
5'-most EST	uC-zmflmo17241c09b1
Method	BLASTX
NCBI GI	g4522004
BLAST score	510
E value	1.0e-51
Match length	202
% identity	55
NCBI Description	(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]

Seq. No.	275543
Contig ID	60282_1.R1011
5'-most EST	uC-zmroteosinte070b02b1

Seq. No.	275544
Contig ID	60282_2.R1011
5'-most EST	nbm700477201.h1

Seq. No.	275545
Contig ID	60282_3.R1011
5'-most EST	nbm700469208.h1

Seq. No.	275546
Contig ID	60294_1.R1011
5'-most EST	LIB3060-002-Q1-K2-C5
Method	BLASTN
NCBI GI	g22372
BLAST score	90
E value	6.0e-43
Match length	113
% identity	96
NCBI Description	Maize Mu5 transposable element

Seq. No.	275547
Contig ID	60301_1.R1011
5'-most EST	xjt700094445.h1

Seq. No.	275548

Contig ID	60304_1.R1011
5'-most EST	LIB83-015-Q1-E1-A3
Method	BLASTX
NCBI GI	g2754849
BLAST score	1205
E value	1.0e-133
Match length	274
% identity	84
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	275549
Contig ID	60306_1.R1011
5'-most EST	fwa700097234.h1
Method	BLASTX
NCBI GI	g2129941
BLAST score	1686
E value	0.0e+00
Match length	463
% identity	70
NCBI Description	zeaxanthin epoxidase precursor - curled-leaved tobacco >gi_1370274_emb_CAA65048_ (X95732) zeaxanthin epoxidase [Nicotiana plumbaginifolia]

Seq. No.	275550
Contig ID	60306_2.R1011
5'-most EST	uer700580621.h1
Method	BLASTX
NCBI GI	g2129941
BLAST score	295
E value	9.0e-27
Match length	79
% identity	70
NCBI Description	zeaxanthin epoxidase precursor - curled-leaved tobacco >gi_1370274_emb_CAA65048_ (X95732) zeaxanthin epoxidase [Nicotiana plumbaginifolia]

Seq. No.	275551
Contig ID	60309_1.R1011
5'-most EST	LIB3069-039-Q1-K1-B10

Seq. No.	275552
Contig ID	60317_1.R1011
5'-most EST	uC-zmflb73221f09b1
Method	BLASTX
NCBI GI	g2827630
BLAST score	148
E value	4.0e-09
Match length	36
% identity	72
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	275553
Contig ID	60333_1.R1011
5'-most EST	uC-zmflmo17273a04b1
Method	BLASTX
NCBI GI	g3914005

BLAST score	789
E value	2.0e-84
Match length	185
% identity	89
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]

Seq. No.	275554
Contig ID	60343_1.R1011
5'-most EST	LIB3060-002-Q1-K2-H2

Seq. No.	275555
Contig ID	60343_2.R1011
5'-most EST	tfd700569106.h1

Seq. No.	275556
Contig ID	60348_1.R1011
5'-most EST	LIB3060-006-Q1-K1-H6

Seq. No.	275557
Contig ID	60356_1.R1011
5'-most EST	LIB3060-003-Q1-K1-B1

Seq. No.	275558
Contig ID	60358_1.R1011
5'-most EST	LIB3060-003-Q1-K1-B11

Seq. No.	275559
Contig ID	60373_1.R1011
5'-most EST	LIB3060-003-Q1-K1-C8
Method	BLASTX
NCBI GI	g3021270
BLAST score	341
E value	9.0e-32
Match length	150
% identity	46
NCBI Description	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq. No.	275560
Contig ID	60374_1.R1011
5'-most EST	tzu700204471.h1
Method	BLASTX
NCBI GI	g4455225
BLAST score	2031
E value	0.0e+00
Match length	453
% identity	77
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	275561
Contig ID	60377_1.R1011
5'-most EST	LIB3060-003-Q1-K1-D12
Method	BLASTX
NCBI GI	g431162
BLAST score	403
E value	3.0e-39

Match length	143
% identity	51
NCBI Description	(D21822) ORF [Lilium longiflorum]

Seq. No.	275562
Contig ID	60379_1.R1011
5'-most EST	wyr700241146.h1
Method	BLASTX
NCBI GI	g2062389
BLAST score	566
E value	6.0e-58
Match length	208
% identity	51
NCBI Description	(U77657) pathogenesis-related thaumatin-like protein [Oryza sativa]

Seq. No.	275563
Contig ID	60380_1.R1011
5'-most EST	LIB3060-006-Q1-K1-F11

Seq. No.	275564
Contig ID	60389_1.R1011
5'-most EST	cyk700049036.f1

Seq. No.	275565
Contig ID	60392_1.R1011
5'-most EST	pmx700082815.h1

Seq. No.	275566
Contig ID	60393_1.R1011
5'-most EST	LIB3060-003-Q1-K1-E8
Method	BLASTX
NCBI GI	g4490756
BLAST score	392
E value	1.0e-37
Match length	181
% identity	44
NCBI Description	(AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275567
Contig ID	60397_2.R1011
5'-most EST	LIB3060-003-Q1-K1-F7

Seq. No.	275568
Contig ID	60401_1.R1011
5'-most EST	pmx700086370.h1

Seq. No.	275569
Contig ID	60406_1.R1011
5'-most EST	LIB3060-003-Q1-K1-G2

Seq. No.	275570
Contig ID	60408_1.R1011
5'-most EST	LIB3069-047-Q1-K1-B9

Seq. No.	275571
Contig ID	60410_1.R1011

5'-most EST	LIB3060-003-Q1-K1-H10
Seq. No.	275572
Contig ID	60414_1.R1011
5'-most EST	nbm700469428.h1
Method	BLASTX
NCBI GI	g1362051
BLAST score	1194
E value	1.0e-131
Match length	258
% identity	86
NCBI Description	protein kinase 3 - soybean >gi_310582 (L19361) protein kinase 3 [Glycine max]
Seq. No.	275573
Contig ID	60427_1.R1011
5'-most EST	yyf700348988.h1
Method	BLASTX
NCBI GI	g4567262
BLAST score	767
E value	1.0e-81
Match length	172
% identity	80
NCBI Description	(AC006841) putative ubiquitin [Arabidopsis thaliana]
Seq. No.	275574
Contig ID	60427_2.R1011
5'-most EST	LIB3137-003-Q1-K1-D7
Method	BLASTX
NCBI GI	g4539312
BLAST score	165
E value	2.0e-18
Match length	69
% identity	71
NCBI Description	(AL035679) putative ubiquitin-dependent proteolytic protein [Arabidopsis thaliana]
Seq. No.	275575
Contig ID	60428_1.R1011
5'-most EST	uC-zmflmo17051f02b1
Seq. No.	275576
Contig ID	60434_1.R1011
5'-most EST	LIB3617-Q1-E1-G2
Seq. No.	275577
Contig ID	60444_1.R1011
5'-most EST	fwa700101244.h1
Seq. No.	275578
Contig ID	60461_1.R1011
5'-most EST	gct701170801.h1
Method	BLASTX
NCBI GI	g1684913
BLAST score	223
E value	4.0e-18
Match length	148

% identity	34
NCBI Description	(U77888) receptor-like protein kinase [Ipomoea nil]

Seq. No.	275579
Contig ID	60468_1.R1011
5'-most EST	uer700582209.h1
Method	BLASTN
NCBI GI	g4160401
BLAST score	36
E value	2.0e-10
Match length	56
% identity	91
NCBI Description	Zea mays eIF-5 gene, exons 1-2

Seq. No.	275580
Contig ID	60468_2.R1011
5'-most EST	nwy700444533.h1

Seq. No.	275581
Contig ID	60491_1.R1011
5'-most EST	gwl700613348.h1
Method	BLASTX
NCBI GI	g3668092
BLAST score	414
E value	1.0e-40
Match length	118
% identity	71
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	275582
Contig ID	60494_1.R1011
5'-most EST	LIB3060-005-Q1-K1-A12

Seq. No.	275583
Contig ID	60498_1.R1011
5'-most EST	LIB3060-005-Q1-K1-A5

Seq. No.	275584
Contig ID	60502_1.R1011
5'-most EST	LIB3060-005-Q1-K1-A9
Method	BLASTX
NCBI GI	g4038044
BLAST score	243
E value	2.0e-20
Match length	77
% identity	61
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana] >gi_4406788_gb_AAD20098_ (AC006532) unknown protein [Arabidopsis thaliana]

Seq. No.	275585
Contig ID	60504_1.R1011
5'-most EST	xmt700265112.h1

Seq. No.	275586
Contig ID	60509_1.R1011
5'-most EST	uC-zmflB73045c08b1

Seq. No. 275587
Contig ID 60525_1.R1011
5'-most EST LIB3060-005-Q1-K1-D11

Seq. No. 275588
Contig ID 60531_1.R1011
5'-most EST LIB3067-039-Q1-K1-G9
Method BLASTX
NCBI GI g1729938
BLAST score 199
E value 2.0e-15
Match length 59
% identity 63
NCBI Description THIOREDOXIN-LIKE PROTEIN SLR0233 >gi_1001610_dbj_BAA10238_ (D64000) thioredoxin M [Synechocystis sp.]

Seq. No. 275589
Contig ID 60534_1.R1011
5'-most EST LIB3060-005-Q1-K1-E12

Seq. No. 275590
Contig ID 60541_1.R1011
5'-most EST LIB3060-005-Q1-K1-E9

Seq. No. 275591
Contig ID 60553_1.R1011
5'-most EST ceu700429776.h1

Seq. No. 275592
Contig ID 60559_1.R1011
5'-most EST uC-zmflmo17259d10b1

Seq. No. 275593
Contig ID 60559_2.R1011
5'-most EST uC-zmflmo17068d11b2

Seq. No. 275594
Contig ID 60563_1.R1011
5'-most EST LIB3060-005-Q1-K1-H12

Seq. No. 275595
Contig ID 60573_1.R1011
5'-most EST uC-zmroteosinte042b02b1

Seq. No. 275596
Contig ID 60573_2.R1011
5'-most EST uC-zmflmo17377a08a1

Seq. No. 275597
Contig ID 60606_1.R1011
5'-most EST LIB3060-049-Q1-K1-E2
Method BLASTX
NCBI GI g3176098
BLAST score 354
E value 3.0e-33
Match length 150

% identity	50
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	275598
Contig ID	60630_1.R1011
5'-most EST	LIB3060-006-Q1-K1-G11
Method	BLASTX
NCBI GI	g2984004
BLAST score	768
E value	1.0e-81
Match length	265
% identity	53
NCBI Description	(AE000750) threonyl-tRNA synthetase [Aquifex aeolicus]

Seq. No.	275599
Contig ID	60631_1.R1011
5'-most EST	pmx70083193.h1
Method	BLASTX
NCBI GI	g4006875
BLAST score	337
E value	3.0e-31
Match length	129
% identity	54
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	275600
Contig ID	60634_1.R1011
5'-most EST	LIB3060-006-Q1-K1-G6
Method	BLASTX
NCBI GI	g2290782
BLAST score	252
E value	1.0e-21
Match length	103
% identity	50
NCBI Description	(AF002692) glutathione S-transferase, class-phi [Solanum commersonii]

Seq. No.	275601
Contig ID	60635_1.R1011
5'-most EST	LIB3060-006-Q1-K1-G7
Method	BLASTX
NCBI GI	g4455312
BLAST score	277
E value	3.0e-24
Match length	126
% identity	47
NCBI Description	(AL035528) DnaJ-like protein [Arabidopsis thaliana]

Seq. No.	275602
Contig ID	60648_1.R1011
5'-most EST	LIB3060-007-Q1-K1-A11
Method	BLASTX
NCBI GI	g1546817
BLAST score	223
E value	3.0e-18
Match length	57
% identity	74

NCBI Description	(U68484) patatin homolog [Nicotiana tabacum]

Seq. No.	275603
Contig ID	60650_1.R1011
5'-most EST	pmx700084919.h1
Method	BLASTX
NCBI GI	g3402711
BLAST score	383
E value	8.0e-37
Match length	127
% identity	38
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	275604
Contig ID	60656_1.R1011
5'-most EST	LIB3060-049-Q1-K1-A3

Seq. No.	275605
Contig ID	60659_1.R1011
5'-most EST	uC-zmflb73167b01b2

Seq. No.	275606
Contig ID	60665_1.R1011
5'-most EST	ntr700076886.h1
Method	BLASTX
NCBI GI	g2244998
BLAST score	447
E value	3.0e-44
Match length	190
% identity	57
NCBI Description	(Z97341) similarity to probable transcriptional adaptor ADA2 [Arabidopsis thaliana]

Seq. No.	275607
Contig ID	60670_1.R1011
5'-most EST	LIB3136-014-Q1-K2-G2
Method	BLASTX
NCBI GI	g1362172
BLAST score	250
E value	3.0e-21
Match length	85
% identity	62
NCBI Description	hook-containing protein AT1 - rice >gi_871496_emb_CAA61276_ (X88798) putative [Oryza sativa]

Seq. No.	275608
Contig ID	60675_1.R1011
5'-most EST	mwy700439722.h1

Seq. No.	275609
Contig ID	60677_1.R1011
5'-most EST	ceu700431195.h1
Method	BLASTX
NCBI GI	g1402876
BLAST score	597
E value	4.0e-62

Match length	132
% identity	88
NCBI Description	(X98130) putative phosphate permease [Arabidopsis thaliana] >gi_1495255_emb_CAA66116_ (X97484) orf01 [Arabidopsis thaliana]

Seq. No.	275610
Contig ID	60679_1.R1011
5'-most EST	LIB3060-007-Q1-K1-D3

Seq. No.	275611
Contig ID	60682_1.R1011
5'-most EST	uer700584243.h1

Seq. No.	275612
Contig ID	60686_1.R1011
5'-most EST	uC-zmflb73413c07a1

Seq. No.	275613
Contig ID	60695_1.R1011
5'-most EST	LIB3060-007-Q1-K1-F12

Seq. No.	275614
Contig ID	60698_1.R1011
5'-most EST	LIB3060-024-Q1-K1-A6
Method	BLASTX
NCBI GI	g2252830
BLAST score	212
E value	5.0e-17
Match length	130
% identity	44
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	275615
Contig ID	60699_1.R1011
5'-most EST	wyr700237304.h1

Seq. No.	275616
Contig ID	60699_2.R1011
5'-most EST	nbm700473021.h1

Seq. No.	275617
Contig ID	60701_1.R1011
5'-most EST	LIB3060-007-Q1-K1-F7

Seq. No.	275618
Contig ID	60719_1.R1011
5'-most EST	fwa700097321.h1
Method	BLASTX
NCBI GI	g4206195
BLAST score	418
E value	8.0e-41
Match length	99
% identity	73
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein

[Arabidopsis thaliana]

Seq. No.	275619
Contig ID	60722_1.R1011
5'-most EST	LIB3060-044-Q1-K1-D10
Method	BLASTX
NCBI GI	g3337367
BLAST score	237
E value	7.0e-20
Match length	102
% identity	48
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275620
Contig ID	60736_1.R1011
5'-most EST	LIB3060-008-Q1-K1-B11
Method	BLASTX
NCBI GI	g2541876
BLAST score	240
E value	2.0e-31
Match length	132
% identity	57
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	275621
Contig ID	60743_1.R1011
5'-most EST	LIB3069-036-Q1-K1-A6

Seq. No.	275622
Contig ID	60744_1.R1011
5'-most EST	LIB3068-014-Q1-K1-C5
Method	BLASTX
NCBI GI	g2618699
BLAST score	267
E value	4.0e-23
Match length	183
% identity	35
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	275623
Contig ID	60745_1.R1011
5'-most EST	uC-zmf1mo17163c05a1

Seq. No.	275624
Contig ID	60745_2.R1011
5'-most EST	LIB3060-009-Q1-K1-B9
Method	BLASTN
NCBI GI	g4206305
BLAST score	48
E value	7.0e-18
Match length	97
% identity	89
NCBI Description	Zea mays retrotransposon Cinful-1, complete sequence

Seq. No.	275625
Contig ID	60748_1.R1011

5'-most EST	uC-zmflb73226g11b1
Method	BLASTX
NCBI GI	g2194132
BLAST score	919
E value	2.0e-99
Match length	245
% identity	70
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	275626
Contig ID	60751_1.R1011
5'-most EST	uC-zmflmo17023d01b1

Seq. No.	275627
Contig ID	60751_2.R1011
5'-most EST	xmt700259029.h1

Seq. No.	275628
Contig ID	60756_1.R1011
5'-most EST	LIB3069-039-Q1-K1-F10
Method	BLASTX
NCBI GI	g2289786
BLAST score	147
E value	2.0e-11
Match length	140
% identity	37
NCBI Description	(D88153) HYA22 [Homo sapiens]

Seq. No.	275629
Contig ID	60775_1.R1011
5'-most EST	uC-zmflb73206a12b1

Seq. No.	275630
Contig ID	60795_1.R1011
5'-most EST	LIB3060-008-Q1-K1-G5

Seq. No.	275631
Contig ID	60804_1.R1011
5'-most EST	LIB3060-008-Q1-K1-H4

Seq. No.	275632
Contig ID	60804_2.R1011
5'-most EST	LIB3066-017-Q1-K1-G7

Seq. No.	275633
Contig ID	60807_1.R1011
5'-most EST	LIB3060-008-Q1-K1-H7
Method	BLASTX
NCBI GI	g3367596
BLAST score	710
E value	8.0e-75
Match length	238
% identity	56
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	275634
Contig ID	60807_2.R1011

5'-most EST	fC-zmle700578206f1
Method	BLASTX
NCBI GI	g3367596
BLAST score	619
E value	2.0e-64
Match length	182
% identity	61
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	275635
Contig ID	60813_1.R1011
5'-most EST	gw1700613648.h1

Seq. No.	275636
Contig ID	60814_1.R1011
5'-most EST	lhp700053351.r1
Method	BLASTX
NCBI GI	g3822403
BLAST score	480
E value	5.0e-48
Match length	175
% identity	51
NCBI Description	(AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No.	275637
Contig ID	60837_1.R1011
5'-most EST	LIB3060-009-Q1-K1-D6

Seq. No.	275638
Contig ID	60840_1.R1011
5'-most EST	clt700042308.f1
Method	BLASTX
NCBI GI	g2213620
BLAST score	702
E value	3.0e-74
Match length	175
% identity	76
NCBI Description	(AC000103) F21J9.13 [Arabidopsis thaliana]

Seq. No.	275639
Contig ID	60850_1.R1011
5'-most EST	uC-zmflb73177h11b1
Method	BLASTX
NCBI GI	g3021508
BLAST score	651
E value	4.0e-68
Match length	142
% identity	86
NCBI Description	(AJ001769) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	275640
Contig ID	60850_2.R1011
5'-most EST	uC-zmflb73063a02b1
Method	BLASTX
NCBI GI	g585165
BLAST score	1667

E value	0.0e+00
Match length	405
% identity	79
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]

Seq. No.	275641
Contig ID	60850_3.R1011
5'-most EST	LIB3069-049-Q1-K1-G4
Method	BLASTX
NCBI GI	g3021508
BLAST score	588
E value	1.0e-60
Match length	157
% identity	71
NCBI Description	(AJ001769) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	275642
Contig ID	60855_1.R1011
5'-most EST	LIB3060-009-Q1-K1-F6
Method	BLASTX
NCBI GI	g3982632
BLAST score	412
E value	2.0e-40
Match length	87
% identity	89
NCBI Description	(AF056160) disease resistance gene analog PIC20 [Zea mays]

Seq. No.	275643
Contig ID	60858_1.R1011
5'-most EST	LIB3137-033-Q1-K1-A4
Method	BLASTX
NCBI GI	g2829918
BLAST score	287
E value	2.0e-25
Match length	96
% identity	58
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	275644
Contig ID	60864_1.R1011
5'-most EST	LIB3060-009-Q1-K1-G9

Seq. No.	275645
Contig ID	60866_1.R1011
5'-most EST	LIB84-016-Q1-E1-G6

Seq. No.	275646
Contig ID	60868_1.R1011
5'-most EST	uC-zmflmo17289h05b1
Method	BLASTX
NCBI GI	g1737218

BLAST score	173
E value	4.0e-12
Match length	37
% identity	84
NCBI Description	(U79959) vacuolar sorting receptor homolog [Arabidopsis thaliana]

Seq. No.	275647
Contig ID	60882_1.R1011
5'-most EST	nbm700474768.h1
Method	BLASTX
NCBI GI	g4455340
BLAST score	303
E value	1.0e-27
Match length	103
% identity	52
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	275648
Contig ID	60890_1.R1011
5'-most EST	uC-zmflmo17108g12b1

Seq. No.	275649
Contig ID	60892_1.R1011
5'-most EST	LIB3060-010-Q1-K1-C11

Seq. No.	275650
Contig ID	60902_1.R1011
5'-most EST	LIB3060-010-Q1-K1-D11
Method	BLASTX
NCBI GI	g3395431
BLAST score	148
E value	2.0e-09
Match length	81
% identity	38
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	275651
Contig ID	60916_1.R1011
5'-most EST	vux700160360.h1
Method	BLASTX
NCBI GI	g4006915
BLAST score	296
E value	1.0e-26
Match length	170
% identity	36
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275652
Contig ID	60926_1.R1011
5'-most EST	hvj700619164.h1
Method	BLASTX
NCBI GI	g629562
BLAST score	911
E value	2.0e-98
Match length	186
% identity	89

NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir__S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	275653
Contig ID	60929_1.R1011
5'-most EST	uC-zmflmo17281c07b1

Seq. No.	275654
Contig ID	60929_2.R1011
5'-most EST	xsy700211476.h1

Seq. No.	275655
Contig ID	60936_1.R1011
5'-most EST	uC-zmflmo17136e10b1
Method	BLASTX
NCBI GI	g2262115
BLAST score	455
E value	4.0e-45
Match length	232
% identity	41
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.	275656
Contig ID	60946_1.R1011
5'-most EST	LIB3060-011-Q1-K1-A11
Method	BLASTX
NCBI GI	g4210504
BLAST score	201
E value	3.0e-15
Match length	86
% identity	52
NCBI Description	(AC002392) putative cadmium-transporting ATPase [Arabidopsis thaliana]

Seq. No.	275657
Contig ID	60963_1.R1011
5'-most EST	LIB3060-011-Q1-K1-B6
Method	BLASTX
NCBI GI	g4558549
BLAST score	931
E value	1.0e-101
Match length	210
% identity	86
NCBI Description	(AC007138) putative SecA-type chloroplast protein transport factor [Arabidopsis thaliana]

Seq. No.	275658
Contig ID	60967_1.R1011
5'-most EST	uC-zmflmo17248g07b1

Seq. No.	275659
Contig ID	60970_1.R1011
5'-most EST	LIB3060-011-Q1-K1-C12
Method	BLASTX
NCBI GI	g2764524
BLAST score	420
E value	1.0e-44
Match length	158
% identity	56
NCBI Description	(AJ000520) Rieske iron-sulfur protein Tic55 [Pisum sativum]

Seq. No.	275660
Contig ID	60973_1.R1011
5'-most EST	tzu7000201371.h1
Method	BLASTX
NCBI GI	g3184061
BLAST score	188
E value	7.0e-14
Match length	111
% identity	41
NCBI Description	(AL023776) atp dependent helicase [Schizosaccharomyces pombe]

Seq. No.	275661
Contig ID	60990_1.R1011
5'-most EST	LIB3060-011-Q1-K1-E2
Method	BLASTX
NCBI GI	g2129855
BLAST score	301
E value	3.0e-27
Match length	69
% identity	72
NCBI Description	mitogen-activated protein kinase MMK2 (EC 2.7.1.-) - alfalfa

Seq. No.	275662
Contig ID	61001_1.R1011
5'-most EST	fdz7010160458.h1
Method	BLASTX
NCBI GI	g2979554
BLAST score	704
E value	3.0e-74
Match length	255
% identity	53
NCBI Description	(AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No.	275663
Contig ID	61003_1.R1011
5'-most EST	qmh7000026865.f1

Seq. No.	275664
Contig ID	61007_1.R1011
5'-most EST	pwr7000451316.h1
Method	BLASTX
NCBI GI	g4056568
BLAST score	240
E value	4.0e-20

Match length	116
% identity	14
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	275665
Contig ID	61012_1.R1011
5'-most EST	xmt700257752.h1

Seq. No.	275666
Contig ID	61021_1.R1011
5'-most EST	uC-zmflMo17004f08b1

Seq. No.	275667
Contig ID	61022_1.R1011
5'-most EST	LIB3136-006-Q1-K1-B4
Method	BLASTX
NCBI GI	g2088647
BLAST score	306
E value	1.0e-27
Match length	104
% identity	58
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	275668
Contig ID	61022_2.R1011
5'-most EST	nbm700470648.h1

Seq. No.	275669
Contig ID	61027_1.R1011
5'-most EST	ntr700074650.h1
Method	BLASTX
NCBI GI	g1652434
BLAST score	273
E value	9.0e-33
Match length	101
% identity	71
NCBI Description	(D90905) N-acetylglutamate kinase [Synechocystis sp.]

Seq. No.	275670
Contig ID	61032_1.R1011
5'-most EST	LIB3060-018-Q1-K1-C1
Method	BLASTX
NCBI GI	g1172704
BLAST score	194
E value	8.0e-15
Match length	86
% identity	45
NCBI Description	PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN) >gi_633940 (L39082) transport protein [Arabidopsis thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine transport protein PTR2-B [Arabidopsis thaliana]

Seq. No.	275671
Contig ID	61037_1.R1011
5'-most EST	uC-zmflb73046g05b1

Method	BLASTX
NCBI GI	g2408068
BLAST score	542
E value	3.0e-55
Match length	291
% identity	34
NCBI Description	(Z99165) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	275672
Contig ID	61042_1.R1011
5'-most EST	xjt700093121.h1
Method	BLASTX
NCBI GI	g2736155
BLAST score	825
E value	2.0e-88
Match length	206
% identity	76
NCBI Description	(AF022082) sulfolipid biosynthesis protein [Arabidopsis thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid biosynthesis protein SQD1 [Arabidopsis thaliana]

Seq. No.	275673
Contig ID	61046_1.R1011
5'-most EST	LIB3137-005-Q1-K1-H8

Seq. No.	275674
Contig ID	61060_1.R1011
5'-most EST	uC-zmflb73126g10b1
Method	BLASTX
NCBI GI	g2529686
BLAST score	504
E value	6.0e-51
Match length	196
% identity	49
NCBI Description	(AC002535) putative G-beta-repeat containing protein, 5' partial [Arabidopsis thaliana]

Seq. No.	275675
Contig ID	61081_1.R1011
5'-most EST	uC-zmflmo17159d04b1
Method	BLASTX
NCBI GI	g1653162
BLAST score	264
E value	9.0e-23
Match length	154
% identity	41
NCBI Description	(D90911) (p)ppGpp 3-pyrophosphohydrolase [Synechocystis sp.]

Seq. No.	275676
Contig ID	61082_1.R1011
5'-most EST	xsy700210189.h1

Seq. No.	275677
Contig ID	61087_1.R1011
5'-most EST	uC-zmflb73014g03b1

Seq. No.	275678
Contig ID	61130_1.R1011
5'-most EST	vux700161930.h1
Method	BLASTX
NCBI GI	g2696221
BLAST score	262
E value	8.0e-23
Match length	89
% identity	57
NCBI Description	(D55708) chitinase [Oryza sativa]

Seq. No.	275679
Contig ID	61145_1.R1011
5'-most EST	LIB3060-013-Q1-K1-E6

Seq. No.	275680
Contig ID	61162_1.R1011
5'-most EST	uwc700150727.h1

Seq. No.	275681
Contig ID	61162_2.R1011
5'-most EST	uwc700156169.h1

Seq. No.	275682
Contig ID	61165_1.R1011
5'-most EST	LIB36-018-Q1-E1-D11
Method	BLASTN
NCBI GI	g2062705
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	275683
Contig ID	61165_2.R1011
5'-most EST	LIB3060-013-Q1-K1-G9

Seq. No.	275684
Contig ID	61172_3.R1011
5'-most EST	hvj700619569.h1

Seq. No.	275685
Contig ID	61183_1.R1011
5'-most EST	ymt700219928.h1
Method	BLASTX
NCBI GI	g3775987
BLAST score	488
E value	3.0e-49
Match length	154
% identity	68
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.	275686
Contig ID	61190_1.R1011
5'-most EST	LIB36-003-Q1-E1-D7

Seq. No.	275687
Contig ID	61203_1.R1011
5'-most EST	LIB3060-014-Q1-K1-D11

Seq. No.	275688
Contig ID	61214_1.R1011
5'-most EST	uC-zmflb73017h03b1
Method	BLASTX
NCBI GI	g3980416
BLAST score	343
E value	3.0e-32
Match length	109
% identity	62
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	275689
Contig ID	61214_2.R1011
5'-most EST	uC-zmflmo17020e04b1
Method	BLASTX
NCBI GI	g3980399
BLAST score	292
E value	2.0e-26
Match length	91
% identity	64
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	275690
Contig ID	61216_1.R1011
5'-most EST	uC-zmflmo17342a04b1

Seq. No.	275691
Contig ID	61222_1.R1011
5'-most EST	LIB3060-014-Q1-K1-E9
Method	BLASTX
NCBI GI	g3024871
BLAST score	299
E value	1.0e-26
Match length	171
% identity	40
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	275692
Contig ID	61224_1.R1011
5'-most EST	pmx700091572.h1
Method	BLASTX
NCBI GI	g3808235
BLAST score	224
E value	4.0e-18
Match length	165
% identity	33
NCBI Description	(AF058718) putative 13 S Golgi transport complex 90kD subunit brain-specific isoform [Homo sapiens]

Seq. No.	275693
Contig ID	61244_1.R1011
5'-most EST	LIB3060-014-Q1-K1-H8

Seq. No.	275694
Contig ID	61251_1.R1011
5'-most EST	LIB3060-015-Q1-K1-A2
Method	BLASTX
NCBI GI	g3935185
BLAST score	142
E value	8.0e-09
Match length	70
% identity	44
NCBI Description	(AC004557) F17L21.28 [Arabidopsis thaliana]

Seq. No.	275695
Contig ID	61256_1.R1011
5'-most EST	hbs701182842.h1
Method	BLASTX
NCBI GI	g1699023
BLAST score	515
E value	3.0e-52
Match length	154
% identity	68
NCBI Description	(U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi_1699051 (U78867) putative aspartate-arginine-rich mRNA binding protein [Arabidopsis thaliana]

Seq. No.	275696
Contig ID	61262_1.R1011
5'-most EST	uC-zmflMo17084c04b1

Seq. No.	275697
Contig ID	61270_1.R1011
5'-most EST	rvl700454541.h1

Seq. No.	275698
Contig ID	61273_1.R1011
5'-most EST	uC-zmflmo17291d07a1

Seq. No.	275699
Contig ID	61277_1.R1011
5'-most EST	LIB3060-015-Q1-K1-D5
Method	BLASTX
NCBI GI	g3341679
BLAST score	391
E value	6.0e-40
Match length	151
% identity	62
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	275700
Contig ID	61282_1.R1011
5'-most EST	uC-zmflmo17184c03b1
Method	BLASTX

NCBI GI	g1680686
BLAST score	618
E value	2.0e-64
Match length	171
% identity	74
NCBI Description	(U51330) rust resistance kinase Lr10 [Triticum aestivum]

Seq. No.	275701
Contig ID	61300_1.R1011
5'-most EST	nwy700446621.h1
Method	BLASTX
NCBI GI	g3522946
BLAST score	515
E value	1.0e-80
Match length	321
% identity	51
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	275702
Contig ID	61303_1.R1011
5'-most EST	LIB3060-015-Q1-K1-G9

Seq. No.	275703
Contig ID	61320_1.R1011
5'-most EST	uC-zmflm017214g08b1
Method	BLASTX
NCBI GI	g2959767
BLAST score	612
E value	2.0e-63
Match length	163
% identity	71
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	275704
Contig ID	61334_1.R1011
5'-most EST	LIB3060-016-Q1-K1-B10

Seq. No.	275705
Contig ID	61340_1.R1011
5'-most EST	LIB3060-016-Q1-K1-C1

Seq. No.	275706
Contig ID	61340_3.R1011
5'-most EST	uer700581472.h1

Seq. No.	275707
Contig ID	61343_1.R1011
5'-most EST	LIB3060-016-Q1-K1-B8

Seq. No.	275708
Contig ID	61349_1.R1011
5'-most EST	LIB3060-016-Q1-K1-C2
Method	BLASTX
NCBI GI	g3643598
BLAST score	871

E value	5.0e-94
Match length	190
% identity	83
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	275709
Contig ID	61349_2.R1011
5'-most EST	rvt700552833.h1

Seq. No.	275710
Contig ID	61353_1.R1011
5'-most EST	LIB3069-036-Q1-K1-H10
Method	BLASTX
NCBI GI	g3273764
BLAST score	387
E value	9.0e-37
Match length	214
% identity	48
NCBI Description	(AF061870) Dc3 promoter-binding factor-3 [Helianthus annuus]

Seq. No.	275711
Contig ID	61354_1.R1011
5'-most EST	uC-zmflb73283g04b2

Seq. No.	275712
Contig ID	61357_1.R1011
5'-most EST	wyr700235625.h1

Seq. No.	275713
Contig ID	61366_1.R1011
5'-most EST	fwa700097976.h1

Seq. No.	275714
Contig ID	61372_1.R1011
5'-most EST	fwa700099019.h1
Method	BLASTX
NCBI GI	g1706082
BLAST score	425
E value	1.0e-41
Match length	162
% identity	56
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	275715
Contig ID	61373_1.R1011
5'-most EST	LIB3060-016-Q1-K1-E6

Seq. No.	275716
Contig ID	61376_1.R1011

5'-most EST	uC-zmflmo17330d06b1
Method	BLASTX
NCBI GI	g4512651
BLAST score	159
E value	1.0e-10
Match length	102
% identity	34
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	275717
Contig ID	61383_1.R1011
5'-most EST	qmh700029091.f1

Seq. No.	275718
Contig ID	61383_2.R1011
5'-most EST	LIB3060-016-Q1-K1-F5

Seq. No.	275719
Contig ID	61385_1.R1011
5'-most EST	LIB3060-016-Q1-K1-F7

Seq. No.	275720
Contig ID	61391_1.R1011
5'-most EST	LIB3060-016-Q1-K1-G12
Method	BLASTX
NCBI GI	g4572671
BLAST score	250
E value	4.0e-21
Match length	112
% identity	46
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	275721
Contig ID	61394_1.R1011
5'-most EST	xsy700211587.h1

Seq. No.	275722
Contig ID	61399_1.R1011
5'-most EST	wyr700235404.h1

Seq. No.	275723
Contig ID	61400_1.R1011
5'-most EST	LIB3060-016-Q1-K1-H10

Seq. No.	275724
Contig ID	61413_1.R1011
5'-most EST	LIB3060-017-Q1-K1-A11

Seq. No.	275725
Contig ID	61414_1.R1011
5'-most EST	LIB3060-017-Q1-K1-A2

Seq. No.	275726
Contig ID	61427_1.R1011
5'-most EST	LIB84-003-Q1-E1-G3

Seq. No.	275727
Contig ID	61433_1.R1011
5'-most EST	uC-zmflmo17180d07b1

Seq. No.	275728
Contig ID	61434_1.R1011
5'-most EST	uC-zmflmo17041g06b1

Seq. No.	275729
Contig ID	61437_1.R1011
5'-most EST	uC-zmflb73143a04b1

Seq. No.	275730
Contig ID	61437_2.R1011
5'-most EST	LIB3060-017-Q1-K1-C5
Method	BLASTX
NCBI GI	g2505876
BLAST score	232
E value	3.0e-19
Match length	50
% identity	88
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	275731
Contig ID	61445_1.R1011
5'-most EST	uC-zmflMo17063g12b1
Method	BLASTX
NCBI GI	g4263711
BLAST score	316
E value	8.0e-44
Match length	137
% identity	64
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	275732
Contig ID	61455_1.R1011
5'-most EST	LIB3060-017-Q1-K1-E3

Seq. No.	275733
Contig ID	61463_1.R1011
5'-most EST	LIB3060-017-Q1-K1-F10

Seq. No.	275734
Contig ID	61471_1.R1011
5'-most EST	ntr700077032.h1
Method	BLASTX
NCBI GI	g136632
BLAST score	166
E value	2.0e-11
Match length	69
% identity	58
NCBI Description	UBIQUITIN-ACTIVATING ENZYME E1 1 >gi_100841_pir__A38373 ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat >gi_285451_pir__A42873 ubiquitin-activating enzyme E1, UBA1 - Wheat >gi_170780 (M55604) ubiquitin-activating enzyme E1

[Triticum aestivum]

Seq. No.	275735
Contig ID	61483_1.R1011
5'-most EST	LIB3060-017-Q1-K1-G7

Seq. No.	275736
Contig ID	61483_3.R1011
5'-most EST	uer700580573.h1
Method	BLASTX
NCBI GI	g4469020
BLAST score	693
E value	3.0e-73
Match length	146
% identity	89
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	275737
Contig ID	61489_1.R1011
5'-most EST	LIB3060-017-Q1-K1-H2
Method	BLASTX
NCBI GI	g2462826
BLAST score	395
E value	3.0e-38
Match length	198
% identity	47
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	275738
Contig ID	61502_1.R1011
5'-most EST	LIB3060-018-Q1-K1-A4
Method	BLASTX
NCBI GI	g893294
BLAST score	151
E value	9.0e-10
Match length	124
% identity	37
NCBI Description	(L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa]

Seq. No.	275739
Contig ID	61506_1.R1011
5'-most EST	uC-zmroB73014b02b1

Seq. No.	275740
Contig ID	61509_1.R1011
5'-most EST	LIB3068-050-Q1-K1-H11
Method	BLASTX
NCBI GI	g4038055
BLAST score	368
E value	6.0e-35
Match length	166
% identity	44
NCBI Description	(AC005897) putative cytochrome P450 [Arabidopsis thaliana] >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	275741
Contig ID	61512_1.R1011
5'-most EST	pmx700084893.h1
Method	BLASTX
NCBI GI	g3417448
BLAST score	164
E value	4.0e-11
Match length	58
% identity	52
NCBI Description	(AB010087) UMP kinase [Pseudomonas aeruginosa]

Seq. No.	275742
Contig ID	61515_1.R1011
5'-most EST	LIB3060-018-Q1-K1-B6

Seq. No.	275743
Contig ID	61521_1.R1011
5'-most EST	LIB3060-018-Q1-K1-C11

Seq. No.	275744
Contig ID	61536_1.R1011
5'-most EST	LIB3060-018-Q1-K1-D8

Seq. No.	275745
Contig ID	61537_1.R1011
5'-most EST	uwc700155001.h1

Seq. No.	275746
Contig ID	61543_1.R1011
5'-most EST	uC-zmflb73012d09b1

Seq. No.	275747
Contig ID	61543_2.R1011
5'-most EST	LIB3066-034-Q1-K1-G2

Seq. No.	275748
Contig ID	61544_1.R1011
5'-most EST	LIB3060-018-Q1-K1-E6
Method	BLASTX
NCBI GI	g2982453
BLAST score	559
E value	1.0e-57
Match length	130
% identity	82
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	275749
Contig ID	61554_1.R1011
5'-most EST	cat700021296.r1
Method	BLASTX
NCBI GI	g1848225
BLAST score	154
E value	4.0e-10
Match length	61
% identity	46
NCBI Description	(U88090) nonspecific lipid transfer protein [Hordeum

vulgare]

Seq. No.	275750
Contig ID	61568_1.R1011
5'-most EST	LIB3136-032-Q1-K1-D4
Method	BLASTX
NCBI GI	g4580470
BLAST score	179
E value	5.0e-13
Match length	122
% identity	34
NCBI Description	(AC006081) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275751
Contig ID	61576_2.R1011
5'-most EST	wen700335560.h1
Method	BLASTX
NCBI GI	g4490702
BLAST score	381
E value	2.0e-36
Match length	232
% identity	43
NCBI Description	(AL035680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275752
Contig ID	61592_1.R1011
5'-most EST	LIB84-014-Q1-E1-E8

Seq. No.	275753
Contig ID	61594_1.R1011
5'-most EST	xmt700263095.h1
Method	BLASTX
NCBI GI	g3641837
BLAST score	456
E value	2.0e-45
Match length	103
% identity	87
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	275754
Contig ID	61596_1.R1011
5'-most EST	LIB3061-038-Q1-K1-G8
Method	BLASTX
NCBI GI	g3413719
BLAST score	255
E value	1.0e-21
Match length	85
% identity	62
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643592 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	275755
Contig ID	61620_1.R1011
5'-most EST	LIB3060-019-Q1-K1-E4

Seq. No.	275756
Contig ID	61620_2.R1011
5'-most EST	uC-zmflb73126h06a1
Method	BLASTN
NCBI GI	g949979
BLAST score	124
E value	5.0e-63
Match length	309
% identity	94
NCBI Description	Z.mays Glossy2 locus DNA

Seq. No.	275757
Contig ID	61625_1.R1011
5'-most EST	rvl700454049.h1
Method	BLASTX
NCBI GI	g2832643
BLAST score	168
E value	1.0e-11
Match length	102
% identity	39
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275758
Contig ID	61634_1.R1011
5'-most EST	LIB3060-045-Q1-K1-A3
Method	BLASTX
NCBI GI	g283038
BLAST score	533
E value	2.0e-54
Match length	114
% identity	89
NCBI Description	chlorophyll a/b-binding protein (cab-m7) precursor - maize >gi_22230_emb_CAA37474_ (X53398) light harvesting chlorophyll a /b binding protein [Zea mays]

Seq. No.	275759
Contig ID	61644_1.R1011
5'-most EST	LIB3060-019-Q1-K1-G6

Seq. No.	275760
Contig ID	61669_1.R1011
5'-most EST	xjt700095571.h1

Seq. No.	275761
Contig ID	61672_1.R1011
5'-most EST	dyk700106776.h1

Seq. No.	275762
Contig ID	61672_2.R1011
5'-most EST	tzu700204523.h1

Seq. No.	275763
Contig ID	61673_1.R1011
5'-most EST	LIB3060-020-Q1-K1-C9

Seq. No.	275764
Contig ID	61679_1.R1011

5'-most EST	uC-zmflm017092d04b1
Seq. No.	275765
Contig ID	61686_1.R1011
5'-most EST	LIB36-022-Q1-E1-E6
Seq. No.	275766
Contig ID	61688_1.R1011
5'-most EST	LIB3060-020-Q1-K1-H4
Method	BLASTX
NCBI GI	g115771
BLAST score	490
E value	1.0e-49
Match length	96
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
Seq. No.	275767
Contig ID	61708_1.R1011
5'-most EST	uC-zmflmo17238g12b1
Method	BLASTX
NCBI GI	g4262234
BLAST score	381
E value	1.0e-36
Match length	153
% identity	53
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]
Seq. No.	275768
Contig ID	61708_2.R1011
5'-most EST	LIB3060-020-Q1-K1-H12
Method	BLASTX
NCBI GI	g4262234
BLAST score	359
E value	2.0e-34
Match length	135
% identity	59
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]
Seq. No.	275769
Contig ID	61721_1.R1011
5'-most EST	LIB3060-046-Q1-K1-F1
Method	BLASTX
NCBI GI	g2979555
BLAST score	193
E value	1.0e-14
Match length	120
% identity	39
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]
Seq. No.	275770
Contig ID	61724_1.R1011
5'-most EST	ymt700218649.h1

Seq. No.	275771
Contig ID	61731_1.R1011
5'-most EST	uwc700154137.h1

Seq. No.	275772
Contig ID	61756_1.R1011
5'-most EST	LIB3060-021-Q1-K1-E7

Seq. No.	275773
Contig ID	61760_1.R1011
5'-most EST	mwy700441126.h1
Method	BLASTX
NCBI GI	g4544389
BLAST score	688
E value	2.0e-72
Match length	242
% identity	57
NCBI Description	(AC007047) putative homeodomain protein [Arabidopsis thaliana]

Seq. No.	275774
Contig ID	61781_1.R1011
5'-most EST	uC-zmflmo17297c04b1

Seq. No.	275775
Contig ID	61785_1.R1011
5'-most EST	fwa700097728.h1
Method	BLASTX
NCBI GI	g2286121
BLAST score	280
E value	5.0e-31
Match length	102
% identity	70
NCBI Description	(U88068) sec14 like protein [Oryza sativa]

Seq. No.	275776
Contig ID	61795_1.R1011
5'-most EST	ceu700423149.h1
Method	BLASTX
NCBI GI	g2213590
BLAST score	190
E value	2.0e-14
Match length	94
% identity	43
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	275777
Contig ID	61802_1.R1011
5'-most EST	yyf700348928.h1
Method	BLASTX
NCBI GI	g1362152
BLAST score	293
E value	4.0e-26
Match length	105
% identity	59
NCBI Description	ribosomal protein S6 kinase homolog (clone Aspk11) - oat

>gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]

Seq. No.	275778
Contig ID	61803_1.R1011
5'-most EST	LIB3137-021-Q1-K1-B5
Method	BLASTX
NCBI GI	g2244814
BLAST score	304
E value	1.0e-27
Match length	125
% identity	53
NCBI Description	(Z97336) protein kinase [Arabidopsis thaliana]

Seq. No.	275779
Contig ID	61805_1.R1011
5'-most EST	LIB3060-022-Q1-K1-B2

Seq. No.	275780
Contig ID	61811_1.R1011
5'-most EST	LIB3060-022-Q1-K1-B9
Method	BLASTX
NCBI GI	g4406759
BLAST score	371
E value	2.0e-35
Match length	117
% identity	61
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275781
Contig ID	61813_1.R1011
5'-most EST	uC-zmflmo17118c11b1
Method	BLASTX
NCBI GI	g1800219
BLAST score	501
E value	2.0e-54
Match length	151
% identity	77
NCBI Description	(U56731) phytochrome C [Sorghum bicolor]

Seq. No.	275782
Contig ID	61827_1.R1011
5'-most EST	LIB3060-022-Q1-K1-D7

Seq. No.	275783
Contig ID	61834_1.R1011
5'-most EST	LIB3060-022-Q1-K1-E4
Method	BLASTX
NCBI GI	g3461850
BLAST score	263
E value	1.0e-39
Match length	155
% identity	54
NCBI Description	(AC005315) putative ligand-gated ionic channel [Arabidopsis thaliana]

Seq. No. 275784

Contig ID	61859_1.R1011
5'-most EST	ceu700431943.h1
Method	BLASTX
NCBI GI	g3258575
BLAST score	145
E value	5.0e-09
Match length	40
% identity	68
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	275785
Contig ID	61864_1.R1011
5'-most EST	afb700381008.h1

Seq. No.	275786
Contig ID	61871_1.R1011
5'-most EST	LIB3060-023-Q1-K1-A8

Seq. No.	275787
Contig ID	61872_1.R1011
5'-most EST	LIB3060-023-Q1-K1-B1

Seq. No.	275788
Contig ID	61873_1.R1011
5'-most EST	LIB3060-023-Q1-K1-B10
Method	BLASTX
NCBI GI	g478422
BLAST score	315
E value	8.0e-29
Match length	168
% identity	40
NCBI Description	S-locus-specific receptor kinase (EC 2.7.1.-) - rape

Seq. No.	275789
Contig ID	61876_1.R1011
5'-most EST	uC-zmflmo17335f12b1

Seq. No.	275790
Contig ID	61884_1.R1011
5'-most EST	uC-zmroteosinte034b05b1

Seq. No.	275791
Contig ID	61885_1.R1011
5'-most EST	LIB3060-023-Q1-K1-C4
Method	BLASTX
NCBI GI	g3036801
BLAST score	167
E value	2.0e-11
Match length	100
% identity	41
NCBI Description	(AL022373) putative ascorbate peroxidase [Arabidopsis thaliana] >gi_3805863_emb_CAA21483_ (AL031986) putative ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	275792
Contig ID	61888_1.R1011
5'-most EST	LIB3060-023-Q1-K1-C7

Method	BLASTX
NCBI GI	g2190540
BLAST score	359
E value	5.0e-34
Match length	98
% identity	64
NCBI Description	(AC001229) Similar to Arabidopsis TFL1 (gb_U77674). [Arabidopsis thaliana]

Seq. No.	275793
Contig ID	61908_1.R1011
5'-most EST	hbs701182236.h1

Seq. No.	275794
Contig ID	61947_1.R1011
5'-most EST	LIB3060-024-Q1-K1-A7
Method	BLASTX
NCBI GI	g4512708
BLAST score	360
E value	6.0e-34
Match length	107
% identity	62
NCBI Description	(AC006569) putative glutaredoxin [Arabidopsis thaliana]

Seq. No.	275795
Contig ID	61957_1.R1011
5'-most EST	LIB3060-024-Q1-K1-C1

Seq. No.	275796
Contig ID	61959_1.R1011
5'-most EST	uC-zmflb73051c03b1
Method	BLASTX
NCBI GI	g4102839
BLAST score	463
E value	1.0e-45
Match length	237
% identity	42
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	275797
Contig ID	61959_2.R1011
5'-most EST	uC-zmflmo17175a01a1
Method	BLASTX
NCBI GI	g2651310
BLAST score	238
E value	6.0e-20
Match length	91
% identity	45
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	275798
Contig ID	61961_1.R1011
5'-most EST	LIB83-002-Q1-E1-D8

Seq. No.	275799
Contig ID	61963_1.R1011

5'-most EST	zuv700356284.h1
Method	BLASTX
NCBI GI	g2739028
BLAST score	192
E value	5.0e-14
Match length	248
% identity	25
NCBI Description	(AF023919) PK-120 precursor [Mus musculus]

Seq. No.	275800
Contig ID	61963_2.R1011
5'-most EST	LIB3060-024-Q1-K1-C5

Seq. No.	275801
Contig ID	61965_1.R1011
5'-most EST	LIB3060-024-Q1-K1-D1
Method	BLASTX
NCBI GI	g1001478
BLAST score	278
E value	3.0e-24
Match length	183
% identity	34
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	275802
Contig ID	61966_1.R1011
5'-most EST	LIB3060-024-Q1-K1-C9
Method	BLASTX
NCBI GI	g1652807
BLAST score	181
E value	4.0e-13
Match length	77
% identity	49
NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]

Seq. No.	275803
Contig ID	61968_1.R1011
5'-most EST	nwy700443503.h1

Seq. No.	275804
Contig ID	61969_1.R1011
5'-most EST	LIB3060-024-Q1-K1-D11
Method	BLASTX
NCBI GI	g3831441
BLAST score	190
E value	3.0e-14
Match length	61
% identity	74
NCBI Description	(AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275805
Contig ID	61976_1.R1011
5'-most EST	LIB3060-024-Q1-K1-E1
Method	BLASTX
NCBI GI	g2586083
BLAST score	161
E value	2.0e-12

Match length	127
% identity	32
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	275806
Contig ID	61977_1.R1011
5'-most EST	uC-zmroB73030d12b1
Method	BLASTX
NCBI GI	g4056506
BLAST score	393
E value	8.0e-38
Match length	211
% identity	40
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	275807
Contig ID	61977_2.R1011
5'-most EST	uC-zmrob73006c12b1
Method	BLASTX
NCBI GI	g2598575
BLAST score	168
E value	7.0e-12
Match length	57
% identity	54
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	275808
Contig ID	61988_1.R1011
5'-most EST	fC-zmro700449008d4

Seq. No.	275809
Contig ID	61991_1.R1011
5'-most EST	uC-zmflm017209f03b1
Method	BLASTX
NCBI GI	g4249386
BLAST score	454
E value	2.0e-85
Match length	330
% identity	55
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	275810
Contig ID	61991_2.R1011
5'-most EST	LIB3137-047-Q1-K1-F1
Method	BLASTX
NCBI GI	g4249386
BLAST score	639
E value	1.0e-66
Match length	221
% identity	57
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	275811
Contig ID	61997_1.R1011
5'-most EST	LIB3060-024-Q1-K1-F4
Method	BLASTX
NCBI GI	g2501231
BLAST score	577
E value	1.0e-59
Match length	142
% identity	71
NCBI Description	HYPOTHETICAL 38.1 KD PROTEIN >gi_99505_pir__S24930 hypothetical protein - pink corydalis >gi_18258_emb_CAA45139_ (X63595) protein of unknown function [Corydalis sempervirens] >gi_444333_prf__1906382A pCSC71 protein [Corydalis sempervirens]

Seq. No.	275812
Contig ID	61998_1.R1011
5'-most EST	LIB3060-024-Q1-K1-F5
Method	BLASTX
NCBI GI	g4539520
BLAST score	260
E value	2.0e-22
Match length	184
% identity	11
NCBI Description	(AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins) [Homo sapiens]

Seq. No.	275813
Contig ID	62002_1.R1011
5'-most EST	uC-zmflb73040c05b1
Method	BLASTX
NCBI GI	g4335735
BLAST score	239
E value	6.0e-20
Match length	110
% identity	45
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275814
Contig ID	62006_1.R1011
5'-most EST	hbs701182018.h1

Seq. No.	275815
Contig ID	62006_2.R1011
5'-most EST	uC-zmflb73287h08b1

Seq. No.	275816
Contig ID	62008_1.R1011
5'-most EST	tzu700202541.h1
Method	BLASTX
NCBI GI	g3169171
BLAST score	887
E value	2.0e-95
Match length	422
% identity	42
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi_3445213 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	275817
Contig ID	62026_1.R1011
5'-most EST	uC-zmflmo17103f03b1

Seq. No.	275818
Contig ID	62026_3.R1011
5'-most EST	LIB3060-025-Q1-K1-A6
Method	BLASTX
NCBI GI	g2505870
BLAST score	224
E value	8.0e-29
Match length	108
% identity	60
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275819
Contig ID	62036_1.R1011
5'-most EST	uC-zmflb73032e12b1
Method	BLASTX
NCBI GI	g3877951
BLAST score	255
E value	8.0e-22
Match length	131
% identity	36
NCBI Description	(Z81555) predicted using Genefinder [Caenorhabditis elegans]

Seq. No.	275820
Contig ID	62039_1.R1011
5'-most EST	LIB3060-025-Q1-K1-C1

Seq. No.	275821
Contig ID	62043_1.R1011
5'-most EST	uC-zmflmo17179h04a1
Method	BLASTX
NCBI GI	g2618686
BLAST score	260
E value	5.0e-32
Match length	153
% identity	61
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275822
Contig ID	62043_2.R1011
5'-most EST	mwy700442358.h1
Method	BLASTX
NCBI GI	g2618686
BLAST score	805
E value	4.0e-86
Match length	241
% identity	61
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	275823

Contig ID	62051_1.R1011
5'-most EST	hbs701182987.h1
Method	BLASTX
NCBI GI	g3158376
BLAST score	169
E value	6.0e-12
Match length	105
% identity	41
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	275824
Contig ID	62070_1.R1011
5'-most EST	LIB3060-025-Q1-K1-F11

Seq. No.	275825
Contig ID	62082_1.R1011
5'-most EST	uC-zmflb73055e08b1

Seq. No.	275826
Contig ID	62091_1.R1011
5'-most EST	uC-zmrob73066d04b1

Seq. No.	275827
Contig ID	62093_1.R1011
5'-most EST	wyr700240201.h1
Method	BLASTX
NCBI GI	g3258575
BLAST score	184
E value	2.0e-13
Match length	87
% identity	48
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	275828
Contig ID	62097_1.R1011
5'-most EST	uC-zmrob73076a08b1
Method	BLASTX
NCBI GI	g4336436
BLAST score	639
E value	1.0e-66
Match length	202
% identity	64
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	275829
Contig ID	62102_1.R1011
5'-most EST	LIB3060-026-Q1-K1-H7

Seq. No.	275830
Contig ID	62103_1.R1011
5'-most EST	LIB3060-026-Q1-K1-A3
Method	BLASTX
NCBI GI	g3894176
BLAST score	282
E value	3.0e-42
Match length	102
% identity	76

NCBI Description	(AC005312) putative NAM (no apical meristem) protein [Arabidopsis thaliana]
Seq. No.	275831
Contig ID	62104_1.R1011
5'-most EST	LIB3060-026-Q1-K1-A4
Method	BLASTX
NCBI GI	g3355474
BLAST score	300
E value	3.0e-27
Match length	115
% identity	57
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.	275832
Contig ID	62107_1.R1011
5'-most EST	LIB3060-026-Q1-K1-A7
Seq. No.	275833
Contig ID	62117_1.R1011
5'-most EST	LIB3060-026-Q1-K1-B8
Seq. No.	275834
Contig ID	62118_1.R1011
5'-most EST	LIB3060-026-Q1-K1-C1
Seq. No.	275835
Contig ID	62121_1.R1011
5'-most EST	uC-zmflb73237h07b2
Seq. No.	275836
Contig ID	62125_1.R1011
5'-most EST	yyf700347471.h1
Seq. No.	275837
Contig ID	62131_1.R1011
5'-most EST	LIB3060-026-Q1-K1-D10
Seq. No.	275838
Contig ID	62132_1.R1011
5'-most EST	LIB3069-005-Q1-K1-C12
Method	BLASTX
NCBI GI	g2454302
BLAST score	352
E value	1.0e-32
Match length	149
% identity	46
NCBI Description	(AF000152) OS-4 protein [Homo sapiens]
Seq. No.	275839
Contig ID	62132_2.R1011
5'-most EST	uC-zmflmo17223h09b1
Seq. No.	275840
Contig ID	62132_3.R1011
5'-most EST	LIB3060-026-Q1-K1-D11

Seq. No.	275841
Contig ID	62133_2.R1011
5'-most EST	LIB3060-026-Q1-K1-D12
Seq. No.	275842
Contig ID	62137_1.R1011
5'-most EST	dyk700102343.h1
Seq. No.	275843
Contig ID	62149_1.R1011
5'-most EST	uC-zmflb73029f02b1
Seq. No.	275844
Contig ID	62162_1.R1011
5'-most EST	uC-zmflmo17246g02b1
Seq. No.	275845
Contig ID	62170_1.R1011
5'-most EST	xsy700209180.h1
Seq. No.	275846
Contig ID	62175_1.R1011
5'-most EST	uC-zmflb73119b07b1
Seq. No.	275847
Contig ID	62202_1.R1011
5'-most EST	xmt700263321.h1
Seq. No.	275848
Contig ID	62206_1.R1011
5'-most EST	LIB3060-027-Q1-K1-C8
Seq. No.	275849
Contig ID	62212_1.R1011
5'-most EST	LIB3060-027-Q1-K1-D3
Method	BLASTX
NCBI GI	g2130141
BLAST score	365
E value	2.0e-42
Match length	227
% identity	43
NCBI Description	mudrA protein - maize transposon MuDR >gi_540581 (M76978) mudrA [Zea mays] >gi_595816 (U14597) mudrA gene product [Zea mays]
Seq. No.	275850
Contig ID	62230_1.R1011
5'-most EST	LIB3060-027-Q1-K1-F11
Seq. No.	275851
Contig ID	62232_1.R1011
5'-most EST	LIB3062-017-Q1-K1-D12
Seq. No.	275852
Contig ID	62234_1.R1011
5'-most EST	LIB3060-027-Q1-K1-F4
Method	BLASTX

NCBI GI	g4512613
BLAST score	253
E value	2.0e-21
Match length	86
% identity	63
NCBI Description	(AC004793) F28K20.12 [Arabidopsis thaliana]

Seq. No.	275853
Contig ID	62234_2.R1011
5'-most EST	uer700580694.h1
Method	BLASTX
NCBI GI	g4512613
BLAST score	273
E value	4.0e-24
Match length	72
% identity	72
NCBI Description	(AC004793) F28K20.12 [Arabidopsis thaliana]

Seq. No.	275854
Contig ID	62237_1.R1011
5'-most EST	LIB3062-013-Q1-K1-B8
Method	BLASTX
NCBI GI	g3080740
BLAST score	976
E value	1.0e-106
Match length	257
% identity	70
NCBI Description	(U77366) pasticcino 1-D [Arabidopsis thaliana]

Seq. No.	275855
Contig ID	62241_1.R1011
5'-most EST	uC-zmflb73177f04b1

Seq. No.	275856
Contig ID	62251_1.R1011
5'-most EST	uC-zmflb73194g02b2

Seq. No.	275857
Contig ID	62259_1.R1011
5'-most EST	LIB3060-028-Q1-K1-A3

Seq. No.	275858
Contig ID	62270_1.R1011
5'-most EST	uC-zmflmo17263h02b1

Seq. No.	275859
Contig ID	62275_1.R1011
5'-most EST	LIB3067-007-Q1-K1-G2
Method	BLASTX
NCBI GI	g4512651
BLAST score	198
E value	3.0e-15
Match length	101
% identity	38
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	275860
Contig ID	62286_1.R1011
5'-most EST	LIB3137-039-Q1-K1-E11
Method	BLASTX
NCBI GI	g3775987
BLAST score	220
E value	7.0e-18
Match length	82
% identity	62
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.	275861
Contig ID	62306_1.R1011
5'-most EST	uC-zmflm017212b02b1

Seq. No.	275862
Contig ID	62313_1.R1011
5'-most EST	LIB3060-028-Q1-K1-G12
Method	BLASTX
NCBI GI	g2131505
BLAST score	187
E value	6.0e-14
Match length	118
% identity	35
NCBI Description	hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae) >gi_927738 (U33050) Tom1p; CAI: 0.16 [Saccharomyces cerevisiae]

Seq. No.	275863
Contig ID	62316_1.R1011
5'-most EST	uC-zmflb73225a08b1

Seq. No.	275864
Contig ID	62318_1.R1011
5'-most EST	nbm700469720.h1
Method	BLASTX
NCBI GI	g4335731
BLAST score	338
E value	1.0e-31
Match length	173
% identity	44
NCBI Description	(AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No.	275865
Contig ID	62320_1.R1011
5'-most EST	LIB3060-028-Q1-K1-H1
Method	BLASTX
NCBI GI	g1903364
BLAST score	297
E value	1.0e-26
Match length	152
% identity	44
NCBI Description	(AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No.	275866
Contig ID	62328_1.R1011

5'-most EST	LIB3060-028-Q1-K1-H9
Seq. No.	275867
Contig ID	62343_1.R1011
5'-most EST	wty700167257.h1
Seq. No.	275868
Contig ID	62366_1.R1011
5'-most EST	LIB3060-029-Q1-K1-D6
Seq. No.	275869
Contig ID	62370_1.R1011
5'-most EST	LIB3060-029-Q1-K1-E11
Method	BLASTX
NCBI GI	g2959767
BLAST score	528
E value	5.0e-54
Match length	131
% identity	74
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]
Seq. No.	275870
Contig ID	62374_1.R1011
5'-most EST	LIB3060-029-Q1-K1-E5
Seq. No.	275871
Contig ID	62379_2.R1011
5'-most EST	uC-zmflb73292h10b1
Seq. No.	275872
Contig ID	62384_1.R1011
5'-most EST	LIB3060-029-Q1-K1-F4
Seq. No.	275873
Contig ID	62388_1.R1011
5'-most EST	uC-zmflmo17033d09b2
Method	BLASTX
NCBI GI	g3461835
BLAST score	1064
E value	1.0e-116
Match length	258
% identity	76
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]
Seq. No.	275874
Contig ID	62397_1.R1011
5'-most EST	LIB3067-047-Q1-K1-C11
Method	BLASTX
NCBI GI	g1076660
BLAST score	353
E value	6.0e-33
Match length	147
% identity	54

NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]
Seq. No.	275875
Contig ID	62404_1.R1011
5'-most EST	LIB3060-029-Q1-K1-H4
Method	BLASTX
NCBI GI	g3540201
BLAST score	160
E value	1.0e-10
Match length	63
% identity	52
NCBI Description	(AC004260) Putative nuclear protein [Arabidopsis thaliana]
Seq. No.	275876
Contig ID	62412_1.R1011
5'-most EST	uC-zmflmo17023d09b1
Seq. No.	275877
Contig ID	62434_1.R1011
5'-most EST	afb700381432.h1
Method	BLASTX
NCBI GI	g1652057
BLAST score	171
E value	5.0e-12
Match length	122
% identity	34
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]
Seq. No.	275878
Contig ID	62439_1.R1011
5'-most EST	uC-zmflmo17159f01b1
Method	BLASTN
NCBI GI	g2801535
BLAST score	136
E value	2.0e-70
Match length	303
% identity	87
NCBI Description	Oryza sativa lysophospholipase homolog (LPL1) mRNA, complete cds
Seq. No.	275879
Contig ID	62439_2.R1011
5'-most EST	uC-zmroteosinte028e03b1
Method	BLASTX
NCBI GI	g2801536
BLAST score	733
E value	1.0e-77
Match length	152
% identity	90
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]
Seq. No.	275880
Contig ID	62453_1.R1011
5'-most EST	pmx700089203.h1

Method	BLASTX
NCBI GI	g2244996
BLAST score	311
E value	2.0e-28
Match length	173
% identity	38
NCBI Description	(Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]

Seq. No.	275881
Contig ID	62463_1.R1011
5'-most EST	uC-zmflb73069c01b1
Method	BLASTX
NCBI GI	g738309
BLAST score	223
E value	5.0e-18
Match length	171
% identity	34
NCBI Description	nucler protein GRB1 [Homo sapiens]

Seq. No.	275882
Contig ID	62464_1.R1011
5'-most EST	LIB3060-037-Q1-K1-F7

Seq. No.	275883
Contig ID	62472_1.R1011
5'-most EST	uwc700150959.h1
Method	BLASTN
NCBI GI	g4589409
BLAST score	37
E value	6.0e-11
Match length	77
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	275884
Contig ID	62482_1.R1011
5'-most EST	LIB3060-032-Q1-K1-A2
Method	BLASTX
NCBI GI	g3249064
BLAST score	1184
E value	1.0e-130
Match length	332
% identity	64
NCBI Description	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4 contig gb_Z97344. [Arabidopsis thaliana]

Seq. No.	275885
Contig ID	62492_1.R1011
5'-most EST	LIB3060-032-Q1-K1-B4
Method	BLASTX
NCBI GI	g4249411
BLAST score	229
E value	5.0e-21
Match length	115

% identity 50
NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 275886
Contig ID 62509_1.R1011
5'-most EST LIB3060-032-Q1-K1-D8

Seq. No. 275887
Contig ID 62520_1.R1011
5'-most EST uC-zmroteosinte022a01b1
Method BLASTX
NCBI GI g4263507
BLAST score 754
E value 4.0e-80
Match length 215
% identity 66
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 275888
Contig ID 62527_1.R1011
5'-most EST LIB3060-032-Q1-K1-H1

Seq. No. 275889
Contig ID 62536_1.R1011
5'-most EST LIB3067-017-Q1-K1-H1
Method BLASTX
NCBI GI g3169012
BLAST score 814
E value 3.0e-87
Match length 207
% identity 74
NCBI Description (AJ002610) putative calmodulin binding transporter protein [Hordeum vulgare]

Seq. No. 275890
Contig ID 62553_1.R1011
5'-most EST uC-zmflm017016c06b1
Method BLASTX
NCBI GI g1076793
BLAST score 496
E value 3.0e-50
Match length 115
% identity 51
NCBI Description calmodulin cam2 - maize >gi_747917_emb_CAA54583_ (X77397) calmodulin [Zea mays]

Seq. No. 275891
Contig ID 62553_2.R1011
5'-most EST uC-zmflb73008h02b1
Method BLASTX
NCBI GI g1754999
BLAST score 469
E value 4.0e-47
Match length 113
% identity 81
NCBI Description (U48691) calmodulin TaCaM2-2 [Triticum aestivum] >gi_1755001 (U48692) calmodulin TaCaM2-3 [Triticum

aestivum]

Seq. No.	275892
Contig ID	62563_1.R1011
5'-most EST	LIB3060-034-Q1-K1-E3
Method	BLASTX
NCBI GI	g114551
BLAST score	435
E value	6.0e-73
Match length	161
% identity	89
NCBI Description	ATP SYNTHASE BETA CHAIN >gi_67833_pir__PWZMB H+-transporting ATP synthase (EC 3.6.1.34) beta chain - maize chloroplast >gi_552732 (J01421) coupling factor beta-subunit [Zea mays] >gi_902229_emb_CAA60293_ (X86563) ATPase beta subunit [Zea mays]

Seq. No.	275893
Contig ID	62570_1.R1011
5'-most EST	uC-zmflb73270c11a1

Seq. No.	275894
Contig ID	62570_2.R1011
5'-most EST	yyf700347536.h1
Method	BLASTX
NCBI GI	g3041758
BLAST score	171
E value	5.0e-12
Match length	136
% identity	29
NCBI Description	(D85081) unnamed protein product [Escherichia coli]

Seq. No.	275895
Contig ID	62570_3.R1011
5'-most EST	LIB3137-033-Q1-K1-B11

Seq. No.	275896
Contig ID	62599_1.R1011
5'-most EST	LIB3060-035-Q1-K1-B11
Method	BLASTX
NCBI GI	g2213884
BLAST score	477
E value	5.0e-48
Match length	136
% identity	68
NCBI Description	(AF004166) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	275897
Contig ID	62613_1.R1011
5'-most EST	xsy700212537.h1
Method	BLASTX
NCBI GI	g1170659
BLAST score	190
E value	3.0e-14
Match length	77
% identity	49

NCBI Description	KINESIN-LIKE PROTEIN KIF4 >gi_1083417_pir__A54803 microtubule-associated motor KIF4 - mouse >gi_563773_dbj_BAA02167_ (D12646) KIF4 [Mus musculus]

Seq. No.	275898
Contig ID	62622_1.R1011
5'-most EST	uwc700156383.h1

Seq. No.	275899
Contig ID	62628_1.R1011
5'-most EST	fC-zmse700618106a1
Method	BLASTX
NCBI GI	g3128225
BLAST score	919
E value	3.0e-99
Match length	264
% identity	71
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.	275900
Contig ID	62633_1.R1011
5'-most EST	LIB3060-035-Q1-K1-E4

Seq. No.	275901
Contig ID	62643_1.R1011
5'-most EST	LIB3060-035-Q1-K1-F5

Seq. No.	275902
Contig ID	62650_1.R1011
5'-most EST	uC-zmflmo17129c05a1
Method	BLASTX
NCBI GI	g4008372
BLAST score	270
E value	3.0e-23
Match length	188
% identity	34
NCBI Description	(Z27079) cDNA EST CEMSF67FB comes from this gene; cDNA EST CEMSF67R comes from this gene; cDNA EST yk195e10.3 comes from this gene; cDNA EST yk195e10.5 comes from this gene; cDNA EST yk397a5.3 comes from this gene; cDNA EST yk3

Seq. No.	275903
Contig ID	62650_2.R1011
5'-most EST	LIB3060-035-Q1-K1-G3

Seq. No.	275904
Contig ID	62658_1.R1011
5'-most EST	vqh700053179.r1

Seq. No.	275905
Contig ID	62661_1.R1011
5'-most EST	LIB3061-039-Q1-K1-D8
Method	BLASTX
NCBI GI	g4586118
BLAST score	538
E value	7.0e-55
Match length	181

% identity	58
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	275906
Contig ID	62664_1.R1011
5'-most EST	LIB3060-036-Q1-K1-A9
Method	BLASTX
NCBI GI	g2651310
BLAST score	271
E value	7.0e-24
Match length	135
% identity	41
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	275907
Contig ID	62676_1.R1011
5'-most EST	LIB3060-036-Q1-K1-B3

Seq. No.	275908
Contig ID	62677_1.R1011
5'-most EST	uC-zmflb73009c12a2

Seq. No.	275909
Contig ID	62682_1.R1011
5'-most EST	LIB3060-036-Q1-K1-C1
Method	BLASTX
NCBI GI	g4063750
BLAST score	149
E value	3.0e-09
Match length	138
% identity	34
NCBI Description	(AC005851) putative indole-3-acetate beta-glucosyltransferase synthetase [Arabidopsis thaliana]

Seq. No.	275910
Contig ID	62684_1.R1011
5'-most EST	LIB3062-007-Q1-K1-E10
Method	BLASTX
NCBI GI	g2864618
BLAST score	702
E value	7.0e-74
Match length	248
% identity	57
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	275911
Contig ID	62685_1.R1011
5'-most EST	LIB36-018-Q1-E1-D1

Seq. No.	275912
Contig ID	62699_1.R1011
5'-most EST	nbm700467903.h1
Method	BLASTX
NCBI GI	g2262105
BLAST score	1244
E value	1.0e-137

Match length	408
% identity	54
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	275913
Contig ID	62701_1.R1011
5'-most EST	ceu700426301.h1
Method	BLASTX
NCBI GI	g1363488
BLAST score	337
E value	3.0e-31
Match length	101
% identity	60
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	275914
Contig ID	62701_2.R1011
5'-most EST	uC-zmrob73036d01b1

Seq. No.	275915
Contig ID	62712_1.R1011
5'-most EST	LIB84-028-Q1-E1-H3
Method	BLASTX
NCBI GI	g4512678
BLAST score	281
E value	5.0e-25
Match length	80
% identity	65
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	275916
Contig ID	62721_2.R1011
5'-most EST	LIB3136-026-Q1-K1-C10
Method	BLASTX
NCBI GI	g3688598
BLAST score	210
E value	1.0e-16
Match length	88
% identity	51
NCBI Description	(AB009029) Cycloartenol Synthase [Panax ginseng]

Seq. No.	275917
Contig ID	62723_1.R1011
5'-most EST	LIB3062-002-Q1-K2-A1

Seq. No.	275918
Contig ID	62724_1.R1011
5'-most EST	LIB3060-036-Q1-K1-G6

Seq. No.	275919
Contig ID	62746_1.R1011
5'-most EST	uC-zmrob73004b07b1

Seq. No.	275920

Contig ID 62753_1.R1011
5'-most EST uC-zmflb73052f03b1
Method BLASTX
NCBI GI g3873551
BLAST score 193
E value 3.0e-14
Match length 204
% identity 26
NCBI Description (AL033534) putative vacuolar protein sorting protein subunit [Schizosaccharomyces pombe]

Seq. No. 275921
Contig ID 62753_2.R1011
5'-most EST LIB3068-031-Q1-K1-A9

Seq. No. 275922
Contig ID 62759_1.R1011
5'-most EST dyk700105083.h1

Seq. No. 275923
Contig ID 62766_1.R1011
5'-most EST LIB3069-050-Q1-K1-E2
Method BLASTX
NCBI GI g4467145
BLAST score 154
E value 5.0e-10
Match length 66
% identity 44
NCBI Description (AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No. 275924
Contig ID 62766_2.R1011
5'-most EST uC-zmroB73014f01b1

Seq. No. 275925
Contig ID 62786_1.R1011
5'-most EST LIB3060-038-Q1-K1-A2

Seq. No. 275926
Contig ID 62787_1.R1011
5'-most EST nbm700474511.h1

Seq. No. 275927
Contig ID 62802_1.R1011
5'-most EST nbm700468547.h1

Seq. No. 275928
Contig ID 62806_1.R1011
5'-most EST uC-zmflmo17164g04b1

Seq. No. 275929
Contig ID 62806_2.R1011
5'-most EST uC-zmflMo17014f10b1

Seq. No. 275930
Contig ID 62806_3.R1011

5'-most EST	hvj700619225.h1
Seq. No.	275931
Contig ID	62806_4.R1011
5'-most EST	wyr700243970.h1
Seq. No.	275932
Contig ID	62809_1.R1011
5'-most EST	LIB3060-038-Q1-K1-D6
Seq. No.	275933
Contig ID	62813_1.R1011
5'-most EST	mwy700440513.h1
Method	BLASTX
NCBI GI	g4455296
BLAST score	298
E value	1.0e-45
Match length	174
% identity	63
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]
Seq. No.	275934
Contig ID	62841_1.R1011
5'-most EST	LIB3060-038-Q1-K1-H4
Method	BLASTX
NCBI GI	g1871187
BLAST score	175
E value	8.0e-13
Match length	53
% identity	64
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]
Seq. No.	275935
Contig ID	62844_1.R1011
5'-most EST	LIB3060-039-Q1-K1-H5
Method	BLASTX
NCBI GI	g1346883
BLAST score	459
E value	7.0e-46
Match length	110
% identity	84
NCBI Description	PHYTOENE SYNTHASE PRECURSOR >gi_2130144_pir__S68307 phytoene synthase - maize >gi_1098665 (U32636) phytoene synthase [Zea mays]
Seq. No.	275936
Contig ID	62844_2.R1011
5'-most EST	ymt700221554.h2
Method	BLASTX
NCBI GI	g1346883
BLAST score	592
E value	1.0e-61
Match length	116
% identity	100
NCBI Description	PHYTOENE SYNTHASE PRECURSOR >gi_2130144_pir__S68307 phytoene synthase - maize >gi_1098665 (U32636) phytoene synthase [Zea mays]

Seq. No.	275937
Contig ID	62852_1.R1011
5'-most EST	LIB3660-019-Q1-E1-E3

Seq. No.	275938
Contig ID	62879_1.R1011
5'-most EST	LIB3060-039-Q1-K1-F11

Seq. No.	275939
Contig ID	62890_1.R1011
5'-most EST	pmx700082979.h1

Seq. No.	275940
Contig ID	62920_1.R1011
5'-most EST	LIB3060-041-Q1-K1-D11
Method	BLASTX
NCBI GI	g4249402
BLAST score	661
E value	2.0e-69
Match length	180
% identity	69
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	275941
Contig ID	62931_1.R1011
5'-most EST	LIB3060-041-Q1-K1-A3
Method	BLASTX
NCBI GI	g3152568
BLAST score	480
E value	4.0e-48
Match length	202
% identity	49
NCBI Description	(AC002986) Similar to hypothetical protein product gb_Z97337 from A. thaliana. EST gb_H76597 comes from this gene. [Arabidopsis thaliana]

Seq. No.	275942
Contig ID	62943_1.R1011
5'-most EST	LIB3069-025-Q1-K1-F8
Method	BLASTX
NCBI GI	g3522941
BLAST score	306
E value	2.0e-32
Match length	148
% identity	60
NCBI Description	(AC004411) putative peptide chain release factor [Arabidopsis thaliana]

Seq. No.	275943
Contig ID	62945_1.R1011
5'-most EST	LIB3060-041-Q1-K1-C2
Method	BLASTX
NCBI GI	g1724114
BLAST score	831
E value	4.0e-89
Match length	301

% identity	56
NCBI Description	(U80041) Af10-protein [Avena fatua]

Seq. No.	275944
Contig ID	62945_2.R1011
5'-most EST	uC-zmf1b73026d12b1
Method	BLASTX
NCBI GI	g1724114
BLAST score	289
E value	1.0e-44
Match length	154
% identity	64
NCBI Description	(U80041) Af10-protein [Avena fatua]

Seq. No.	275945
Contig ID	62957_2.R1011
5'-most EST	hbs701182458.h1

Seq. No.	275946
Contig ID	62963_1.R1011
5'-most EST	LIB3060-041-Q1-K1-E11
Method	BLASTX
NCBI GI	g2655098
BLAST score	150
E value	9.0e-10
Match length	61
% identity	48
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	275947
Contig ID	62976_1.R1011
5'-most EST	cat700018290.r1
Method	BLASTX
NCBI GI	g2245092
BLAST score	176
E value	1.0e-14
Match length	223
% identity	38
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	275948
Contig ID	62977_1.R1011
5'-most EST	cyk700048413.f1
Method	BLASTX
NCBI GI	g4539383
BLAST score	698
E value	2.0e-76
Match length	207
% identity	69
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	275949
Contig ID	62987_1.R1011
5'-most EST	LIB3060-041-Q1-K1-H10
Method	BLASTX
NCBI GI	g4115938

BLAST score	432
E value	2.0e-42
Match length	110
% identity	81
NCBI Description	(AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana]

Seq. No.	275950
Contig ID	62988_1.R1011
5'-most EST	LIB3060-041-Q1-K1-H11
Method	BLASTX
NCBI GI	g4164576
BLAST score	414
E value	1.0e-41
Match length	126
% identity	66
NCBI Description	(AF098946) CTF2A [Arabidopsis thaliana]

Seq. No.	275951
Contig ID	62989_1.R1011
5'-most EST	LIB3060-041-Q1-K1-H12
Method	BLASTX
NCBI GI	g3033397
BLAST score	156
E value	2.0e-10
Match length	122
% identity	33
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	275952
Contig ID	62991_1.R1011
5'-most EST	LIB3060-041-Q1-K1-H3

Seq. No.	275953
Contig ID	62993_1.R1011
5'-most EST	uC-zmflmo17242g04b1

Seq. No.	275954
Contig ID	63004_1.R1011
5'-most EST	hvj700624062.h1

Seq. No.	275955
Contig ID	63011_1.R1011
5'-most EST	LIB3067-026-Q1-K1-A3

Seq. No.	275956
Contig ID	63015_1.R1011
5'-most EST	LIB3060-045-Q1-K1-F8
Method	BLASTX
NCBI GI	g4106538
BLAST score	379
E value	2.0e-36
Match length	108
% identity	67
NCBI Description	(AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]

Seq. No.	275957
Contig ID	63016_1.R1011
5'-most EST	gct70l178402.h1
Method	BLASTX
NCBI GI	g3435096
BLAST score	254
E value	2.0e-21
Match length	101
% identity	52
NCBI Description	(AF033587) SRZ-80 [Arabidopsis thaliana]

Seq. No.	275958
Contig ID	63016_2.R1011
5'-most EST	xmt70O268122.h1
Method	BLASTX
NCBI GI	g3281869
BLAST score	261
E value	3.0e-22
Match length	101
% identity	54
NCBI Description	(AL031004) RSZp22 splicing factor [Arabidopsis thaliana] >gi_3435094 (AF033586) 9G8-like SR protein [Arabidopsis thaliana]

Seq. No.	275959
Contig ID	63024_1.R1011
5'-most EST	LIB30O0-042-Q1-K1-D10

Seq. No.	275960
Contig ID	63033_1.R1011
5'-most EST	LIB30O0-042-Q1-K1-E1
Method	BLASTX
NCBI GI	g3201680
BLAST score	290
E value	3.0e-26
Match length	118
% identity	52
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	275961
Contig ID	63053_1.R1011
5'-most EST	uC-zmflmo17153g04b1

Seq. No.	275962
Contig ID	63071_1.R1011
5'-most EST	LIB36-002-Q1-E1-B9
Method	BLASTN
NCBI GI	g11957
BLAST score	177
E value	5.0e-95
Match length	185
% identity	49
NCBI Description	Rice complete chloroplast genome

Seq. No.	275963
Contig ID	63128_1.R1011

5'-most EST	yne700378737.h1
Seq. No.	275964
Contig ID	63129_1.R1011
5'-most EST	dyk700104686.h1
Seq. No.	275965
Contig ID	63141_1.R1011
5'-most EST	LIB3060-043-Q1-K1-H10
Seq. No.	275966
Contig ID	63143_1.R1011
5'-most EST	rvt700550495.h1
Method	BLASTX
NCBI GI	g4574137
BLAST score	546
E value	6.0e-56
Match length	147
% identity	71
NCBI Description	(AF073696) cysteine synthase [Oryza sativa]
Seq. No.	275967
Contig ID	63156_1.R1011
5'-most EST	xjt700095377.h1
Seq. No.	275968
Contig ID	63157_1.R1011
5'-most EST	LIB3060-044-Q1-K1-A8
Method	BLASTX
NCBI GI	g4376203
BLAST score	559
E value	1.0e-107
Match length	418
% identity	48
NCBI Description	(U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]
Seq. No.	275969
Contig ID	63157_2.R1011
5'-most EST	uC-zmflb73233b11b1
Method	BLASTX
NCBI GI	g4376203
BLAST score	405
E value	3.0e-39
Match length	245
% identity	40
NCBI Description	(U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]
Seq. No.	275970
Contig ID	63159_1.R1011
5'-most EST	uC-zmroteosinte022g05b1
Method	BLASTX
NCBI GI	g3522948
BLAST score	1103
E value	1.0e-121
Match length	374

% identity	56
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]
Seq. No.	275971
Contig ID	63190_1.R1011
5'-most EST	LIB3060-044-Q1-K1-E11
Seq. No.	275972
Contig ID	63218_1.R1011
5'-most EST	LIB3060-044-Q1-K1-H10
Method	BLASTN
NCBI GI	g1061307
BLAST score	370
E value	0.0e+00
Match length	393
% identity	99
NCBI Description	Z.mays Dof3 mRNA
Seq. No.	275973
Contig ID	63222_1.R1011
5'-most EST	wyr700237389.h1
Method	BLASTX
NCBI GI	g4587517
BLAST score	255
E value	2.0e-21
Match length	186
% identity	34
NCBI Description	(AC007060) T5I8.6 [Arabidopsis thaliana]
Seq. No.	275974
Contig ID	63227_1.R1011
5'-most EST	uwc700154576.h1
Method	BLASTX
NCBI GI	g3024871
BLAST score	482
E value	7.0e-90
Match length	290
% identity	56
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]
Seq. No.	275975
Contig ID	63228_1.R1011
5'-most EST	LIB3060-045-Q1-K1-A11
Method	BLASTX
NCBI GI	g2739373
BLAST score	154
E value	4.0e-10
Match length	113
% identity	40
NCBI Description	(AC002505) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
Seq. No.	275976
Contig ID	63229_1.R1011
5'-most EST	LIB3060-045-Q1-K1-A12

Seq. No.	275977
Contig ID	63258_1.R1011
5'-most EST	LIB3060-045-Q1-K1-D10
Seq. No.	275978
Contig ID	63262_1.R1011
5'-most EST	LIB3060-045-Q1-K1-D3
Seq. No.	275979
Contig ID	63263_1.R1011
5'-most EST	yyf700350428.h1
Seq. No.	275980
Contig ID	63264_1.R1011
5'-most EST	LIB83-001-Q1-E1-B3
Method	BLASTX
NCBI GI	g298750
BLAST score	730
E value	4.0e-77
Match length	135
% identity	99
NCBI Description	photosystem I reaction center protein psaA product [Sorghum bicolor, Qiuji No. 5, Peptide Chloroplast, 750 aa]
Seq. No.	275981
Contig ID	63265_1.R1011
5'-most EST	uC-zmflB73046d03b1
Seq. No.	275982
Contig ID	63265_2.R1011
5'-most EST	ntr700074927.h1
Method	BLASTX
NCBI GI	g3668091
BLAST score	680
E value	3.0e-71
Match length	237
% identity	26
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]
Seq. No.	275983
Contig ID	63284_1.R1011
5'-most EST	uer700583922.h1
Seq. No.	275984
Contig ID	63284_2.R1011
5'-most EST	LIB3060-048-Q1-K1-E12
Seq. No.	275985
Contig ID	63299_1.R1011
5'-most EST	nbm700471664.h1
Seq. No.	275986
Contig ID	63315_1.R1011
5'-most EST	uC-zmflb73019b04b1
Seq. No.	275987

Contig ID	63316_1.R1011
5'-most EST	xmt70263636.h1
Method	BLASTX
NCBI GI	g1208886
BLAST score	147
E value	3.0e-12
Match length	121
% identity	37
NCBI Description	(U50135) coded for by C. elegans cDNA yk46f1.3; coded for by C. elegans cDNA yk46f1.5; weakly similar to S. cerevisiae vanadate resistance protein G0G5/VRG4 (GB:L33915) [Caenorhabditis elegans]

Seq. No.	275988
Contig ID	63316_2.R1011
5'-most EST	LIB3060-046-Q1-K1-A8
Method	BLASTX
NCBI GI	g1665787
BLAST score	173
E value	4.0e-12
Match length	144
% identity	32
NCBI Description	(D87449) Similar to a C.elegans protein encoded in cosmid C52E12 (U50135) [Homo sapiens]

Seq. No.	275989
Contig ID	63318_1.R1011
5'-most EST	LIB3060-046-Q1-K1-B1

Seq. No.	275990
Contig ID	63335_1.R1011
5'-most EST	uC-zmroteosinte097h02b1
Method	BLASTN
NCBI GI	g902585
BLAST score	40
E value	8.0e-13
Match length	44
% identity	98
NCBI Description	Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No.	275991
Contig ID	63335_2.R1011
5'-most EST	uC-zmflb73184h02b1
Method	BLASTN
NCBI GI	g998429
BLAST score	37
E value	5.0e-11
Match length	73
% identity	88
NCBI Description	GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]

Seq. No.	275992
Contig ID	63339_1.R1011
5'-most EST	uC-zmflb73272a05b1

Seq. No. 275993

Contig ID	63339_2.R1011
5'-most EST	uC-zmflb73298b03b1
Seq. No.	275994
Contig ID	63341_1.R1011
5'-most EST	uC-zmflmo17267a01b1
Seq. No.	275995
Contig ID	63341_2.R1011
5'-most EST	uC-zmflmo17344a07a1
Seq. No.	275996
Contig ID	63341_3.R1011
5'-most EST	gct701167118.h1
Seq. No.	275997
Contig ID	63344_1.R1011
5'-most EST	xsy700217031.h1
Method	BLASTX
NCBI GI	g2980765
BLAST score	504
E value	5.0e-51
Match length	160
% identity	59
NCBI Description	(AL022198) hypothetical protein [Arabidopsis thaliana]
Seq. No.	275998
Contig ID	63353_1.R1011
5'-most EST	LIB3060-046-Q1-K1-E4
Seq. No.	275999
Contig ID	63354_1.R1011
5'-most EST	uC-zmrob73004h12b1
Seq. No.	276000
Contig ID	63355_1.R1011
5'-most EST	uC-zmflmo17287g11b1
Seq. No.	276001
Contig ID	63355_2.R1011
5'-most EST	LIB3060-046-Q1-K1-E7
Seq. No.	276002
Contig ID	63366_1.R1011
5'-most EST	uC-zmflmo17242e10b1
Method	BLASTX
NCBI GI	g3355308
BLAST score	475
E value	2.0e-47
Match length	180
% identity	52
NCBI Description	(AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
Seq. No.	276003
Contig ID	63367_1.R1011
5'-most EST	LIB3066-031-Q1-K1-H3

Seq. No.	276004
Contig ID	63368_1.R1011
5'-most EST	LIB3060-046-Q1-K1-G11

Seq. No.	276005
Contig ID	63369_1.R1011
5'-most EST	LIB3060-046-Q1-K1-G12
Method	BLASTX
NCBI GI	g2047324
BLAST score	534
E value	1.0e-54
Match length	130
% identity	73
NCBI Description	(U80192) HAL3 homolog [Arabidopsis thaliana]

Seq. No.	276006
Contig ID	63375_1.R1011
5'-most EST	uC-zmflb73125h10b2
Method	BLASTX
NCBI GI	g2105137
BLAST score	1156
E value	1.0e-127
Match length	258
% identity	86
NCBI Description	(U66876) ADP-glucose pyrophosphorylase large subunit [Hordeum vulgare]

Seq. No.	276007
Contig ID	63377_1.R1011
5'-most EST	uC-zmflb73151f11b1

Seq. No.	276008
Contig ID	63380_1.R1011
5'-most EST	LIB83-008-Q1-E1-G4

Seq. No.	276009
Contig ID	63383_1.R1011
5'-most EST	uwc700150510.h1

Seq. No.	276010
Contig ID	63401_1.R1011
5'-most EST	uC-zmflMo17065g11b1
Method	BLASTX
NCBI GI	g3885340
BLAST score	528
E value	1.0e-53
Match length	235
% identity	63
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	276011
Contig ID	63401_2.R1011
5'-most EST	LIB3060-047-Q1-K1-B4
Method	BLASTX
NCBI GI	g3885340
BLAST score	394
E value	3.0e-38

Match length	143
% identity	59
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	276012
Contig ID	63407_1.R1011
5'-most EST	LIB3060-047-Q1-K1-C10
Method	BLASTX
NCBI GI	g4589389
BLAST score	358
E value	3.0e-39
Match length	165
% identity	51
NCBI Description	(AB025433) beta-galactosidase [Psychromonas sp. 4-22]

Seq. No.	276013
Contig ID	63409_1.R1011
5'-most EST	ceu700430576.h1

Seq. No.	276014
Contig ID	63410_1.R1011
5'-most EST	LIB3060-047-Q1-K1-C2
Method	BLASTX
NCBI GI	g3413425
BLAST score	443
E value	9.0e-44
Match length	175
% identity	53
NCBI Description	(AJ006309) protein tyrosine phosphatase [Arabidopsis thaliana]

Seq. No.	276015
Contig ID	63415_1.R1011
5'-most EST	ypc700805296.h1
Method	BLASTX
NCBI GI	g1730576
BLAST score	297
E value	7.0e-27
Match length	122
% identity	50
NCBI Description	PROLINE IMINOPEPTIDASE (PROLYL AMINOPEPTIDASE) >gi_1084134_pir__JC4184 prolyl aminopeptidase (EC 3.4.11.5) - Aeromonas sobria >gi_1236731_dbj_BAA06380_ (D30714) prolyl aminopeptidase [Aeromonas sobria]

Seq. No.	276016
Contig ID	63421_1.R1011
5'-most EST	LIB36-021-Q1-E1-B4

Seq. No.	276017
Contig ID	63425_1.R1011
5'-most EST	xmt700260657.h1
Method	BLASTX
NCBI GI	g3540196
BLAST score	408
E value	7.0e-40
Match length	125

% identity	66
NCBI Description	(AC004260) Putative amp-binding protein [Arabidopsis thaliana]
Seq. No.	276018
Contig ID	63433_1.R1011
5'-most EST	fdz701159587.h1
Seq. No.	276019
Contig ID	63437_1.R1011
5'-most EST	fwa700099501.h1
Seq. No.	276020
Contig ID	63440_1.R1011
5'-most EST	tfd700572448.h1
Method	BLASTX
NCBI GI	g2462749
BLAST score	623
E value	5.0e-81
Match length	219
% identity	73
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
Seq. No.	276021
Contig ID	63446_1.R1011
5'-most EST	LIB3060-047-Q1-K1-G10
Method	BLASTX
NCBI GI	g2827528
BLAST score	186
E value	6.0e-14
Match length	63
% identity	52
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.	276022
Contig ID	63447_1.R1011
5'-most EST	LIB3060-047-Q1-K1-G11
Method	BLASTX
NCBI GI	g2501493
BLAST score	211
E value	9.0e-17
Match length	66
% identity	58
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 4 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 4) >gi_458547_emb_CAA54610_ (X77460) UTP-glucose glucosyltransferase [Manihot esculenta]
Seq. No.	276023
Contig ID	63447_2.R1011
5'-most EST	fwa700101608.h1
Seq. No.	276024
Contig ID	63460_1.R1011
5'-most EST	LIB3060-047-Q1-K1-H5
Method	BLASTX

NCBI GI	g2245109
BLAST score	261
E value	1.0e-22
Match length	104
% identity	51
NCBI Description	(Z97343) carboxyl-terminal proteinase homolog [Arabidopsis thaliana]

Seq. No.	276025
Contig ID	63471_1.R1011
5'-most EST	uC-zmflmo17259e10b1

Seq. No.	276026
Contig ID	63485_1.R1011
5'-most EST	LIB3060-048-Q1-K1-C11

Seq. No.	276027
Contig ID	63507_1.R1011
5'-most EST	uC-zmflb73222b12b1
Method	BLASTX
NCBI GI	g4335745
BLAST score	378
E value	4.0e-36
Match length	148
% identity	48
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	276028
Contig ID	63507_4.R1011
5'-most EST	uC-zmflmo17022b08b1
Method	BLASTX
NCBI GI	g4335745
BLAST score	193
E value	1.0e-14
Match length	98
% identity	41
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	276029
Contig ID	63514_1.R1011
5'-most EST	uC-zmroteosinte053a06b2
Method	BLASTX
NCBI GI	g2576363
BLAST score	645
E value	1.0e-73
Match length	304
% identity	50
NCBI Description	(U39783) amino acid transport protein [Arabidopsis thaliana]

Seq. No.	276030
Contig ID	63531_1.R1011
5'-most EST	LIB3060-048-Q1-K1-G7

Seq. No.	276031
Contig ID	63548_1.R1011
5'-most EST	uC-zmroteosinte068c02b1
Method	BLASTX
NCBI GI	g3882321
BLAST score	225
E value	4.0e-18
Match length	102
% identity	46
NCBI Description	(AB018343) KIAA0800 protein [Homo sapiens]

Seq. No.	276032
Contig ID	63564_1.R1011
5'-most EST	uC-zmflmo17265h01b1

Seq. No.	276033
Contig ID	63568_1.R1011
5'-most EST	uC-zmflmo17320e02b1
Method	BLASTX
NCBI GI	g1841966
BLAST score	186
E value	2.0e-13
Match length	166
% identity	17
NCBI Description	(U65916) ankyrin [Rattus norvegicus]

Seq. No.	276034
Contig ID	63571_1.R1011
5'-most EST	LIB3060-049-Q1-K1-D10

Seq. No.	276035
Contig ID	63588_1.R1011
5'-most EST	uC-zmflmo17048d06b1
Method	BLASTX
NCBI GI	g4584527
BLAST score	165
E value	3.0e-11
Match length	55
% identity	55
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	276036
Contig ID	63597_1.R1011
5'-most EST	LIB3060-049-Q1-K1-G10
Method	BLASTX
NCBI GI	g4406814
BLAST score	375
E value	1.0e-35
Match length	114
% identity	64
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	276037
Contig ID	63600_1.R1011
5'-most EST	LIB3060-049-Q1-K1-G2

Method	BLASTX
NCBI GI	g3603230
BLAST score	218
E value	1.0e-17
Match length	93
% identity	46
NCBI Description	(AF026850) cytochrome oxidase assembly factor [Homo sapiens]

Seq. No.	276038
Contig ID	63601_1.R1011
5'-most EST	uer700579651.h1

Seq. No.	276039
Contig ID	63620_1.R1011
5'-most EST	LIB84-008-Q1-E1-E9

Seq. No.	276040
Contig ID	63663_1.R1011
5'-most EST	xjt700095935.h1
Method	BLASTX
NCBI GI	g1143445
BLAST score	227
E value	1.0e-18
Match length	120
% identity	43
NCBI Description	(X88797) cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]

Seq. No.	276041
Contig ID	63666_1.R1011
5'-most EST	LIB3060-051-Q1-K1-A4

Seq. No.	276042
Contig ID	63670_1.R1011
5'-most EST	uC-zmflb73100b11b1
Method	BLASTX
NCBI GI	g4539008
BLAST score	348
E value	1.0e-32
Match length	177
% identity	46
NCBI Description	(AL049481) lipase-like protein [Arabidopsis thaliana]

Seq. No.	276043
Contig ID	63680_1.R1011
5'-most EST	LIB3060-051-Q1-K1-C11

Seq. No.	276044
Contig ID	63682_1.R1011
5'-most EST	LIB3060-051-Q1-K1-C2
Method	BLASTX
NCBI GI	g2832661
BLAST score	247
E value	2.0e-31
Match length	131
% identity	62
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No.	276045
Contig ID	63683_1.R1011
5'-most EST	LIB3060-051-Q1-K1-C3
Method	BLASTX
NCBI GI	g1653089
BLAST score	233
E value	4.0e-19
Match length	67
% identity	63
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	276046
Contig ID	63686_1.R1011
5'-most EST	LIB3060-051-Q1-K1-C6
Method	BLASTX
NCBI GI	g3395424
BLAST score	186
E value	9.0e-14
Match length	128
% identity	31
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana] >gi_3786024 (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276047
Contig ID	63695_1.R1011
5'-most EST	LIB3060-051-Q1-K1-D3
Method	BLASTX
NCBI GI	g3702337
BLAST score	355
E value	2.0e-34
Match length	188
% identity	49
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	276048
Contig ID	63717_1.R1011
5'-most EST	uC-zmflmo17206b11a1
Method	BLASTX
NCBI GI	g4490308
BLAST score	779
E value	1.0e-106
Match length	303
% identity	67
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	276049
Contig ID	63717_3.R1011
5'-most EST	xmt700257696.h1

Seq. No.	276050
Contig ID	63717_7.R1011
5'-most EST	tfd700569636.h1
Method	BLASTN
NCBI GI	g902585

BLAST score	38
E value	8.0e-12
Match length	66
% identity	89
NCBI Description	Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No.	276051
Contig ID	63727_1.R1011
5'-most EST	wty700167019.h1

Seq. No.	276052
Contig ID	63746_1.R1011
5'-most EST	LIB3061-045-Q1-K1-G8

Seq. No.	276053
Contig ID	63746_2.R1011
5'-most EST	cyk700050212.f1

Seq. No.	276054
Contig ID	63756_1.R1011
5'-most EST	LIB3060-052-Q1-K1-B11

Seq. No.	276055
Contig ID	63757_1.R1011
5'-most EST	uC-zmflmo17222f01a1

Seq. No.	276056
Contig ID	63764_1.R1011
5'-most EST	LIB3060-052-Q1-K1-C2
Method	BLASTX
NCBI GI	g3877536
BLAST score	166
E value	2.0e-11
Match length	124
% identity	31
NCBI Description	(Z77663) Similarity to Rabbit dimethylaniline monooxygenase (SW:FMO2_RABIT); cDNA EST EMBL:M89097 comes from this gene; cDNA EST yk290c2.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	276057
Contig ID	63773_1.R1011
5'-most EST	LIB3060-052-Q1-K1-C7

Seq. No.	276058
Contig ID	63780_1.R1011
5'-most EST	LIB3060-052-Q1-K1-D2
Method	BLASTX
NCBI GI	g1708191
BLAST score	707
E value	1.0e-74
Match length	232
% identity	57
NCBI Description	HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No.	276059

Contig ID	63785_1.R1011
5'-most EST	LIB3060-052-Q1-K1-D7
Seq. No.	276060
Contig ID	63803_1.R1011
5'-most EST	LIB3060-052-Q1-K1-F2
Seq. No.	276061
Contig ID	63805_1.R1011
5'-most EST	uC-zmflmo17136h05b1
Seq. No.	276062
Contig ID	63816_1.R1011
5'-most EST	tfd700575289.h1
Method	BLASTX
NCBI GI	g2760349
BLAST score	488
E value	2.0e-49
Match length	99
% identity	21
NCBI Description	(U84969) ubiquitin [Arabidopsis thaliana]
Seq. No.	276063
Contig ID	63817_1.R1011
5'-most EST	LIB3062-039-Q1-K1-C12
Method	BLASTX
NCBI GI	g4539459
BLAST score	662
E value	3.0e-69
Match length	193
% identity	64
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]
Seq. No.	276064
Contig ID	63823_1.R1011
5'-most EST	LIB3060-052-Q1-K1-H2
Seq. No.	276065
Contig ID	63825_1.R1011
5'-most EST	LIB3060-052-Q1-K1-H11
Method	BLASTX
NCBI GI	g2462753
BLAST score	220
E value	2.0e-17
Match length	81
% identity	57
NCBI Description	(AC002292) putative polygalacturonase [Arabidopsis thaliana]
Seq. No.	276066
Contig ID	63836_1.R1011
5'-most EST	xmt700262777.h1
Seq. No.	276067
Contig ID	63839_1.R1011
5'-most EST	LIB3060-053-Q1-K1-A5

Seq. No.	276068
Contig ID	63848_1.R1011
5'-most EST	LIB3060-053-Q1-K1-B2

Seq. No.	276069
Contig ID	63850_1.R1011
5'-most EST	wyr700244205.h1

Seq. No.	276070
Contig ID	63855_1.R1011
5'-most EST	LIB3136-040-P1-K1-B6
Method	BLASTX
NCBI GI	g4559372
BLAST score	201
E value	1.0e-15
Match length	90
% identity	44
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana] >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No.	276071
Contig ID	63866_1.R1011
5'-most EST	LIB3060-053-Q1-K1-C8
Method	BLASTX
NCBI GI	g3445397
BLAST score	657
E value	9.0e-69
Match length	197
% identity	62
NCBI Description	(AJ010166) S-domain receptor-like protein kinase [Zea mays]

Seq. No.	276072
Contig ID	63868_1.R1011
5'-most EST	uC-zmflmo17201c09b1
Method	BLASTX
NCBI GI	g4220514
BLAST score	417
E value	8.0e-41
Match length	149
% identity	52
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	276073
Contig ID	63874_1.R1011
5'-most EST	LIB84-017-Q1-E1-B5
Method	BLASTX
NCBI GI	g3777602
BLAST score	437
E value	3.0e-43
Match length	94
% identity	90
NCBI Description	(AF095709) 50S ribosomal protein L10 [Oryza sativa]

Seq. No.	276074
Contig ID	63883_1.R1011
5'-most EST	fwa700098304.h1

Method	BLASTX
NCBI GI	g3582333
BLAST score	624
E value	3.0e-65
Match length	147
% identity	78
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276075
Contig ID	63894_1.R1011
5'-most EST	LIB3060-053-Q1-K1-F2

Seq. No.	276076
Contig ID	63897_1.R1011
5'-most EST	uC-zmflb73015b06b1

Seq. No.	276077
Contig ID	63898_1.R1011
5'-most EST	LIB3060-053-Q1-K1-F8
Method	BLASTX
NCBI GI	g2213581
BLAST score	196
E value	7.0e-15
Match length	55
% identity	62
NCBI Description	(AC000348) T7N9.1 [Arabidopsis thaliana]

Seq. No.	276078
Contig ID	63902_1.R1011
5'-most EST	LIB3060-053-Q1-K1-G11

Seq. No.	276079
Contig ID	63912_1.R1011
5'-most EST	gct701179349.h1

Seq. No.	276080
Contig ID	63918_1.R1011
5'-most EST	LIB3060-053-Q1-K1-H7
Method	BLASTX
NCBI GI	g3128234
BLAST score	390
E value	9.0e-38
Match length	151
% identity	54
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276081
Contig ID	63936_1.R1011
5'-most EST	LIB3060-054-Q1-K1-B4

Seq. No.	276082
Contig ID	63946_1.R1011
5'-most EST	ypc700803483.h1

Seq. No.	276083
Contig ID	63957_1.R1011
5'-most EST	LIB3060-054-Q1-K1-D3

Method	BLASTX
NCBI GI	g3176664
BLAST score	170
E value	1.0e-11
Match length	88
% identity	41
NCBI Description	(AC004393) Contains similarity to beta scruin gb_Z47541 from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955 come from this gene. [Arabidopsis thaliana]

Seq. No.	276084
Contig ID	63972_1.R1011
5'-most EST	LIB3060-054-Q1-K1-F1
Method	BLASTX
NCBI GI	g2244806
BLAST score	392
E value	1.0e-37
Match length	225
% identity	42
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276085
Contig ID	63973_1.R1011
5'-most EST	vux700158227.h1
Method	BLASTX
NCBI GI	g4455285
BLAST score	471
E value	3.0e-47
Match length	153
% identity	56
NCBI Description	(AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276086
Contig ID	63982_1.R1011
5'-most EST	uC-zmroteosinte080g03b1
Method	BLASTX
NCBI GI	g2828293
BLAST score	355
E value	2.0e-33
Match length	121
% identity	59
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	276087
Contig ID	63992_1.R1011
5'-most EST	LIB83-001-Q1-E1-H5

Seq. No.	276088
Contig ID	63993_1.R1011
5'-most EST	LIB3060-054-Q1-K1-H10

Seq. No.	276089
Contig ID	64001_1.R1011
5'-most EST	uC-zmflmo17270h06b1

Seq. No.	276090
Contig ID	64005_2.R1011

5'-most EST	LIB3061-001-Q1-K1-A12
Seq. No.	276091
Contig ID	64006_1.R1011
5'-most EST	LIB3061-001-Q1-K1-A9
Method	BLASTN
NCBI GI	g1840117
BLAST score	88
E value	5.0e-42
Match length	104
% identity	97
NCBI Description	Zea mays PIF-12 transposable element in r-1 (r-p) locus, complete sequence
Seq. No.	276092
Contig ID	64034_1.R1011
5'-most EST	uC-zmflb73137h09b1
Method	BLASTX
NCBI GI	g2130442
BLAST score	173
E value	5.0e-12
Match length	183
% identity	28
NCBI Description	hypothetical protein SPAC8A4.01c - fission yeast (Schizosaccharomyces pombe) (fragment) >gi_1052534_emb_CAA91511_ (Z66569) unknown [Schizosaccharomyces pombe]
Seq. No.	276093
Contig ID	64052_1.R1011
5'-most EST	yyf700350790.h1
Method	BLASTX
NCBI GI	g3786011
BLAST score	524
E value	3.0e-53
Match length	169
% identity	63
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]
Seq. No.	276094
Contig ID	64066_1.R1011
5'-most EST	uwc700152904.h1
Method	BLASTX
NCBI GI	g3218544
BLAST score	458
E value	2.0e-45
Match length	168
% identity	64
NCBI Description	(AB004813) alternative oxidase [Oryza sativa] >gi_3218546_dbj_BAA28773_ (AB004864) alternative oxidase [Oryza sativa]
Seq. No.	276095
Contig ID	64068_1.R1011
5'-most EST	uC-zmflb73149b09b1
Method	BLASTX

NCBI GI g3928869
BLAST score 148
E value 7.0e-09
Match length 235
% identity 24
NCBI Description (AF093420) Hsp70 binding protein HspBP1 [Homo sapiens]

Seq. No. 276096
Contig ID 64073_1.R1011
5'-most EST pmx700083287.h1

Seq. No. 276097
Contig ID 64074_1.R1011
5'-most EST LIB3061-002-Q1-K2-B10

Seq. No. 276098
Contig ID 64083_1.R1011
5'-most EST mwy700442001.h1
Method BLASTX
NCBI GI g584707
BLAST score 299
E value 1.0e-26
Match length 102
% identity 56
NCBI Description ABSCISIC ACID-INSENSITIVE PROTEIN 3 >gi_320551_pir__JQ1676 ABI3 protein - Arabidopsis thaliana >gi_16146_emb_CAA48241_ (X68141) ABI3 protein [Arabidopsis thaliana]

Seq. No. 276099
Contig ID 64083_2.R1011
5'-most EST LIB3061-002-Q1-K2-F12
Method BLASTN
NCBI GI g535019
BLAST score 127
E value 5.0e-65
Match length 199
% identity 45
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 276100
Contig ID 64083_3.R1011
5'-most EST uC-zmroteosinte093h10b2
Method BLASTX
NCBI GI g584707
BLAST score 245
E value 2.0e-20
Match length 100
% identity 48
NCBI Description ABSCISIC ACID-INSENSITIVE PROTEIN 3 >gi_320551_pir__JQ1676 ABI3 protein - Arabidopsis thaliana >gi_16146_emb_CAA48241_ (X68141) ABI3 protein [Arabidopsis thaliana]

Seq. No. 276101
Contig ID 64093_1.R1011
5'-most EST uC-zmflb73088f05b2
Method BLASTX
NCBI GI g4539335

BLAST score	1090
E value	1.0e-123
Match length	296
% identity	67
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	276102
Contig ID	64093_2.R1011
5'-most EST	uC-zmflmo17219b11a1
Method	BLASTX
NCBI GI	g4539335
BLAST score	240
E value	4.0e-20
Match length	64
% identity	56
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	276103
Contig ID	64108_1.R1011
5'-most EST	LIB3061-002-Q1-K2-C2
Method	BLASTX
NCBI GI	g3377842
BLAST score	270
E value	1.0e-23
Match length	125
% identity	49
NCBI Description	(AF076274) No definition line found [Arabidopsis thaliana]

Seq. No.	276104
Contig ID	64108_2.R1011
5'-most EST	uer700579977.h1

Seq. No.	276105
Contig ID	64109_1.R1011
5'-most EST	yne700378661.h1
Method	BLASTX
NCBI GI	g4417276
BLAST score	209
E value	1.0e-16
Match length	68
% identity	60
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	276106
Contig ID	64112_1.R1011
5'-most EST	uC-zmroB73030c10b1
Method	BLASTX
NCBI GI	g3540206
BLAST score	349
E value	1.0e-42
Match length	124
% identity	66
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	276107
Contig ID	64124_1.R1011
5'-most EST	uC-zmflmo17164c07b1

Seq. No.	276108
Contig ID	64241_1.R1011
5'-most EST	uC-zmflmo17240b04b1
Method	BLASTX
NCBI GI	g3451474
BLAST score	985
E value	1.0e-107
Match length	416
% identity	45
NCBI Description	(AL031349) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	276109
Contig ID	64258_1.R1011
5'-most EST	LIB3069-001-Q1-K1-A4
Method	BLASTX
NCBI GI	g2088651
BLAST score	326
E value	9.0e-30
Match length	173
% identity	40
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	276110
Contig ID	64270_1.R1011
5'-most EST	zuv700353862.h1

Seq. No.	276111
Contig ID	64272_1.R1011
5'-most EST	LIB84-025-Q1-E1-A11

Seq. No.	276112
Contig ID	64284_1.R1011
5'-most EST	LIB3061-006-Q1-K1-C9

Seq. No.	276113
Contig ID	64301_1.R1011
5'-most EST	LIB3137-007-Q1-K1-A5
Method	BLASTX
NCBI GI	g4512664
BLAST score	1202
E value	1.0e-132
Match length	313
% identity	71
NCBI Description	(AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	276114
Contig ID	64316_1.R1011
5'-most EST	LIB3061-006-Q1-K1-G3
Method	BLASTX
NCBI GI	g4262162
BLAST score	152

E value	1.0e-09
Match length	79
% identity	38
NCBI Description	(AC005275) putative glycosylation enzyme [Arabidopsis thaliana]

Seq. No.	276115
Contig ID	64319_1.R1011
5'-most EST	LIB3061-006-Q1-K1-G9
Method	BLASTX
NCBI GI	g961442
BLAST score	191
E value	2.0e-14
Match length	101
% identity	46
NCBI Description	(D63875) KIAA0155 gene product is related to C.elegans B0464.2 protein. [Homo sapiens]

Seq. No.	276116
Contig ID	64324_1.R1011
5'-most EST	ntr700071935.h1
Method	BLASTX
NCBI GI	g1730910
BLAST score	248
E value	1.0e-20
Match length	200
% identity	35
NCBI Description	HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION >gi_1256633 (L77246) putative [Bacillus subtilis] >gi_2634609_emb_CAB14107_ (Z99115) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	276117
Contig ID	64324_2.R1011
5'-most EST	LIB3137-036-Q1-K1-H9

Seq. No.	276118
Contig ID	64324_3.R1011
5'-most EST	uC-zmflmo17055g09b1

Seq. No.	276119
Contig ID	64345_1.R1011
5'-most EST	LIB3061-007-Q1-K1-C4
Method	BLASTX
NCBI GI	g3023275
BLAST score	203
E value	9.0e-16
Match length	108
% identity	45
NCBI Description	ALPHA-GLUCOSIDASE PRECURSOR (MALTASE) >gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) - barley >gi_944901 (U22450) alpha-glucosidase [Hordeum vulgare]

Seq. No.	276120
Contig ID	64349_1.R1011
5'-most EST	LIB3061-007-Q1-K1-C9

Method	BLASTX
NCBI GI	g129808
BLAST score	315
E value	8.0e-29
Match length	177
% identity	42
NCBI Description	CATIONIC PEROXIDASE 2 PRECURSOR >gi_99873_pir__B38265 peroxidase (EC 1.11.1.7) precursor, cationic (clone PNC2) - peanut >gi_166475 (M37637) cationic peroxidase [Arachis hypogaea]

Seq. No.	276121
Contig ID	64354_1.R1011
5'-most EST	LIB3061-007-Q1-K1-E12
Method	BLASTX
NCBI GI	g100905
BLAST score	619
E value	2.0e-64
Match length	171
% identity	77
NCBI Description	Opaque-2 protein - maize

Seq. No.	276122
Contig ID	64359_1.R1011
5'-most EST	LIB3061-007-Q1-K1-F11

Seq. No.	276123
Contig ID	64367_1.R1011
5'-most EST	LIB3061-007-Q1-K1-G4
Method	BLASTX
NCBI GI	g3046695
BLAST score	258
E value	5.0e-22
Match length	104
% identity	61
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	276124
Contig ID	64367_2.R1011
5'-most EST	LIB3137-009-Q1-K1-H9
Method	BLASTX
NCBI GI	g3046695
BLAST score	148
E value	3.0e-09
Match length	74
% identity	45
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	276125
Contig ID	64375_1.R1011
5'-most EST	fC-zmle700441928a4
Method	BLASTX
NCBI GI	g169363
BLAST score	150
E value	1.0e-09
Match length	35
% identity	71

NCBI Description	(M75856) PVPR3 [Phaseolus vulgaris]
Seq. No.	276126
Contig ID	64378_1.R1011
5'-most EST	uC-zmflb73068g05b1
Seq. No.	276127
Contig ID	64383_1.R1011
5'-most EST	uC-zmflmo17183g11a1
Seq. No.	276128
Contig ID	64384_1.R1011
5'-most EST	uC-zmflmo17258h05b1
Seq. No.	276129
Contig ID	64393_1.R1011
5'-most EST	LIB3061-008-Q1-K1-D5
Seq. No.	276130
Contig ID	64394_1.R1011
5'-most EST	LIB3061-008-Q1-K1-D9
Seq. No.	276131
Contig ID	64404_1.R1011
5'-most EST	uC-zmflmo17105a02b1
Method	BLASTX
NCBI GI	g4586249
BLAST score	590
E value	2.0e-60
Match length	311
% identity	43
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]
Seq. No.	276132
Contig ID	64440_1.R1011
5'-most EST	uC-zmflMo17009d02b1
Method	BLASTX
NCBI GI	g3510253
BLAST score	188
E value	1.0e-26
Match length	140
% identity	49
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276133
Contig ID	64440_2.R1011
5'-most EST	xmt700267756.h1
Method	BLASTX
NCBI GI	g3510253
BLAST score	180
E value	6.0e-13
Match length	50
% identity	66
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276134

Contig ID	64463_1.R1011
5'-most EST	uC-zmflmo17015e08b1
Method	BLASTX
NCBI GI	g3107903
BLAST score	242
E value	1.0e-19
Match length	180
% identity	44
NCBI Description	(D83719) polycomb-like protein [Daucus carota]

Seq. No.	276135
Contig ID	64466_1.R1011
5'-most EST	LIB3061-009-Q1-K1-H12
Method	BLASTX
NCBI GI	g4539009
BLAST score	255
E value	1.0e-24
Match length	173
% identity	43
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	276136
Contig ID	64472_1.R1011
5'-most EST	uC-zmroteosinte017d05b1
Method	BLASTX
NCBI GI	g4455359
BLAST score	216
E value	2.0e-17
Match length	65
% identity	65
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	276137
Contig ID	64481_1.R1011
5'-most EST	LIB3061-010-Q1-K1-B9

Seq. No.	276138
Contig ID	64485_1.R1011
5'-most EST	fdz701166789.h1

Seq. No.	276139
Contig ID	64489_1.R1011
5'-most EST	uC-zmflb73122e01b2

Seq. No.	276140
Contig ID	64492_1.R1011
5'-most EST	fdz701158812.h1

Seq. No.	276141
Contig ID	64502_1.R1011
5'-most EST	LIB3061-010-Q1-K1-F8

Seq. No.	276142
Contig ID	64510_1.R1011
5'-most EST	uC-zmroteosinte033f01b1

Seq. No.	276143

Contig ID	64545_1.R1011
5'-most EST	LIB3061-011-Q1-K1-E9
Seq. No.	276144
Contig ID	64548_1.R1011
5'-most EST	uC-zmroB73001c09b1
Seq. No.	276145
Contig ID	64559_1.R1011
5'-most EST	LIB3062-004-Q1-K1-E12
Seq. No.	276146
Contig ID	64559_2.R1011
5'-most EST	hvj700620071.h1
Seq. No.	276147
Contig ID	64594_1.R1011
5'-most EST	LIB3061-012-Q1-K1-E2
Method	BLASTX
NCBI GI	g2289002
BLAST score	357
E value	2.0e-33
Match length	115
% identity	62
NCBI Description	(AC002335) unknown protein [Arabidopsis thaliana]
Seq. No.	276148
Contig ID	64606_1.R1011
5'-most EST	uC-zmflmo17105g11b1
Seq. No.	276149
Contig ID	64624_1.R1011
5'-most EST	LIB3067-039-Q1-K1-G6
Method	BLASTX
NCBI GI	g3374509
BLAST score	226
E value	5.0e-21
Match length	226
% identity	36
NCBI Description	(AB016529) Ku70 [Gallus gallus]
Seq. No.	276150
Contig ID	64624_2.R1011
5'-most EST	pmx700083273.h1
Seq. No.	276151
Contig ID	64629_1.R1011
5'-most EST	LIB3061-013-Q1-K1-A6
Seq. No.	276152
Contig ID	64636_1.R1011
5'-most EST	xyt700344039.h1
Method	BLASTX
NCBI GI	g4263710
BLAST score	761
E value	8.0e-81
Match length	260

% identity	61
NCBI Description	(AC006223) putative pur-alpha transcriptional activator protein [Arabidopsis thaliana]

Seq. No.	276153
Contig ID	64650_1.R1011
5'-most EST	tfd700571048.h1
Method	BLASTX
NCBI GI	g4581164
BLAST score	327
E value	5.0e-30
Match length	133
% identity	50
NCBI Description	(AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No.	276154
Contig ID	64663_1.R1011
5'-most EST	LIB3069-037-Q1-K1-E3
Method	BLASTX
NCBI GI	g1552379
BLAST score	430
E value	8.0e-66
Match length	220
% identity	55
NCBI Description	(Y08155) pectin methylesterase [Silene latifolia ssp. alba]

Seq. No.	276155
Contig ID	64663_2.R1011
5'-most EST	uC-zmrob73036e07b1

Seq. No.	276156
Contig ID	64669_1.R1011
5'-most EST	LIB3061-057-Q1-K1-H5

Seq. No.	276157
Contig ID	64669_2.R1011
5'-most EST	zla700380204.h1
Method	BLASTX
NCBI GI	g1353000
BLAST score	158
E value	2.0e-10
Match length	152
% identity	33
NCBI Description	HYPOTHETICAL 56.4 KD PROTEIN IN SRS2-SIP4 INTERGENIC REGION >gi_1078241_pir__S56868 probable membrane protein YJL091c - yeast (Saccharomyces cerevisiae) >gi_1008262_emb_CAA89384_ (Z49366) ORF YJL091c [Saccharomyces cerevisiae]

Seq. No.	276158
Contig ID	64669_3.R1011
5'-most EST	wyr700241563.h1

Seq. No.	276159
Contig ID	64670_1.R1011
5'-most EST	LIB3067-054-Q1-K1-E9

Seq. No.	276160

Contig ID	64688_1.R1011
5'-most EST	LIB3061-014-Q1-K1-C10
Seq. No.	276161
Contig ID	64689_1.R1011
5'-most EST	cyk700048277.f1
Seq. No.	276162
Contig ID	64708_1.R1011
5'-most EST	xmt700260815.h1
Seq. No.	276163
Contig ID	64724_1.R1011
5'-most EST	uC-zmroteosinte003a02b1
Method	BLASTX
NCBI GI	g3122357
BLAST score	269
E value	2.0e-23
Match length	75
% identity	71
NCBI Description	PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS PROTEIN B) >gi_2494127 (AC002376) Contains similarity to Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis thaliana]
Seq. No.	276164
Contig ID	64724_3.R1011
5'-most EST	wty700162884.h1
Seq. No.	276165
Contig ID	64760_2.R1011
5'-most EST	LIB3066-006-Q1-K1-E11
Method	BLASTX
NCBI GI	g4512685
BLAST score	325
E value	5.0e-30
Match length	166
% identity	42
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276166
Contig ID	64768_1.R1011
5'-most EST	uC-zmroB73014c12b1
Seq. No.	276167
Contig ID	64783_1.R1011
5'-most EST	LIB3061-016-Q1-K1-A1
Seq. No.	276168
Contig ID	64799_1.R1011
5'-most EST	uC-zmroteosinte120a09b2
Method	BLASTX
NCBI GI	g3790252
BLAST score	203
E value	3.0e-15

Match length	116
% identity	38
NCBI Description	(AL031966) putative Zn-protease [Schizosaccharomyces pombe]

Seq. No.	276169
Contig ID	64828_1.R1011
5'-most EST	qmh700030271.f1

Seq. No.	276170
Contig ID	64839_1.R1011
5'-most EST	uC-zmflmo17129c09a1
Method	BLASTX
NCBI GI	g2522534
BLAST score	485
E value	2.0e-48
Match length	228
% identity	45
NCBI Description	(AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]

Seq. No.	276171
Contig ID	64845_1.R1011
5'-most EST	wty700170626.h1
Method	BLASTX
NCBI GI	g2347100
BLAST score	1214
E value	1.0e-134
Match length	285
% identity	83
NCBI Description	(U76846) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4567196_gb_AAD23612.1_AC007168_3 (AC007168) putative ubiquitin-specific protease [Arabidopsis thaliana]

Seq. No.	276172
Contig ID	64866_1.R1011
5'-most EST	LIB3069-034-Q1-K1-H10
Method	BLASTX
NCBI GI	g1903364
BLAST score	281
E value	1.0e-24
Match length	123
% identity	49
NCBI Description	(AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No.	276173
Contig ID	64902_1.R1011
5'-most EST	LIB3068-021-Q1-K1-C7
Method	BLASTX
NCBI GI	g2827699
BLAST score	474
E value	2.0e-47
Match length	192
% identity	53
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	276174
Contig ID	64918_1.R1011

5'-most EST	LIB3061-018-Q1-K1-D2
Method	BLASTX
NCBI GI	g3894178
BLAST score	470
E value	8.0e-47
Match length	169
% identity	53
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	276175
Contig ID	64926_1.R1011
5'-most EST	pmx700086638.h1
Method	BLASTX
NCBI GI	g4582488
BLAST score	459
E value	2.0e-45
Match length	164
% identity	49
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	276176
Contig ID	64926_2.R1011
5'-most EST	xsy700213864.h1

Seq. No.	276177
Contig ID	64952_1.R1011
5'-most EST	LIB3061-020-Q1-K1-A1
Method	BLASTX
NCBI GI	g141605
BLAST score	484
E value	8.0e-49
Match length	119
% identity	87
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No.	276178
Contig ID	64959_1.R1011
5'-most EST	LIB3067-034-Q1-K1-H1
Method	BLASTX
NCBI GI	g80783
BLAST score	193
E value	5.0e-14
Match length	275
% identity	25
NCBI Description	hypothetical 31.7K protein (aphE region) - Streptomyces griseus >gi_153164 (M37378) streptomycin-3'-phosphotransferase [Streptomyces griseus]

Seq. No.	276179
Contig ID	64967_1.R1011
5'-most EST	LIB3061-020-Q1-K1-B6

Seq. No.	276180
Contig ID	64968_1.R1011

5'-most EST	uC-zmflb73119e06b1
Seq. No.	276181
Contig ID	64983_1.R1011
5'-most EST	xjt700095468.h1
Seq. No.	276182
Contig ID	64988_1.R1011
5'-most EST	xsy700214790.h1
Method	BLASTX
NCBI GI	g4337175
BLAST score	274
E value	5.0e-24
Match length	112
% identity	46
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.	276183
Contig ID	65001_1.R1011
5'-most EST	LIB3061-020-Q1-K1-G7
Method	BLASTX
NCBI GI	g1430846
BLAST score	557
E value	2.0e-57
Match length	117
% identity	84
NCBI Description	(X99210) myb-related transcription factor [Lycopersicon esculentum]
Seq. No.	276184
Contig ID	65029_1.R1011
5'-most EST	LIB3061-021-Q1-K1-C2
Seq. No.	276185
Contig ID	65049_1.R1011
5'-most EST	LIB3067-023-Q1-K1-F10
Method	BLASTX
NCBI GI	g2224605
BLAST score	286
E value	2.0e-25
Match length	144
% identity	46
NCBI Description	(AB002330) KIAA0332 [Homo sapiens]
Seq. No.	276186
Contig ID	65061_1.R1011
5'-most EST	LIB3061-021-Q1-K1-G9
Method	BLASTX
NCBI GI	g3309583
BLAST score	961
E value	1.0e-104
Match length	210
% identity	86
NCBI Description	(AF073830) fructose-6-phosphate

2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No.	276187
Contig ID	65065_1.R1011
5'-most EST	gwl700615429.h1

Seq. No.	276188
Contig ID	65067_1.R1011
5'-most EST	LIB3061-022-Q1-K1-A12

Seq. No.	276189
Contig ID	65083_1.R1011
5'-most EST	LIB3061-022-Q1-K1-C5
Method	BLASTX
NCBI GI	g4263715
BLAST score	207
E value	2.0e-16
Match length	86
% identity	48
NCBI Description	(AC006223) putative alanine acetyl transferase [Arabidopsis thaliana]

Seq. No.	276190
Contig ID	65087_1.R1011
5'-most EST	tfd700573370.h1
Method	BLASTX
NCBI GI	g4056490
BLAST score	487
E value	1.0e-48
Match length	322
% identity	39
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276191
Contig ID	65098_1.R1011
5'-most EST	gct701179902.h1
Method	BLASTX
NCBI GI	g4455331
BLAST score	314
E value	1.0e-28
Match length	116
% identity	53
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	276192
Contig ID	65099_1.R1011
5'-most EST	wyr700237018.h1

Seq. No.	276193
Contig ID	65117_1.R1011
5'-most EST	uC-zmflmo17044a07b1

Seq. No.	276194
Contig ID	65149_1.R1011
5'-most EST	LIB3061-050-Q1-K1-B5
Method	BLASTX
NCBI GI	g4006871

BLAST score	500
E value	2.0e-62
Match length	231
% identity	56
NCBI Description	(Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.	276195
Contig ID	65149_3.R1011
5'-most EST	ypc700801127.h1
Method	BLASTX
NCBI GI	g4539677
BLAST score	262
E value	3.0e-23
Match length	66
% identity	74
NCBI Description	(AF061282) patatin-like protein [Sorghum bicolor]

Seq. No.	276196
Contig ID	65153_1.R1011
5'-most EST	xmt700262242.h1
Method	BLASTX
NCBI GI	g2632129
BLAST score	177
E value	1.0e-12
Match length	124
% identity	33
NCBI Description	(AJ222589) poly(ADP-ribose) polymerase [Zea mays]

Seq. No.	276197
Contig ID	65153_2.R1011
5'-most EST	ypc700806645.h1
Method	BLASTX
NCBI GI	g4038491
BLAST score	183
E value	2.0e-13
Match length	141
% identity	36
NCBI Description	(AJ131705) poly(ADP-ribose) polymerase [Arabidopsis thaliana]

Seq. No.	276198
Contig ID	65160_1.R1011
5'-most EST	hbs701183891.h1
Method	BLASTX
NCBI GI	g3063709
BLAST score	215
E value	3.0e-17
Match length	52
% identity	71
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	276199
Contig ID	65171_1.R1011
5'-most EST	LIB83-001-Q1-E1-E5

Seq. No.	276200
Contig ID	65179_1.R1011

5'-most EST	LIB3061-024-Q1-K1-C9
Seq. No.	276201
Contig ID	65186_1.R1011
5'-most EST	uC-zmf1b73054d01b1
Method	BLASTX
NCBI GI	g2317725
BLAST score	217
E value	4.0e-17
Match length	184
% identity	33
NCBI Description	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]
Seq. No.	276202
Contig ID	65186_3.R1011
5'-most EST	zla700379650.h1
Seq. No.	276203
Contig ID	65188_1.R1011
5'-most EST	ntr700072086.h1
Method	BLASTX
NCBI GI	g1946366
BLAST score	152
E value	1.0e-09
Match length	115
% identity	35
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]
Seq. No.	276204
Contig ID	65191_1.R1011
5'-most EST	pmx700087071.h1
Seq. No.	276205
Contig ID	65228_1.R1011
5'-most EST	LIB3061-025-Q1-K1-B6
Seq. No.	276206
Contig ID	65233_1.R1011
5'-most EST	uC-zmroteosinte067g11b1
Method	BLASTX
NCBI GI	g4588012
BLAST score	616
E value	7.0e-67
Match length	189
% identity	75
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]
Seq. No.	276207
Contig ID	65233_2.R1011
5'-most EST	LIB3061-025-Q1-K1-C3
Method	BLASTX
NCBI GI	g4588012
BLAST score	575
E value	2.0e-59
Match length	150

% identity	77
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	276208
Contig ID	65262_1.R1011
5'-most EST	uwc700154473.h1
Method	BLASTX
NCBI GI	g728592
BLAST score	604
E value	8.0e-63
Match length	144
% identity	81
NCBI Description	(Z48360) aldose reductase [Hordeum vulgare]

Seq. No.	276209
Contig ID	65267_1.R1011
5'-most EST	dyk700104706.h1
Method	BLASTX
NCBI GI	g1524383
BLAST score	1205
E value	1.0e-133
Match length	248
% identity	95
NCBI Description	(X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]

Seq. No.	276210
Contig ID	65286_1.R1011
5'-most EST	xsy700208127.h1
Method	BLASTX
NCBI GI	g2760844
BLAST score	285
E value	4.0e-25
Match length	153
% identity	38
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276211
Contig ID	65287_1.R1011
5'-most EST	gct701175030.h1
Method	BLASTX
NCBI GI	g2462760
BLAST score	165
E value	4.0e-11
Match length	84
% identity	42
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	276212
Contig ID	65296_1.R1011
5'-most EST	uC-zmflmo17113e06b1
Method	BLASTX
NCBI GI	g3978462
BLAST score	155
E value	8.0e-10
Match length	129

% identity	37
NCBI Description	(AF084535) laforin [Homo sapiens]

Seq. No.	276213
Contig ID	65311_1.R1011
5'-most EST	LIB3061-026-Q1-K1-F3

Seq. No.	276214
Contig ID	65330_1.R1011
5'-most EST	LIB3061-027-Q1-K1-A5
Method	BLASTX
NCBI GI	g4006899
BLAST score	468
E value	8.0e-47
Match length	170
% identity	52
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	276215
Contig ID	65341_1.R1011
5'-most EST	wyr700241026.h1

Seq. No.	276216
Contig ID	65422_1.R1011
5'-most EST	uC-zmflb73118c12b1

Seq. No.	276217
Contig ID	65422_2.R1011
5'-most EST	uC-zmflmo17222f09b1

Seq. No.	276218
Contig ID	65422_3.R1011
5'-most EST	LIB3068-008-Q1-K1-E8
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	276219
Contig ID	65451_1.R1011
5'-most EST	uC-zmflb73059h01b1
Method	BLASTX
NCBI GI	g4510349
BLAST score	225
E value	4.0e-18
Match length	83
% identity	59
NCBI Description	(AC006921) putative bZIP transcription factor [Arabidopsis thaliana]

Seq. No.	276220
Contig ID	65451_2.R1011
5'-most EST	uC-zmroteosinte087h09b2

Seq. No.	276221
Contig ID	65454_1.R1011
5'-most EST	uC-zmf1b73186c03b1
Seq. No.	276222
Contig ID	65458_1.R1011
5'-most EST	LIB3061-029-Q1-K1-E10
Seq. No.	276223
Contig ID	65474_1.R1011
5'-most EST	fdz701163030.h1
Seq. No.	276224
Contig ID	65474_2.R1011
5'-most EST	tfd700576612.h1
Seq. No.	276225
Contig ID	65475_1.R1011
5'-most EST	xyt700346405.h1
Method	BLASTX
NCBI GI	g3702338
BLAST score	448
E value	1.0e-44
Match length	105
% identity	76
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	276226
Contig ID	65482_1.R1011
5'-most EST	LIB3061-030-Q1-K1-A11
Method	BLASTX
NCBI GI	g3548810
BLAST score	210
E value	1.0e-16
Match length	103
% identity	38
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
Seq. No.	276227
Contig ID	65502_1.R1011
5'-most EST	LIB3061-030-Q1-K1-C8
Method	BLASTN
NCBI GI	g1181295
BLAST score	38
E value	6.0e-12
Match length	88
% identity	86
NCBI Description	T.durum Desf. (Siliana) Dehydrin mRNA, clone pTd27e
Seq. No.	276228
Contig ID	65512_1.R1011
5'-most EST	pmx700084462.h1
Method	BLASTX
NCBI GI	g1710599
BLAST score	206
E value	6.0e-16

Match length	153
% identity	35
NCBI Description	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L10 PRECURSOR (YML10) >gi_2133093_pir__S63258 ribosomal protein L15 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) >gi_1302361_emb_CAA96198_ (Z71560) ORF YNL284c [Saccharomyces cerevisiae]

Seq. No.	276229
Contig ID	65517_1.R1011
5'-most EST	LIB3061-030-Q1-K1-E8
Method	BLASTX
NCBI GI	g3790569
BLAST score	163
E value	6.0e-11
Match length	83
% identity	40
NCBI Description	(AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana]

Seq. No.	276230
Contig ID	65571_1.R1011
5'-most EST	LIB3061-031-Q1-K1-E7

Seq. No.	276231
Contig ID	65572_1.R1011
5'-most EST	LIB84-005-Q1-E1-B2

Seq. No.	276232
Contig ID	65575_1.R1011
5'-most EST	LIB3061-052-Q1-K1-C9

Seq. No.	276233
Contig ID	65584_1.R1011
5'-most EST	uC-zmflmo17335d09b1
Method	BLASTX
NCBI GI	g1749516
BLAST score	610
E value	3.0e-63
Match length	198
% identity	57
NCBI Description	(D89154) similar to Saccharomyces cerevisiae ornithine-oxo-acid aminotransferase, SWISS-PROT Accession Number P07991 [Schizosaccharomyces pombe]

Seq. No.	276234
Contig ID	65593_1.R1011
5'-most EST	LIB3061-032-Q1-K1-A6

Seq. No.	276235
Contig ID	65595_1.R1011
5'-most EST	LIB3061-032-Q1-K1-B12
Method	BLASTX
NCBI GI	g4587579
BLAST score	314
E value	8.0e-29
Match length	173

% identity	45
NCBI Description	(AC006550) F10O3.1 [Arabidopsis thaliana]
Seq. No.	276236
Contig ID	65602_1.R1011
5'-most EST	LIB3061-032-Q1-K1-C5
Seq. No.	276237
Contig ID	65611_1.R1011
5'-most EST	LIB3061-032-Q1-K1-D8
Method	BLASTX
NCBI GI	g3033400
BLAST score	549
E value	3.0e-56
Match length	144
% identity	74
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
Seq. No.	276238
Contig ID	65625_1.R1011
5'-most EST	uC-zmroteosinte023g08b2
Method	BLASTX
NCBI GI	g4508069
BLAST score	711
E value	3.0e-75
Match length	206
% identity	62
NCBI Description	(AC005882) 12246 [Arabidopsis thaliana]
Seq. No.	276239
Contig ID	65626_1.R1011
5'-most EST	LIB3061-032-Q1-K1-H11
Method	BLASTX
NCBI GI	g1652892
BLAST score	340
E value	6.0e-32
Match length	104
% identity	60
NCBI Description	(D90909) ABC transporter [Synechocystis sp.]
Seq. No.	276240
Contig ID	65652_1.R1011
5'-most EST	LIB3061-033-Q1-K1-D1
Seq. No.	276241
Contig ID	65655_1.R1011
5'-most EST	LIB3061-033-Q1-K1-D3
Method	BLASTX
NCBI GI	g2828294
BLAST score	551
E value	1.0e-56
Match length	168
% identity	64
NCBI Description	(AL021687) putatative protein [Arabidopsis thaliana]
Seq. No.	276242

Contig ID	65659_1.R1011
5'-most EST	ypc700803121.h1
Seq. No.	276243
Contig ID	65659_2.R1011
5'-most EST	dyk700104626.h1
Seq. No.	276244
Contig ID	65660_1.R1011
5'-most EST	uC-zmroteosinte082g09b1
Method	BLASTX
NCBI GI	g2498882
BLAST score	251
E value	7.0e-21
Match length	191
% identity	39
NCBI Description	SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120) >gi_2146975_pir__S60735 splicing factor SF3a 120K chain - human >gi_899298_emb_CAA59494_ (X85237) human splicing factor [Homo sapiens] >gi_3212998 (AC004997) spliceosome associated protein 114 (SF3a) [Homo sapiens]
Seq. No.	276245
Contig ID	65665_1.R1011
5'-most EST	LIB3061-033-Q1-K1-E7
Method	BLASTN
NCBI GI	g1694832
BLAST score	67
E value	4.0e-29
Match length	82
% identity	96
NCBI Description	H.vulgare Per1 gene
Seq. No.	276246
Contig ID	65682_1.R1011
5'-most EST	uC-zmflb73234g08b2
Method	BLASTX
NCBI GI	g4138343
BLAST score	595
E value	5.0e-68
Match length	273
% identity	51
NCBI Description	(AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]
Seq. No.	276247
Contig ID	65711_1.R1011
5'-most EST	nbm700470281.h1
Method	BLASTX
NCBI GI	g3150239
BLAST score	193
E value	3.0e-14
Match length	91
% identity	46
NCBI Description	(AL023635) hypothetical protein MLCB1243.38 [Mycobacterium leprae]
Seq. No.	276248

Contig ID	65740_1.R1011
5'-most EST	pmx700082248.h1
Method	BLASTX
NCBI GI	g4646203
BLAST score	808
E value	3.0e-86
Match length	306
% identity	48
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No.	276249
Contig ID	65751_1.R1011
5'-most EST	LIB3068-061-Q1-K1-A3

Seq. No.	276250
Contig ID	65751_2.R1011
5'-most EST	LIB3061-035-Q1-K1-A6

Seq. No.	276251
Contig ID	65781_1.R1011
5'-most EST	LIB3061-035-Q1-K1-E12

Seq. No.	276252
Contig ID	65782_1.R1011
5'-most EST	LIB3061-035-Q1-K1-E2
Method	BLASTX
NCBI GI	g3283026
BLAST score	231
E value	4.0e-19
Match length	100
% identity	48
NCBI Description	(AF051562) putative transposase [Arabidopsis thaliana]

Seq. No.	276253
Contig ID	65846_1.R1011
5'-most EST	LIB3061-036-Q1-K1-G2

Seq. No.	276254
Contig ID	65856_1.R1011
5'-most EST	LIB3062-016-Q1-K1-B9
Method	BLASTX
NCBI GI	g499340
BLAST score	191
E value	7.0e-27
Match length	210
% identity	37
NCBI Description	(X78201) 17beta-estradiol dehydrogenase [Sus scrofa]

Seq. No.	276255
Contig ID	65865_1.R1011
5'-most EST	fwa700098059.h1

Seq. No.	276256
Contig ID	65872_1.R1011
5'-most EST	uC-zmf1b73123e01a1

Seq. No.	276257
Contig ID	65886_1.R1011
5'-most EST	uC-zmflmo17127c11b1
Method	BLASTX
NCBI GI	g4206209
BLAST score	1231
E value	1.0e-136
Match length	322
% identity	69
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No.	276258
Contig ID	65894_1.R1011
5'-most EST	LIB3136-037-P1-K1-D8

Seq. No.	276259
Contig ID	65894_2.R1011
5'-most EST	uC-zmflb73025e05a1

Seq. No.	276260
Contig ID	65906_1.R1011
5'-most EST	LIB3061-037-Q1-K1-H1

Seq. No.	276261
Contig ID	65907_1.R1011
5'-most EST	pmx700087877.h1

Seq. No.	276262
Contig ID	65915_1.R1011
5'-most EST	pwr700452646.h1
Method	BLASTX
NCBI GI	g3450842
BLAST score	966
E value	1.0e-105
Match length	245
% identity	74
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	276263
Contig ID	65922_1.R1011
5'-most EST	uC-zmflb73022g12b1
Method	BLASTX
NCBI GI	g3413712
BLAST score	213
E value	9.0e-17
Match length	111
% identity	36
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276264
Contig ID	65964_1.R1011
5'-most EST	uC-zmroteosinte046a05b1
Method	BLASTX
NCBI GI	g3461848

BLAST score	399
E value	1.0e-38
Match length	137
% identity	58
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	276265
Contig ID	65977_1.R1011
5'-most EST	uC-zmflmo17257b12b1
Method	BLASTX
NCBI GI	g586858
BLAST score	342
E value	8.0e-32
Match length	160
% identity	46
NCBI Description	HYPOTHETICAL 21.4 KD PROTEIN IN DACA-SERS INTERGENIC REGION >gi_2127020_pir__S66042 hypothetical protein - Bacillus subtilis >gi_467402_dbj_BAA05248_ (D26185) unknown [Bacillus subtilis] >gi_2632279_emb_CAB11788_ (Z99104) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	276266
Contig ID	65984_1.R1011
5'-most EST	LIB3061-039-Q1-K1-D4

Seq. No.	276267
Contig ID	65992_1.R1011
5'-most EST	wty700169670.h1

Seq. No.	276268
Contig ID	66009_1.R1011
5'-most EST	uC-zmroteosinte015c01b1

Seq. No.	276269
Contig ID	66055_1.R1011
5'-most EST	LIB3061-040-Q1-K1-F9
Method	BLASTX
NCBI GI	g3096945
BLAST score	169
E value	7.0e-12
Match length	79
% identity	49
NCBI Description	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	276270
Contig ID	66057_1.R1011
5'-most EST	LIB3067-052-Q1-K1-F9
Method	BLASTX
NCBI GI	g4336747
BLAST score	496
E value	6.0e-50
Match length	255
% identity	50
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No.	276271

Contig ID	66072_1.R1011
5'-most EST	pmx700090963.h1
Seq. No.	276272
Contig ID	66084_1.R1011
5'-most EST	LIB3136-021-Q1-K1-D8
Method	BLASTX
NCBI GI	g4105798
BLAST score	640
E value	1.0e-68
Match length	195
% identity	50
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.	276273
Contig ID	66094_1.R1011
5'-most EST	uC-zmroteosinte084c12b1
Seq. No.	276274
Contig ID	66094_2.R1011
5'-most EST	LIB3061-041-Q1-K1-E5
Seq. No.	276275
Contig ID	66118_1.R1011
5'-most EST	tzu700204157.h1
Method	BLASTN
NCBI GI	g3256034
BLAST score	52
E value	3.0e-20
Match length	100
% identity	88
NCBI Description	Sorghum bicolor mRNA for SNFL3, putative serine/threonine protein kinase
Seq. No.	276276
Contig ID	66134_1.R1011
5'-most EST	fwa700099910.h1
Method	BLASTX
NCBI GI	g4510377
BLAST score	474
E value	4.0e-47
Match length	234
% identity	41
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]
Seq. No.	276277
Contig ID	66183_1.R1011
5'-most EST	xmt700263748.h1
Method	BLASTN
NCBI GI	g1171347
BLAST score	135
E value	2.0e-69
Match length	413
% identity	84
NCBI Description	Triticum aestivum pMA1951 mRNA, partial cds
Seq. No.	276278

Contig ID	66183_2.R1011
5'-most EST	uC-zmf1b73152c01b1
Method	BLASTN
NCBI GI	g1171347
BLAST score	70
E value	7.0e-31
Match length	173
% identity	85
NCBI Description	Triticum aestivum pMA1951 mRNA, partial cds

Seq. No.	276279
Contig ID	66209_1.R1011
5'-most EST	uer700578273.h1
Method	BLASTX
NCBI GI	g2492863
BLAST score	575
E value	5.0e-59
Match length	207
% identity	53
NCBI Description	ORNITHINE AMINOTRANSFERASE (ORNITHINE--OXO-ACID AMINOTRANSFERASE) >gi_4416517_gb_AAB18259_ (U74303) ornithine transaminase [Emericella nidulans]

Seq. No.	276280
Contig ID	66209_2.R1011
5'-most EST	uC-zmflmo17426f10a1

Seq. No.	276281
Contig ID	66249_1.R1011
5'-most EST	ntr700076180.h1

Seq. No.	276282
Contig ID	66249_2.R1011
5'-most EST	pmx700087765.h1
Method	BLASTX
NCBI GI	g3287944
BLAST score	231
E value	4.0e-19
Match length	76
% identity	57
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN C3D6.08C IN CHROMOSOME II >gi_2117304_emb_CAB09117.1_ (Z95620) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	276283
Contig ID	66251_1.R1011
5'-most EST	LIB3061-044-Q1-K1-F2

Seq. No.	276284
Contig ID	66252_1.R1011
5'-most EST	ymt700223062.h1

Seq. No.	276285
Contig ID	66255_1.R1011
5'-most EST	LIB3061-044-Q1-K1-F8

Seq. No.	276286

Contig ID	66257_1.R1011
5'-most EST	uC-zmflmo17023d04b1
Method	BLASTX
NCBI GI	g2213626
BLAST score	410
E value	2.0e-39
Match length	174
% identity	49
NCBI Description	(AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No.	276287
Contig ID	66260_1.R1011
5'-most EST	LIB84-003-Q1-E1-F12

Seq. No.	276288
Contig ID	66269_1.R1011
5'-most EST	uC-zmflmo17109f02b1

Seq. No.	276289
Contig ID	66277_1.R1011
5'-most EST	LIB3061-045-Q1-K1-B12
Method	BLASTX
NCBI GI	g608567
BLAST score	224
E value	4.0e-18
Match length	97
% identity	25
NCBI Description	(U18116) Bdf1p [Saccharomyces cerevisiae]

Seq. No.	276290
Contig ID	66284_1.R1011
5'-most EST	uC-zmroteosinte041a01b1
Method	BLASTX
NCBI GI	g1705735
BLAST score	1307
E value	1.0e-145
Match length	282
% identity	88
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11) >gi_1362175_pir__S56651 probable calcium-dependent protein kinase (clone OSCPK11) - rice >gi_587500_emb_CAA57156_ (X81393) calcium-dependent protein kinase [Oryza sativa]

Seq. No.	276291
Contig ID	66286_1.R1011
5'-most EST	LIB3061-045-Q1-K1-C3
Method	BLASTX
NCBI GI	g3834314
BLAST score	305
E value	8.0e-39
Match length	134
% identity	68
NCBI Description	(AC005679) Similar to gene pi010 glycosyltransferase gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis thaliana]

Seq. No.	276292
Contig ID	66302_1.R1011
5'-most EST	wty70o164535.h1
Method	BLASTX
NCBI GI	g4508068
BLAST score	174
E value	3.0e-12
Match length	64
% identity	56
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	276293
Contig ID	66302_2.R1011
5'-most EST	LIB3061-045-Q1-K1-F1
Method	BLASTX
NCBI GI	g4508068
BLAST score	203
E value	1.0e-15
Match length	109
% identity	41
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	276294
Contig ID	66323_1.R1011
5'-most EST	uC-zmflmo17072c03b1
Method	BLASTX
NCBI GI	g3063709
BLAST score	226
E value	7.0e-18
Match length	297
% identity	26
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	276295
Contig ID	66327_1.R1011
5'-most EST	LIB3061-055-Q1-K1-A9

Seq. No.	276296
Contig ID	66339_1.R1011
5'-most EST	uC-zmflmo17222b11b1

Seq. No.	276297
Contig ID	66371_1.R1011
5'-most EST	LIB3061-046-Q1-K1-H5

Seq. No.	276298
Contig ID	66374_1.R1011
5'-most EST	uC-zmflmo17288e11b1
Method	BLASTX
NCBI GI	g3738297
BLAST score	280
E value	2.0e-24
Match length	205
% identity	12
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	276299

Contig ID	66376_1.R1011
5'-most EST	mwy700438515.h1
Seq. No.	276300
Contig ID	66376_2.R1011
5'-most EST	LIB3061-047-Q1-K1-A3
Seq. No.	276301
Contig ID	66389_1.R1011
5'-most EST	wyr700242628.h1
Method	BLASTX
NCBI GI	g2435514
BLAST score	304
E value	2.0e-27
Match length	141
% identity	47
NCBI Description	(AF024504) Similar to serine/threonine protein kinase; coded for by A. thaliana cDNA T20930; coded for by A. thaliana cDNA T43472 [Arabidopsis thaliana]
Seq. No.	276302
Contig ID	66399_1.R1011
5'-most EST	uwc700150579.h1
Method	BLASTX
NCBI GI	g4416301
BLAST score	686
E value	2.0e-72
Match length	180
% identity	79
NCBI Description	(AF105716) gag protein [Zea mays]
Seq. No.	276303
Contig ID	66405_1.R1011
5'-most EST	xmt700267018.h1
Method	BLASTX
NCBI GI	g4539005
BLAST score	157
E value	4.0e-13
Match length	118
% identity	42
NCBI Description	(AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.	276304
Contig ID	66425_1.R1011
5'-most EST	LIB3061-047-Q1-K1-H4
Method	BLASTX
NCBI GI	g1943751
BLAST score	905
E value	5.0e-98
Match length	194
% identity	85
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
Seq. No.	276305
Contig ID	66435_1.R1011

5'-most EST	pmx700085585.h1
Method	BLASTX
NCBI GI	g2499735
BLAST score	222
E value	1.0e-17
Match length	124
% identity	39
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE 5 (PP5) (PROTEIN PHOSPHATASE T) (PPT) >gi_567040 (U12204) phosphoprotein phosphatase [Mus musculus]

Seq. No.	276306
Contig ID	66450_1.R1011
5'-most EST	uC-zmflmo17327a12b1

Seq. No.	276307
Contig ID	66450_2.R1011
5'-most EST	uC-zmflmo17163c01b1

Seq. No.	276308
Contig ID	66458_1.R1011
5'-most EST	LIB3061-048-Q1-K1-E12

Seq. No.	276309
Contig ID	66460_1.R1011
5'-most EST	pmx700089767.h1
Method	BLASTX
NCBI GI	g4559333
BLAST score	455
E value	4.0e-45
Match length	163
% identity	55
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	276310
Contig ID	66477_1.R1011
5'-most EST	LIB3061-048-Q1-K1-G9
Method	BLASTX
NCBI GI	g2827497
BLAST score	189
E value	3.0e-14
Match length	119
% identity	32
NCBI Description	(AL009195) EG:30B8.2 [Drosophila melanogaster]

Seq. No.	276311
Contig ID	66498_1.R1011
5'-most EST	uC-zmflb73202a11b1
Method	BLASTX
NCBI GI	g4406809
BLAST score	154
E value	2.0e-09
Match length	78
% identity	45
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 276312

Contig ID	66512_1.R1011
5'-most EST	LIB3061-049-Q1-K1-E10
Method	BLASTX
NCBI GI	g3256068
BLAST score	172
E value	8.0e-12
Match length	89
% identity	51
NCBI Description	(Y14068) Heat Shock Factor 3 [Arabidopsis thaliana]

Seq. No.	276313
Contig ID	66518_1.R1011
5'-most EST	LIB3061-049-Q1-K1-F3

Seq. No.	276314
Contig ID	66525_1.R1011
5'-most EST	uC-zmflmo17259a08b1

Seq. No.	276315
Contig ID	66525_2.R1011
5'-most EST	LIB3061-049-Q1-K1-G10

Seq. No.	276316
Contig ID	66528_1.R1011
5'-most EST	LIB3061-049-Q1-K1-G4
Method	BLASTX
NCBI GI	g4574137
BLAST score	453
E value	4.0e-45
Match length	109
% identity	80
NCBI Description	(AF073696) cysteine synthase [Oryza sativa]

Seq. No.	276317
Contig ID	66566_1.R1011
5'-most EST	uC-zmflB73043b05b1
Method	BLASTX
NCBI GI	g1710805
BLAST score	167
E value	2.0e-11
Match length	200
% identity	31
NCBI Description	RTOA PROTEIN (RATIO-A) >gi_1206019 (U48298) rtoA gene product [Dictyostelium discoideum]

Seq. No.	276318
Contig ID	66568_2.R1011
5'-most EST	uC-zmflb73255g12b1

Seq. No.	276319
Contig ID	66579_1.R1011
5'-most EST	ymt700221578.h2

Seq. No.	276320
Contig ID	66579_2.R1011
5'-most EST	ymt700218627.h1
Method	BLASTX

NCBI GI	g3075391
BLAST score	211
E value	1.0e-16
Match length	105
% identity	50
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	276321
Contig ID	66579_3.R1011
5'-most EST	hbs701180939.h1

Seq. No.	276322
Contig ID	66650_1.R1011
5'-most EST	uwc700151433.h1
Method	BLASTX
NCBI GI	g3953463
BLAST score	536
E value	1.0e-54
Match length	219
% identity	51
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No.	276323
Contig ID	66652_1.R1011
5'-most EST	LIB3061-052-Q1-K1-A12

Seq. No.	276324
Contig ID	66670_1.R1011
5'-most EST	LIB3061-052-Q1-K1-D1

Seq. No.	276325
Contig ID	66683_1.R1011
5'-most EST	uC-zmflmo17297g11b1

Seq. No.	276326
Contig ID	66685_1.R1011
5'-most EST	wyr700236027.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	5.0e-11
Match length	37
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	276327
Contig ID	66721_1.R1011
5'-most EST	LIB3067-045-Q1-K1-H4

Seq. No.	276328
Contig ID	66728_1.R1011
5'-most EST	xmt700264894.h1

Seq. No.	276329
Contig ID	66730_1.R1011
5'-most EST	xmt700266538.h1
Method	BLASTX

NCBI GI	g542182
BLAST score	492
E value	1.0e-67
Match length	136
% identity	99
NCBI Description	vicilin-like storage protein Glb1-L, embryo - maize >gi_22284_emb_CAA41809_ (X59083) vicilin-like embryo storage protein [Zea mays]

Seq. No.	276330
Contig ID	66735_1.R1011
5'-most EST	cjh700196712.h1

Seq. No.	276331
Contig ID	66745_1.R1011
5'-most EST	pmx700087254.h1

Seq. No.	276332
Contig ID	66806_1.R1011
5'-most EST	uC-zmf1Mo17003d01b1
Method	BLASTX
NCBI GI	g3403234
BLAST score	161
E value	1.0e-10
Match length	145
% identity	31
NCBI Description	(AF071543) ribulose-1,5-bisphosphate carboxylase/oxygenase N-methyltransferase [Spinacia oleracea] >gi_3403238 (AF071545) ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase II [Spinacia oleracea]

Seq. No.	276333
Contig ID	66823_1.R1011
5'-most EST	fwa700099354.h1
Method	BLASTX
NCBI GI	g3819699
BLAST score	716
E value	7.0e-76
Match length	174
% identity	81
NCBI Description	(AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No.	276334
Contig ID	66827_1.R1011
5'-most EST	fC-zmf1700356833a1
Method	BLASTX
NCBI GI	g1143069
BLAST score	647
E value	7.0e-68
Match length	163
% identity	73
NCBI Description	(U30600) 3-ketoacyl carrier protein synthase III [Allium porrum]

Seq. No.	276335
Contig ID	66870_1.R1011
5'-most EST	zuv700356484.h1

Seq. No.	276336
Contig ID	66890_1.R1011
5'-most EST	xmt700257543.h1

Seq. No.	276337
Contig ID	66916_1.R1011
5'-most EST	LIB3061-057-Q1-K1-A1
Method	BLASTX
NCBI GI	g4127878
BLAST score	249
E value	3.0e-21
Match length	123
% identity	47
NCBI Description	(AJ011831) NDX1 homeobox protein [Glycine max]

Seq. No.	276338
Contig ID	66927_1.R1011
5'-most EST	LIB3061-057-Q1-K1-B4

Seq. No.	276339
Contig ID	66932_1.R1011
5'-most EST	LIB3061-057-Q1-K1-C2

Seq. No.	276340
Contig ID	66947_1.R1011
5'-most EST	fwa700098547.h1

Seq. No.	276341
Contig ID	66954_1.R1011
5'-most EST	uC-zmflb73256g11b1
Method	BLASTX
NCBI GI	g2129636
BLAST score	311
E value	2.0e-28
Match length	145
% identity	47
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	276342
Contig ID	66954_2.R1011
5'-most EST	tzu700204158.h1
Method	BLASTX
NCBI GI	g2129636
BLAST score	184
E value	2.0e-13
Match length	114
% identity	40
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	276343
Contig ID	66982_1.R1011
5'-most EST	LIB3061-058-Q1-K1-A6

Seq. No.	276344

Contig ID	66984_1.R1011
5'-most EST	clt700044184.f1
Seq. No.	276345
Contig ID	66984_2.R1011
5'-most EST	wty700168069.h1
Seq. No.	276346
Contig ID	66987_1.R1011
5'-most EST	uC-zmflmo17031g01b1
Method	BLASTX
NCBI GI	g2827661
BLAST score	259
E value	3.0e-22
Match length	66
% identity	73
NCBI Description	(AL021637) hyuC-like protein [Arabidopsis thaliana]
Seq. No.	276347
Contig ID	66990_1.R1011
5'-most EST	LIB3069-004-Q1-K1-F8
Method	BLASTX
NCBI GI	g3482972
BLAST score	310
E value	2.0e-29
Match length	168
% identity	44
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]
Seq. No.	276348
Contig ID	66991_1.R1011
5'-most EST	LIB3070-007-Q1-N1-H12
Method	BLASTX
NCBI GI	g3122724
BLAST score	310
E value	3.0e-28
Match length	69
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal protein L38 isolog [Arabidopsis thaliana]
Seq. No.	276349
Contig ID	67023_1.R1011
5'-most EST	uC-zmflm017209f11b1
Seq. No.	276350
Contig ID	67029_1.R1011
5'-most EST	LIB3062-021-Q1-K1-G5
Seq. No.	276351
Contig ID	67036_1.R1011
5'-most EST	uC-zmflb73247f10b3
Method	BLASTX
NCBI GI	g3805853
BLAST score	399
E value	1.0e-38
Match length	162

% identity	51
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	276352
Contig ID	67038_1.R1011
5'-most EST	LIB3068-043-Q1-K1-D5
Seq. No.	276353
Contig ID	67038_2.R1011
5'-most EST	uC-zmflMo17087e09b1
Seq. No.	276354
Contig ID	67057_1.R1011
5'-most EST	LIB3062-001-Q1-K2-C4
Method	BLASTX
NCBI GI	g1087073
BLAST score	226
E value	1.0e-18
Match length	95
% identity	48
NCBI Description	(S79243) calmodulin-binding heat-shock protein, CaMBP [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa] [Nicotiana tabacum]
Seq. No.	276355
Contig ID	67075_1.R1011
5'-most EST	LIB3062-001-Q1-K2-E2
Seq. No.	276356
Contig ID	67094_1.R1011
5'-most EST	LIB3062-001-Q1-K2-G1
Method	BLASTX
NCBI GI	g4455233
BLAST score	237
E value	2.0e-19
Match length	81
% identity	56
NCBI Description	(AL035523) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276357
Contig ID	67095_1.R1011
5'-most EST	pmx700082963.h1
Method	BLASTX
NCBI GI	g4204297
BLAST score	542
E value	1.0e-55
Match length	117
% identity	85
NCBI Description	(AC003027) ADK1 [Arabidopsis thaliana]
Seq. No.	276358
Contig ID	67096_1.R1011
5'-most EST	LIB3066-030-Q1-K1-G10
Method	BLASTX
NCBI GI	g2833378
BLAST score	713
E value	3.0e-75

Match length	291
% identity	54
NCBI Description	HEXOKINASE >gi_619928 (U18754) hexokinase [Arabidopsis thaliana] >gi_1582383_prf__2118367A hexokinase [Arabidopsis thaliana]

Seq. No.	276359
Contig ID	67097_1.R1011
5'-most EST	LIB3062-001-Q1-K2-G12

Seq. No.	276360
Contig ID	67115_1.R1011
5'-most EST	uC-zmflb73284f12b1
Method	BLASTX
NCBI GI	g4559384
BLAST score	677
E value	5.0e-71
Match length	245
% identity	56
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	276361
Contig ID	67137_1.R1011
5'-most EST	LIB3062-002-Q1-K2-C11

Seq. No.	276362
Contig ID	67138_1.R1011
5'-most EST	LIB3062-002-Q1-K2-C12
Method	BLASTX
NCBI GI	g3292824
BLAST score	747
E value	1.0e-105
Match length	302
% identity	64
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	276363
Contig ID	67142_1.R1011
5'-most EST	LIB3062-002-Q1-K2-C7
Method	BLASTX
NCBI GI	g3153205
BLAST score	466
E value	1.0e-46
Match length	106
% identity	77
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	276364
Contig ID	67147_1.R1011
5'-most EST	vux70l161311.h1

Seq. No.	276365
Contig ID	67154_1.R1011
5'-most EST	yyf70l349508.h1

Seq. No.	276366

Contig ID	67154_2.R1011
5'-most EST	LIB3062-002-Q1-K2-D5
Seq. No.	276367
Contig ID	67176_1.R1011
5'-most EST	uC-zmflb73001e05b1
Seq. No.	276368
Contig ID	67179_1.R1011
5'-most EST	ntr700072858.h1
Seq. No.	276369
Contig ID	67192_1.R1011
5'-most EST	xmt700257594.h1
Method	BLASTX
NCBI GI	g3269297
BLAST score	235
E value	2.0e-19
Match length	80
% identity	57
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]
Seq. No.	276370
Contig ID	67206_1.R1011
5'-most EST	LIB3062-003-Q1-K1-A1
Method	BLASTX
NCBI GI	g3152572
BLAST score	597
E value	1.0e-61
Match length	272
% identity	47
NCBI Description	(AC002986) Contains homology to DNAJ heatshock protein gb_U32803 from Haemophilus influenzae. [Arabidopsis thaliana]
Seq. No.	276371
Contig ID	67212_1.R1011
5'-most EST	vux700162159.h1
Seq. No.	276372
Contig ID	67224_1.R1011
5'-most EST	LIB3062-003-Q1-K1-B7
Method	BLASTX
NCBI GI	g4522007
BLAST score	340
E value	6.0e-32
Match length	99
% identity	64
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]
Seq. No.	276373
Contig ID	67232_1.R1011
5'-most EST	dyk700102637.h1
Method	BLASTX
NCBI GI	g719291
BLAST score	169
E value	6.0e-17

Match length	88
% identity	65
NCBI Description	(U19134) unknown [Arabidopsis thaliana] >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]

Seq. No.	276374
Contig ID	67246_1.R1011
5'-most EST	LIB3062-003-Q1-K1-E2

Seq. No.	276375
Contig ID	67247_1.R1011
5'-most EST	LIB3062-003-Q1-K1-E3
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	276376
Contig ID	67250_1.R1011
5'-most EST	LIB3062-003-Q1-K1-E6
Method	BLASTX
NCBI GI	g3859662
BLAST score	149
E value	3.0e-09
Match length	128
% identity	30
NCBI Description	(AL033502) acetyl-coenzyme A synthetase [Candida albicans]

Seq. No.	276377
Contig ID	67253_1.R1011
5'-most EST	uC-zmflmo17295d05b1

Seq. No.	276378
Contig ID	67255_1.R1011
5'-most EST	LIB3062-003-Q1-K1-F3
Method	BLASTX
NCBI GI	g4126473
BLAST score	372
E value	2.0e-70
Match length	240
% identity	61
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	276379
Contig ID	67257_1.R1011
5'-most EST	uC-zmflmo17175c06b1
Method	BLASTX
NCBI GI	g3378661
BLAST score	796
E value	7.0e-86
Match length	249
% identity	62
NCBI Description	(Y13048) putative outward rectifying potassium channel

StKCO1 [Solanum tuberosum]

Seq. No.	276380
Contig ID	67263_1.R1011
5'-most EST	uC-zmflmo17046c12b1
Method	BLASTX
NCBI GI	g3063451
BLAST score	396
E value	3.0e-38
Match length	212
% identity	42
NCBI Description	(AC003981) F22O13.13 [Arabidopsis thaliana]

Seq. No.	276381
Contig ID	67265_2.R1011
5'-most EST	uC-zmflmo17261f09b1

Seq. No.	276382
Contig ID	67266_1.R1011
5'-most EST	LIB3062-024-Q1-K1-B9
Method	BLASTX
NCBI GI	g1944504
BLAST score	742
E value	1.0e-151
Match length	299
% identity	89
NCBI Description	(D64036) protein cdc2 kinase [Oryza sativa]

Seq. No.	276383
Contig ID	67285_1.R1011
5'-most EST	LIB3062-038-Q1-K1-H4

Seq. No.	276384
Contig ID	67292_2.R1011
5'-most EST	ymt700223963.h1
Method	BLASTX
NCBI GI	g3080398
BLAST score	185
E value	1.0e-13
Match length	164
% identity	17
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	276385
Contig ID	67294_1.R1011
5'-most EST	xdb700338259.h1
Method	BLASTN
NCBI GI	g168436
BLAST score	68
E value	1.0e-29
Match length	112
% identity	98
NCBI Description	Zea mays catalase (Cat3) gene, complete cds

Seq. No.	276386
Contig ID	67294_2.R1011
5'-most EST	LIB3062-004-Q1-K1-B7

Seq. No.	276387
Contig ID	67301_1.R1011
5'-most EST	nbm700465380.h1
Method	BLASTX
NCBI GI	g4467098
BLAST score	383
E value	5.0e-37
Match length	128
% identity	53
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	276388
Contig ID	67302_1.R1011
5'-most EST	LIB3062-004-Q1-K1-C7
Method	BLASTX
NCBI GI	g3820578
BLAST score	251
E value	3.0e-21
Match length	112
% identity	46
NCBI Description	(AF084242) GTP-binding protein; CgpA [Caulobacter crescentus]

Seq. No.	276389
Contig ID	67303_1.R1011
5'-most EST	uC-zmflb73151f01a2
Method	BLASTX
NCBI GI	g2204224
BLAST score	259
E value	2.0e-22
Match length	60
% identity	78
NCBI Description	(Y13849) alpha-galactosidase [Hordeum vulgare]

Seq. No.	276390
Contig ID	67306_1.R1011
5'-most EST	fdz701166245.h1
Method	BLASTX
NCBI GI	g4585876
BLAST score	249
E value	4.0e-21
Match length	122
% identity	43
NCBI Description	(AC005850) Putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	276391
Contig ID	67318_1.R1011
5'-most EST	uC-zmflm017205b01b1

Seq. No.	276392
Contig ID	67330_1.R1011
5'-most EST	uC-zmroteosinte073c06b1
Method	BLASTX
NCBI GI	g3913464
BLAST score	1072

E value	1.0e-117
Match length	217
% identity	90
NCBI Description	BETAINE-ALDEHYDE DEHYDROGENASE (BADH) >gi_2244604_dbj_BAA21098_ (AB001348) betaine aldehyde dehydrogenase [Oryza sativa]

Seq. No.	276393
Contig ID	67331_1.R1011
5'-most EST	LIB3062-004-Q1-K1-F8

Seq. No.	276394
Contig ID	67333_1.R1011
5'-most EST	LIB3062-004-Q1-K1-G2

Seq. No.	276395
Contig ID	67334_1.R1011
5'-most EST	LIB3062-004-Q1-K1-G10
Method	BLASTX
NCBI GI	g452357
BLAST score	298
E value	5.0e-27
Match length	90
% identity	67
NCBI Description	(Z29591) guanine nucleotide regulatory protein [Vicia faba] >gi_1098294_prf__2115367B small GTP-binding protein [Vicia faba]

Seq. No.	276396
Contig ID	67344_1.R1011
5'-most EST	LIB3069-047-Q1-K1-A7

Seq. No.	276397
Contig ID	67349_1.R1011
5'-most EST	uC-zmflb73226c07b1

Seq. No.	276398
Contig ID	67356_1.R1011
5'-most EST	LIB3062-005-Q1-K1-A8
Method	BLASTX
NCBI GI	g1323746
BLAST score	193
E value	2.0e-14
Match length	90
% identity	49
NCBI Description	(U32429) sulfur-rich/thionin-like protein [Triticum aestivum]

Seq. No.	276399
Contig ID	67356_2.R1011
5'-most EST	uC-zmflmo17297h08b1
Method	BLASTX
NCBI GI	g1323746
BLAST score	184
E value	2.0e-13
Match length	90
% identity	48

NCBI Description	(U32429) sulfur-rich/thionin-like protein [Triticum aestivum]

Seq. No.	276400
Contig ID	67362_1.R1011
5'-most EST	xyt700342266.h1
Method	BLASTX
NCBI GI	g4587533
BLAST score	446
E value	8.0e-48
Match length	195
% identity	53
NCBI Description	(AC007060) EST gb_AA721821 comes from this gene. [Arabidopsis thaliana]

Seq. No.	276401
Contig ID	67362_2.R1011
5'-most EST	cyk700047448.f1
Method	BLASTX
NCBI GI	g4587533
BLAST score	294
E value	1.0e-26
Match length	88
% identity	62
NCBI Description	(AC007060) EST gb_AA721821 comes from this gene. [Arabidopsis thaliana]

Seq. No.	276402
Contig ID	67364_1.R1011
5'-most EST	uC-zmflMo17019f09b1
Method	BLASTX
NCBI GI	g3935173
BLAST score	315
E value	6.0e-29
Match length	70
% identity	76
NCBI Description	(AC004557) F17L21.16 [Arabidopsis thaliana]

Seq. No.	276403
Contig ID	67378_1.R1011
5'-most EST	nbm700473248.h1
Method	BLASTX
NCBI GI	g4503249
BLAST score	184
E value	4.0e-13
Match length	328
% identity	23
NCBI Description	DEK gene >gi_544150_sp_P35659_DEK_HUMAN DEK PROTEIN >gi_284375_pir__S26059 probable transforming protein (dek) - human >gi_30503_emb_CAA45536_ (X64229) putative oncogene [Homo sapiens] >gi_4007163_emb_CAA21138_ (AL031774) dek (putative oncogene) [Homo sapiens]

Seq. No.	276404
Contig ID	67392_1.R1011
5'-most EST	gct701174366.h1
Method	BLASTX

NCBI GI	g2673918
BLAST score	261
E value	1.0e-22
Match length	94
% identity	60
NCBI Description	(AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No.	276405
Contig ID	67398_1.R1011
5'-most EST	LIB3062-005-Q1-K1-H8

Seq. No.	276406
Contig ID	67400_1.R1011
5'-most EST	cat700019183.r1

Seq. No.	276407
Contig ID	67409_1.R1011
5'-most EST	LIB3069-035-Q1-K1-H2
Method	BLASTX
NCBI GI	g1491776
BLAST score	328
E value	2.0e-30
Match length	96
% identity	69
NCBI Description	(M37636) cationic peroxidase [Arachis hypogaea]

Seq. No.	276408
Contig ID	67415_1.R1011
5'-most EST	uC-zmflmo17054e11b1

Seq. No.	276409
Contig ID	67417_1.R1011
5'-most EST	LIB3062-006-Q1-K1-C7

Seq. No.	276410
Contig ID	67418_1.R1011
5'-most EST	uC-zmrob73006b06b1
Method	BLASTX
NCBI GI	g4240037
BLAST score	447
E value	6.0e-69
Match length	177
% identity	80
NCBI Description	(AB018589) ZmGR2a [Zea mays]

Seq. No.	276411
Contig ID	67418_2.R1011
5'-most EST	wty700167973.h1
Method	BLASTX
NCBI GI	g4240039
BLAST score	346
E value	2.0e-32
Match length	70
% identity	99
NCBI Description	(AB018590) ZmGR2b [Zea mays]

Seq. No.	276412

09854705.040800

Contig ID	67418_3.R1011
5'-most EST	LIB3062-006-Q1-K1-C8
Method	BLASTX
NCBI GI	g4240037
BLAST score	385
E value	3.0e-37
Match length	94
% identity	84
NCBI Description	(AB018589) ZmGR2a [Zea mays]

Seq. No.	276413
Contig ID	67418_4.R1011
5'-most EST	uC-zmflmo17194a03a1
Method	BLASTX
NCBI GI	g4240039
BLAST score	258
E value	3.0e-22
Match length	48
% identity	100
NCBI Description	(AB018590) ZmGR2b [Zea mays]

Seq. No.	276414
Contig ID	67428_1.R1011
5'-most EST	uC-zmromo17010b03a1

Seq. No.	276415
Contig ID	67433_1.R1011
5'-most EST	LIB3062-006-Q1-K1-F2

Seq. No.	276416
Contig ID	67440_1.R1011
5'-most EST	uC-zmflb73126f05b1
Method	BLASTX
NCBI GI	g3777483
BLAST score	611
E value	1.0e-75
Match length	218
% identity	65
NCBI Description	(AB018695) sulfate transporter [Arabidopsis thaliana]

Seq. No.	276417
Contig ID	67442_1.R1011
5'-most EST	uC-zmflb73158c06b2
Method	BLASTX
NCBI GI	g2088651
BLAST score	234
E value	3.0e-19
Match length	174
% identity	36
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	276418
Contig ID	67452_1.R1011
5'-most EST	uC-zmflB73009c09b1

Seq. No.	276419

Contig ID	67457_1.R1011
5'-most EST	xsy700213165.h1
Seq. No.	276420
Contig ID	67475_1.R1011
5'-most EST	LIB3062-007-Q1-K1-C5
Method	BLASTX
NCBI GI	g1877480
BLAST score	247
E value	8.0e-21
Match length	95
% identity	59
NCBI Description	(U89270) short-chain alcohol dehydrogenase [Tripsacum dactyloides]
Seq. No.	276421
Contig ID	67482_1.R1011
5'-most EST	LIB3062-007-Q1-K1-D12
Method	BLASTX
NCBI GI	g3927830
BLAST score	451
E value	3.0e-64
Match length	202
% identity	67
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276422
Contig ID	67485_1.R1011
5'-most EST	xsy700212279.h1
Method	BLASTX
NCBI GI	g4581109
BLAST score	221
E value	1.0e-17
Match length	106
% identity	44
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]
Seq. No.	276423
Contig ID	67492_1.R1011
5'-most EST	dyk700106968.h1
Seq. No.	276424
Contig ID	67497_1.R1011
5'-most EST	LIB3069-029-Q1-K1-D11
Method	BLASTX
NCBI GI	g3402282
BLAST score	198
E value	3.0e-15
Match length	83
% identity	42
NCBI Description	(AJ000997) proline-rich protein [Solanum tuberosum]
Seq. No.	276425
Contig ID	67498_1.R1011
5'-most EST	LIB3062-007-Q1-K1-E9
Method	BLASTX
NCBI GI	g4507943

BLAST score	560
E value	1.0e-57
Match length	185
% identity	56
NCBI Description	exportin 1 (CRM1, yeast, homolog) >gi_2626840_dbj_BAA23415_ (D89729) CRM1 protein [Homo sapiens]

Seq. No.	276426
Contig ID	67502_1.R1011
5'-most EST	LIB3062-007-Q1-K1-F4

Seq. No.	276427
Contig ID	67505_1.R1011
5'-most EST	LIB3136-007-Q1-K1-C6
Method	BLASTX
NCBI GI	g3393022
BLAST score	361
E value	4.0e-34
Match length	195
% identity	43
NCBI Description	(AL031174) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	276428
Contig ID	67524_1.R1011
5'-most EST	uC-zmflmo17297d08b1
Method	BLASTX
NCBI GI	g4416307
BLAST score	249
E value	4.0e-21
Match length	89
% identity	62
NCBI Description	(AF105716) hypothetical protein [Zea mays]

Seq. No.	276429
Contig ID	67537_1.R1011
5'-most EST	LIB3062-008-Q1-K1-B3
Method	BLASTX
NCBI GI	g1703089
BLAST score	450
E value	3.0e-44
Match length	208
% identity	42
NCBI Description	ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE) (APH) (ACYLAMINOACYL-PEPTIDASE) (DNF15S2 PROTEIN) >gi_2118063_pir__JC4655 acylaminoacyl-peptidase (EC 3.4.19.1) - human >gi_556514_dbj_BAA07476_ (D38441) acylamino acid-releasing enzyme [Homo sapiens]

Seq. No.	276430
Contig ID	67551_1.R1011
5'-most EST	LIB3062-008-Q1-K1-C5

Seq. No.	276431
Contig ID	67564_1.R1011
5'-most EST	qmh700030308.f1
Method	BLASTX
NCBI GI	g4580461

BLAST score	827
E value	1.0e-88
Match length	232
% identity	69
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	276432
Contig ID	67570_1.R1011
5'-most EST	LIB3070-001-Q1-N1-H7

Seq. No.	276433
Contig ID	67590_1.R1011
5'-most EST	gwl700615611.h1
Method	BLASTX
NCBI GI	g4218122
BLAST score	153
E value	1.0e-09
Match length	212
% identity	29
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	276434
Contig ID	67608_1.R1011
5'-most EST	LIB3062-009-Q1-K1-A7

Seq. No.	276435
Contig ID	67612_1.R1011
5'-most EST	xmt700260242.h1

Seq. No.	276436
Contig ID	67618_1.R1011
5'-most EST	wev700405038.h1
Method	BLASTX
NCBI GI	g347855
BLAST score	649
E value	4.0e-68
Match length	150
% identity	85
NCBI Description	(L21753) glucose transporter [Saccharum hybrid cultivar H65-7052]

Seq. No.	276437
Contig ID	67621_1.R1011
5'-most EST	uC-zmf1b73142b12b1
Method	BLASTX
NCBI GI	g2194142
BLAST score	231
E value	9.0e-40
Match length	114
% identity	64
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	276438
Contig ID	67621_2.R1011
5'-most EST	qmh700027578.f1
Method	BLASTX

NCBI GI	g2194142
BLAST score	759
E value	8.0e-81
Match length	188
% identity	69
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	276439
Contig ID	67624_1.R1011
5'-most EST	uC-zmrob73053d03a1

Seq. No.	276440
Contig ID	67624_2.R1011
5'-most EST	LIB3062-009-Q1-K1-C11
Method	BLASTX
NCBI GI	g3193287
BLAST score	892
E value	2.0e-96
Match length	188
% identity	83
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	276441
Contig ID	67630_1.R1011
5'-most EST	ymt700224009.h1
Method	BLASTX
NCBI GI	g2498779
BLAST score	179
E value	5.0e-13
Match length	112
% identity	36
NCBI Description	PIR7B PROTEIN >gi_629801_pir__S47087 pir7b protein - rice >gi_498745_emb_CAA84026_ (Z34271) Pir7b [Oryza sativa]

Seq. No.	276442
Contig ID	67642_1.R1011
5'-most EST	nwy700444995.h1
Method	BLASTX
NCBI GI	g4507943
BLAST score	398
E value	2.0e-58
Match length	268
% identity	46
NCBI Description	exportin 1 (CRM1, yeast, homolog) >gi_2626840_dbj_BAA23415_ (D89729) CRM1 protein [Homo sapiens]

Seq. No.	276443
Contig ID	67646_1.R1011
5'-most EST	LIB3062-009-Q1-K1-E11
Method	BLASTX
NCBI GI	g4531444
BLAST score	350
E value	9.0e-33
Match length	87
% identity	75

NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	276444
Contig ID	67647_1.R1011
5'-most EST	xjt700094865.h1
Method	BLASTX
NCBI GI	g3928097
BLAST score	675
E value	7.0e-71
Match length	180
% identity	64
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	276445
Contig ID	67648_1.R1011
5'-most EST	pmx700091744.h1
Method	BLASTX
NCBI GI	g2160191
BLAST score	1019
E value	1.0e-111
Match length	208
% identity	88
NCBI Description	(AC000132) Identical to A. thaliana AtK-1 (gb_X79279). [Arabidopsis thaliana]

Seq. No.	276446
Contig ID	67650_1.R1011
5'-most EST	uC-zmflmo17101d04b1
Method	BLASTX
NCBI GI	g3193292
BLAST score	347
E value	2.0e-66
Match length	241
% identity	51
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	276447
Contig ID	67669_1.R1011
5'-most EST	LIB3062-009-Q1-K1-G12

Seq. No.	276448
Contig ID	67671_1.R1011
5'-most EST	LIB3062-009-Q1-K1-G3
Method	BLASTX
NCBI GI	g2244970
BLAST score	393
E value	6.0e-39
Match length	162
% identity	55
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	276449

Contig ID	67675_1.R1011
5'-most EST	ntr700077449.h1
Seq. No.	276450
Contig ID	67682_1.R1011
5'-most EST	LIB3069-042-Q1-K1-C1
Method	BLASTX
NCBI GI	g4099919
BLAST score	378
E value	2.0e-68
Match length	164
% identity	74
NCBI Description	(U91981) pollen allergen homolog [Triticum aestivum]
Seq. No.	276451
Contig ID	67682_2.R1011
5'-most EST	LIB3067-060-Q1-K1-A3
Method	BLASTX
NCBI GI	g4099919
BLAST score	207
E value	2.0e-16
Match length	49
% identity	76
NCBI Description	(U91981) pollen allergen homolog [Triticum aestivum]
Seq. No.	276452
Contig ID	67698_2.R1011
5'-most EST	pmx700084272.h1
Seq. No.	276453
Contig ID	67700_1.R1011
5'-most EST	cyk700048720.f1
Method	BLASTX
NCBI GI	g3024504
BLAST score	334
E value	6.0e-31
Match length	76
% identity	80
NCBI Description	RAS-RELATED PROTEIN RAB11B >gi_623578 (L29269) putative [Nicotiana tabacum]
Seq. No.	276454
Contig ID	67705_1.R1011
5'-most EST	LIB3062-010-Q1-K1-B5
Seq. No.	276455
Contig ID	67707_1.R1011
5'-most EST	LIB36-006-Q1-E1-C5
Seq. No.	276456
Contig ID	67707_2.R1011
5'-most EST	uC-zmflb73208b11a2
Seq. No.	276457
Contig ID	67716_1.R1011
5'-most EST	uwc700153720.h1
Method	BLASTX

NCBI GI	g4567197
BLAST score	1289
E value	1.0e-142
Match length	582
% identity	47
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	276458
Contig ID	67726_1.R1011
5'-most EST	uC-zmroteosinte080b12b1
Method	BLASTX
NCBI GI	g2909521
BLAST score	194
E value	1.0e-14
Match length	121
% identity	37
NCBI Description	(AL021932) hypothetical protein Rv0446c [Mycobacterium tuberculosis]

Seq. No.	276459
Contig ID	67729_1.R1011
5'-most EST	kem700612203.h1
Method	BLASTX
NCBI GI	g3201615
BLAST score	414
E value	5.0e-40
Match length	271
% identity	41
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	276460
Contig ID	67730_1.R1011
5'-most EST	uC-zmflb73108c02a1

Seq. No.	276461
Contig ID	67735_1.R1011
5'-most EST	LIB3062-010-Q1-K1-E7

Seq. No.	276462
Contig ID	67739_1.R1011
5'-most EST	LIB3062-010-Q1-K1-F10

Seq. No.	276463
Contig ID	67740_1.R1011
5'-most EST	LIB3062-010-Q1-K1-F11
Method	BLASTX
NCBI GI	g3482974
BLAST score	633
E value	3.0e-66
Match length	138
% identity	88
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	276464
Contig ID	67743_1.R1011
5'-most EST	LIB84-024-Q1-E1-B7

Seq. No.	276465
Contig ID	67743_2.R1011
5'-most EST	LIB3069-055-Q1-K1-E12

Seq. No.	276466
Contig ID	67745_1.R1011
5'-most EST	uC-zmflmo17036c08b2
Method	BLASTX
NCBI GI	g1794137
BLAST score	184
E value	2.0e-13
Match length	72
% identity	46
NCBI Description	(AB000402) DMO25 [Drosophila melanogaster]

Seq. No.	276467
Contig ID	67745_2.R1011
5'-most EST	wty700170954.h1
Method	BLASTX
NCBI GI	g547911
BLAST score	569
E value	5.0e-67
Match length	318
% identity	44
NCBI Description	MO25 PROTEIN >gi_2143483_pir__I57997 hypothetical calcium-binding protein - mouse >gi_262934_bbs_121784 (S51858) putative Ca2+ binding protein [mice, embryos, Peptide, 341 aa] [Mus sp.]

Seq. No.	276468
Contig ID	67749_1.R1011
5'-most EST	LIB3062-052-Q1-K1-D6
Method	BLASTX
NCBI GI	g3128213
BLAST score	166
E value	2.0e-11
Match length	59
% identity	56
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276469
Contig ID	67758_1.R1011
5'-most EST	xmt700265973.h1

Seq. No.	276470
Contig ID	67760_1.R1011
5'-most EST	wen700336622.h1
Method	BLASTX
NCBI GI	g2655888
BLAST score	711
E value	3.0e-83
Match length	345
% identity	22
NCBI Description	(AL009171) 62D9.a [Drosophila melanogaster]

Seq. No. 276471

Contig ID	67768_1.R1011
5'-most EST	LIB3069-008-Q1-K1-C10
Method	BLASTX
NCBI GI	g3482914
BLAST score	167
E value	1.0e-11
Match length	52
% identity	60
NCBI Description	(AC003970) Similar to nodulins and lipase [Arabidopsis thaliana]

Seq. No.	276472
Contig ID	67771_1.R1011
5'-most EST	pmx700084960.h1
Method	BLASTX
NCBI GI	g4539291
BLAST score	558
E value	4.0e-57
Match length	267
% identity	49
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	276473
Contig ID	67772_1.R1011
5'-most EST	LIB3062-011-Q1-K1-A8

Seq. No.	276474
Contig ID	67775_1.R1011
5'-most EST	LIB3062-011-Q1-K1-B12

Seq. No.	276475
Contig ID	67777_1.R1011
5'-most EST	LIB3062-011-Q1-K1-B4
Method	BLASTX
NCBI GI	g3540198
BLAST score	271
E value	1.0e-23
Match length	81
% identity	62
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	276476
Contig ID	67779_1.R1011
5'-most EST	qmh700028154.f1
Method	BLASTX
NCBI GI	g465737
BLAST score	169
E value	1.0e-11
Match length	186
% identity	29
NCBI Description	HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III >gi_630510_pir__S44606 C02F5.4 protein - Caenorhabditis elegans >gi_289611 (L14745) coded for by C. elegans cDNA GenBank:CEL16D4 (M89109); putative [Caenorhabditis elegans]

Seq. No.	276477
Contig ID	67785_1.R1011

5'-most EST	LIB3062-011-Q1-K1-C11
Seq. No.	276478
Contig ID	67793_1.R1011
5'-most EST	LIB3137-027-Q1-K1-B7
Seq. No.	276479
Contig ID	67798_1.R1011
5'-most EST	xsy700217040.h1
Seq. No.	276480
Contig ID	67805_1.R1011
5'-most EST	uC-zmflb73247b01a2
Seq. No.	276481
Contig ID	67819_1.R1011
5'-most EST	LIB3062-011-Q1-K1-F11
Method	BLASTX
NCBI GI	g4104058
BLAST score	284
E value	5.0e-25
Match length	90
% identity	56
NCBI Description	(AF031195) blue copper-binding protein homolog [Triticum aestivum]
Seq. No.	276482
Contig ID	67821_1.R1011
5'-most EST	xyt700346227.h1
Method	BLASTX
NCBI GI	g2213594
BLAST score	382
E value	1.0e-36
Match length	188
% identity	39
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.	276483
Contig ID	67831_1.R1011
5'-most EST	LIB3062-011-Q1-K1-G7
Seq. No.	276484
Contig ID	67837_1.R1011
5'-most EST	uC-zmflm017212h05b1
Method	BLASTX
NCBI GI	g4105794
BLAST score	343
E value	6.0e-32
Match length	131
% identity	50
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]
Seq. No.	276485
Contig ID	67849_1.R1011
5'-most EST	uC-zmflmo17223a07b1
Method	BLASTX
NCBI GI	g2262143

BLAST score	1251
E value	1.0e-138
Match length	331
% identity	73
NCBI Description	(AC002330) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	276486
Contig ID	67853_1.R1011
5'-most EST	cat700018319.r1
Method	BLASTX
NCBI GI	g2959358
BLAST score	562
E value	9.0e-58
Match length	110
% identity	97
NCBI Description	(X96758) clathrin coat assembly protein AP17 [Zea mays]

Seq. No.	276487
Contig ID	67856_2.R1011
5'-most EST	LIB3062-012-Q1-K1-B6
Method	BLASTX
NCBI GI	g2829889
BLAST score	243
E value	3.0e-20
Match length	61
% identity	84
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	276488
Contig ID	67862_1.R1011
5'-most EST	gwl700614592.h1
Method	BLASTX
NCBI GI	g2765817
BLAST score	1172
E value	1.0e-129
Match length	369
% identity	62
NCBI Description	(Z95352) AtMlo-h1 [Arabidopsis thaliana] >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No.	276489
Contig ID	67868_1.R1011
5'-most EST	LIB3062-012-Q1-K1-C8
Method	BLASTX
NCBI GI	g4115934
BLAST score	154
E value	3.0e-16
Match length	60
% identity	75
NCBI Description	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No.	276490
Contig ID	67869_1.R1011

5'-most EST	pmx700091013.h1
Seq. No.	276491
Contig ID	67872_1.R1011
5'-most EST	nbm700470995.h1
Seq. No.	276492
Contig ID	67872_2.R1011
5'-most EST	wen700332227.h1
Method	BLASTX
NCBI GI	g4469014
BLAST score	446
E value	5.0e-44
Match length	137
% identity	64
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	276493
Contig ID	67875_1.R1011
5'-most EST	uC-zmflmo17266g08b1
Seq. No.	276494
Contig ID	67875_2.R1011
5'-most EST	LIB3062-019-Q1-K1-G10
Method	BLASTX
NCBI GI	g3643605
BLAST score	163
E value	3.0e-11
Match length	62
% identity	52
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276495
Contig ID	67877_1.R1011
5'-most EST	uC-zmroteosinte070b10b1
Method	BLASTX
NCBI GI	g2190419
BLAST score	661
E value	2.0e-69
Match length	185
% identity	70
NCBI Description	(Y13632) dem [Lycopersicon esculentum]
Seq. No.	276496
Contig ID	67877_2.R1011
5'-most EST	uC-zmflb73083h03b2
Method	BLASTX
NCBI GI	g2190419
BLAST score	598
E value	7.0e-62
Match length	234
% identity	56
NCBI Description	(Y13632) dem [Lycopersicon esculentum]
Seq. No.	276497
Contig ID	67884_1.R1011
5'-most EST	LIB3069-023-Q1-K1-H4

Method	BLASTX
NCBI GI	g3402718
BLAST score	151
E value	2.0e-09
Match length	40
% identity	62
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276498
Contig ID	67885_1.R1011
5'-most EST	LIB3062-012-Q1-K1-E2
Method	BLASTX
NCBI GI	g1931652
BLAST score	217
E value	2.0e-17
Match length	127
% identity	14
NCBI Description	(U95973) phosphatidylinositol-4-phosphate 5-kinase isolog [Arabidopsis thaliana]

Seq. No.	276499
Contig ID	67892_1.R1011
5'-most EST	uC-zmf1b73067d07a1
Method	BLASTX
NCBI GI	g4185499
BLAST score	185
E value	1.0e-13
Match length	66
% identity	44
NCBI Description	(AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.	276500
Contig ID	67897_1.R1011
5'-most EST	LIB3062-012-Q1-K1-F5

Seq. No.	276501
Contig ID	67898_1.R1011
5'-most EST	pwr700452810.h1
Method	BLASTX
NCBI GI	g2498731
BLAST score	631
E value	9.0e-66
Match length	204
% identity	57
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	276502
Contig ID	67907_1.R1011
5'-most EST	uC-zmf1b73235f02b2

Seq. No.	276503

Contig ID	67911_1.R1011
5'-most EST	xsy700210706.h1
Method	BLASTX
NCBI GI	g4455244
BLAST score	429
E value	6.0e-42
Match length	210
% identity	42
NCBI Description	(AL035523) MtN3-like protein [Arabidopsis thaliana]

Seq. No.	276504
Contig ID	67911_2.R1011
5'-most EST	LIB3136-005-Q1-K1-G9
Method	BLASTX
NCBI GI	g4539359
BLAST score	168
E value	2.0e-11
Match length	60
% identity	57
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	276505
Contig ID	67911_3.R1011
5'-most EST	cat700020739.r1

Seq. No.	276506
Contig ID	67922_1.R1011
5'-most EST	LIB3062-012-Q1-K1-H8

Seq. No.	276507
Contig ID	67931_1.R1011
5'-most EST	LIB3062-013-Q1-K1-A7

Seq. No.	276508
Contig ID	67939_1.R1011
5'-most EST	yyf700348335.h1
Method	BLASTX
NCBI GI	g3818624
BLAST score	544
E value	1.0e-55
Match length	118
% identity	86
NCBI Description	(AF095912) actin related protein 2; ARP2 [Arabidopsis thaliana]

Seq. No.	276509
Contig ID	67940_1.R1011
5'-most EST	LIB3062-013-Q1-K1-B6

Seq. No.	276510
Contig ID	67947_1.R1011
5'-most EST	LIB3062-013-Q1-K1-C2
Method	BLASTX
NCBI GI	g3860258
BLAST score	343
E value	5.0e-32
Match length	119

% identity	55
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	276511
Contig ID	67951_1.R1011
5'-most EST	uC-zmflmo17305f01a1
Method	BLASTX
NCBI GI	g3080427
BLAST score	1408
E value	1.0e-156
Match length	410
% identity	65
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	276512
Contig ID	67951_3.R1011
5'-most EST	xyt700343837.h1

Seq. No.	276513
Contig ID	67959_1.R1011
5'-most EST	uC-zmflmo17164f02b1
Method	BLASTX
NCBI GI	g3882215
BLAST score	190
E value	5.0e-14
Match length	134
% identity	36
NCBI Description	(AB018290) KIAA0747 protein [Homo sapiens]

Seq. No.	276514
Contig ID	67969_1.R1011
5'-most EST	xjt700095670.h1
Method	BLASTX
NCBI GI	g3935152
BLAST score	981
E value	1.0e-114
Match length	310
% identity	67
NCBI Description	(AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No.	276515
Contig ID	67971_1.R1011
5'-most EST	uC-zmflb73178d10b1
Method	BLASTX
NCBI GI	g4097948
BLAST score	688
E value	1.0e-142
Match length	327
% identity	82
NCBI Description	(U72255) beta-1,3-glucanase precursor [Oryza sativa]

Seq. No.	276516
Contig ID	67982_1.R1011
5'-most EST	pmx700085079.h1
Method	BLASTX
NCBI GI	g1431629
BLAST score	620

E value	2.0e-64
Match length	168
% identity	62
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	276517
Contig ID	67984_1.R1011
5'-most EST	LIB3069-028-Q1-K1-E9

Seq. No.	276518
Contig ID	67986_1.R1011
5'-most EST	uC-zmroteosinte004f03b1
Method	BLASTX
NCBI GI	g2947063
BLAST score	240
E value	8.0e-20
Match length	153
% identity	37
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	276519
Contig ID	67986_2.R1011
5'-most EST	uC-zmflb73093h09a1

Seq. No.	276520
Contig ID	67989_1.R1011
5'-most EST	ceu700432419.h1

Seq. No.	276521
Contig ID	67993_1.R1011
5'-most EST	uwc700153304.h1

Seq. No.	276522
Contig ID	67996_1.R1011
5'-most EST	LIB3062-013-Q1-K1-H6

Seq. No.	276523
Contig ID	68007_1.R1011
5'-most EST	uC-zmrob73050e06b1

Seq. No.	276524
Contig ID	68007_2.R1011
5'-most EST	xjt700094340.h1
Method	BLASTX
NCBI GI	g3618320
BLAST score	622
E value	1.0e-64
Match length	150
% identity	75
NCBI Description	(AB001888) zinc finger protein [Oryza sativa]

Seq. No.	276525
Contig ID	68013_1.R1011
5'-most EST	hbs701184515.h1
Method	BLASTX
NCBI GI	g4038352

BLAST score	427
E value	6.0e-42
Match length	180
% identity	47
NCBI Description	(AF098951) breast cancer resistance protein [Homo sapiens]

Seq. No.	276526
Contig ID	68017_1.R1011
5'-most EST	rvt700551639.h1
Method	BLASTX
NCBI GI	g3152582
BLAST score	473
E value	3.0e-47
Match length	183
% identity	51
NCBI Description	(AC002986) YUP8H12R.20 [Arabidopsis thaliana]

Seq. No.	276527
Contig ID	68019_1.R1011
5'-most EST	LIB3062-014-Q1-K1-C10

Seq. No.	276528
Contig ID	68022_1.R1011
5'-most EST	uer700582163.h1

Seq. No.	276529
Contig ID	68023_1.R1011
5'-most EST	uC-zmflb73018h04b1
Method	BLASTX
NCBI GI	g1255430
BLAST score	285
E value	2.0e-25
Match length	124
% identity	45
NCBI Description	(U53155) No definition line found [Caenorhabditis elegans]

Seq. No.	276530
Contig ID	68023_3.R1011
5'-most EST	hbs701182122.h1

Seq. No.	276531
Contig ID	68023_4.R1011
5'-most EST	uC-zmflb73185f04b1

Seq. No.	276532
Contig ID	68032_1.R1011
5'-most EST	LIB3062-014-Q1-K1-D4

Seq. No.	276533
Contig ID	68040_1.R1011
5'-most EST	LIB3062-014-Q1-K1-E2

Seq. No.	276534
Contig ID	68043_1.R1011
5'-most EST	LIB3062-014-Q1-K1-E5
Method	BLASTX
NCBI GI	g4574141

BLAST score	574
E value	2.0e-59
Match length	141
% identity	76
NCBI Description	(AF073698) cysteine synthase [Oryza sativa]

Seq. No.	276535
Contig ID	68055_1.R1011
5'-most EST	LIB3062-014-Q1-K1-F6
Method	BLASTX
NCBI GI	g3036807
BLAST score	407
E value	2.0e-39
Match length	140
% identity	57
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana]

Seq. No.	276536
Contig ID	68065_1.R1011
5'-most EST	LIB3062-014-Q1-K1-G5
Method	BLASTX
NCBI GI	g4512671
BLAST score	264
E value	9.0e-23
Match length	111
% identity	50
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	276537
Contig ID	68068_1.R1011
5'-most EST	xjt700092611.h1

Seq. No.	276538
Contig ID	68080_1.R1011
5'-most EST	uC-zmflmo17036b07b2
Method	BLASTX
NCBI GI	g4539459
BLAST score	175
E value	7.0e-12
Match length	183
% identity	31
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	276539
Contig ID	68080_3.R1011
5'-most EST	uC-zmflb73356e06a2

Seq. No.	276540
Contig ID	68080_4.R1011
5'-most EST	rvl700457686.h1

Seq. No.	276541
Contig ID	68081_1.R1011
5'-most EST	LIB3062-015-Q1-K1-A1
Method	BLASTX
NCBI GI	g2618687
BLAST score	190

E value	2.0e-14
Match length	68
% identity	60
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276542
Contig ID	68086_1.R1011
5'-most EST	pmx700091587.h1
Method	BLASTX
NCBI GI	g3687240
BLAST score	251
E value	3.0e-21
Match length	112
% identity	46
NCBI Description	(AC005169) extensin-like protein [Arabidopsis thaliana]

Seq. No.	276543
Contig ID	68086_2.R1011
5'-most EST	ymt700224561.h1

Seq. No.	276544
Contig ID	68107_1.R1011
5'-most EST	LIB3062-015-Q1-K1-C4
Method	BLASTX
NCBI GI	g3386609
BLAST score	168
E value	1.0e-11
Match length	130
% identity	36
NCBI Description	(AC004665) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	276545
Contig ID	68112_1.R1011
5'-most EST	LIB3062-015-Q1-K1-D1
Method	BLASTX
NCBI GI	g3024583
BLAST score	234
E value	2.0e-19
Match length	90
% identity	50
NCBI Description	RT14 PROTEIN HOMOLOG >gi_2347196 (AC002338) RT14 protein isolog [Arabidopsis thaliana]

Seq. No.	276546
Contig ID	68119_1.R1011
5'-most EST	fC-zmst700620845f1
Method	BLASTX
NCBI GI	g2791278
BLAST score	535
E value	4.0e-54
Match length	492
% identity	32
NCBI Description	(Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No.	276547
Contig ID	68120_1.R1011

5'-most EST	uC-zmflb73274d05a1
Seq. No.	276548
Contig ID	68128_1.R1011
5'-most EST	uC-zmflm017086b05b1
Seq. No.	276549
Contig ID	68134_1.R1011
5'-most EST	LIB3062-015-Q1-K1-F12
Seq. No.	276550
Contig ID	68137_1.R1011
5'-most EST	LIB3062-015-Q1-K1-F4
Method	BLASTX
NCBI GI	g99733
BLAST score	324
E value	4.0e-30
Match length	134
% identity	49
NCBI Description	hypothetical protein H1flk - Arabidopsis thaliana (fragment) >gi_16482_emb_CAA44318_ (X62461) H1flk [Arabidopsis thaliana]
Seq. No.	276551
Contig ID	68159_1.R1011
5'-most EST	uC-zmflmo17185e10b1
Method	BLASTX
NCBI GI	g3522945
BLAST score	169
E value	7.0e-12
Match length	116
% identity	34
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	276552
Contig ID	68166_1.R1011
5'-most EST	xsy700208683.h1
Method	BLASTX
NCBI GI	g4455364
BLAST score	189
E value	4.0e-14
Match length	73
% identity	49
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]
Seq. No.	276553
Contig ID	68181_1.R1011
5'-most EST	uC-zmflB73004f05b1
Method	BLASTX
NCBI GI	g3377803
BLAST score	690
E value	1.0e-72
Match length	182
% identity	79
NCBI Description	(AF075597) Similar to (p)ppGpp synthetase; T2H3.9 [Arabidopsis thaliana]

Seq. No.	276554
Contig ID	68195_1.R1011
5'-most EST	LIB3062-016-Q1-K1-D2
Method	BLASTX
NCBI GI	g544184
BLAST score	1166
E value	1.0e-128
Match length	304
% identity	68
NCBI Description	4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) >gi_322785_pir__A45049 4-alpha-glucanotransferase (EC 2.4.1.25) - potato >gi_296692_emb_CAA48630_ (X68664) 4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No.	276555
Contig ID	68205_1.R1011
5'-most EST	uC-zmflb73014h01a1
Method	BLASTX
NCBI GI	g4335745
BLAST score	235
E value	4.0e-33
Match length	179
% identity	43
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	276556
Contig ID	68216_1.R1011
5'-most EST	LIB3062-016-Q1-K1-F12
Method	BLASTX
NCBI GI	g1161566
BLAST score	174
E value	2.0e-12
Match length	53
% identity	58
NCBI Description	(X94943) peroxidase [Lycopersicon esculentum]

Seq. No.	276557
Contig ID	68225_1.R1011
5'-most EST	uC-zmflmo17015h10b1

Seq. No.	276558
Contig ID	68255_1.R1011
5'-most EST	ymt700219782.h1
Method	BLASTX
NCBI GI	g2829888
BLAST score	1138
E value	1.0e-125
Match length	442
% identity	54
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	276559
Contig ID	68255_2.R1011

5'-most EST	uer700580312.h1
Method	BLASTX
NCBI GI	g2829888
BLAST score	254
E value	1.0e-21
Match length	106
% identity	52
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	276560
Contig ID	68261_1.R1011
5'-most EST	pmx700089745.h1
Method	BLASTX
NCBI GI	g2262104
BLAST score	386
E value	3.0e-37
Match length	115
% identity	61
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	276561
Contig ID	68270_1.R1011
5'-most EST	LIB3062-017-Q1-K1-C9
Method	BLASTX
NCBI GI	g4572674
BLAST score	301
E value	3.0e-27
Match length	64
% identity	81
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	276562
Contig ID	68278_1.R1011
5'-most EST	uC-zmflb73317e05b1
Method	BLASTX
NCBI GI	g3414809
BLAST score	183
E value	4.0e-13
Match length	159
% identity	10
NCBI Description	(AF061529) rjs [Mus musculus]

Seq. No.	276563
Contig ID	68278_2.R1011
5'-most EST	uC-zmroteosinte046g06b1
Method	BLASTX
NCBI GI	g4079809
BLAST score	199
E value	3.0e-15
Match length	182
% identity	3
NCBI Description	(AF071172) HERC2 [Homo sapiens]

Seq. No.	276564
Contig ID	68280_1.R1011
5'-most EST	LIB3062-017-Q1-K1-D7

Seq. No.	276565
Contig ID	68281_1.R1011
5'-most EST	kem700612170.h1
Method	BLASTX
NCBI GI	g2275202
BLAST score	561
E value	1.0e-57
Match length	158
% identity	60
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	276566
Contig ID	68281_2.R1011
5'-most EST	zuv700356052.h1
Method	BLASTX
NCBI GI	g1617270
BLAST score	177
E value	5.0e-13
Match length	59
% identity	56
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	276567
Contig ID	68305_1.R1011
5'-most EST	LIB3062-018-Q1-K1-G9
Method	BLASTX
NCBI GI	g2827663
BLAST score	221
E value	7.0e-18
Match length	168
% identity	6
NCBI Description	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]

Seq. No.	276568
Contig ID	68306_1.R1011
5'-most EST	LIB3062-017-Q1-K1-G12
Method	BLASTX
NCBI GI	g4510373
BLAST score	227
E value	2.0e-18
Match length	106
% identity	42
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	276569
Contig ID	68308_1.R1011
5'-most EST	LIB3062-017-Q1-K1-G3
Method	BLASTX
NCBI GI	g3935138
BLAST score	536
E value	3.0e-56
Match length	192
% identity	56
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No.	276570
Contig ID	68308_2.R1011
5'-most EST	uC-zmflmo17045f03b1

Seq. No.	276571
Contig ID	68308_5.R1011
5'-most EST	ckd700461177.h1
Method	BLASTX
NCBI GI	g3935138
BLAST score	188
E value	1.0e-14
Match length	84
% identity	45
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No.	276572
Contig ID	68327_1.R1011
5'-most EST	wen700334926.h1
Method	BLASTX
NCBI GI	g4091008
BLAST score	406
E value	7.0e-40
Match length	76
% identity	96
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	276573
Contig ID	68332_1.R1011
5'-most EST	LIB3062-018-Q1-K1-A7

Seq. No.	276574
Contig ID	68365_1.R1011
5'-most EST	LIB3069-029-Q1-K1-C2
Method	BLASTX
NCBI GI	g2462826
BLAST score	285
E value	4.0e-25
Match length	217
% identity	35
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	276575
Contig ID	68368_1.R1011
5'-most EST	LIB3062-030-Q1-K1-H7
Method	BLASTX
NCBI GI	g2529663
BLAST score	589
E value	8.0e-61
Match length	148
% identity	73
NCBI Description	(AC002535) putative lysophospholipase [Arabidopsis thaliana] >gi_3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	276576
Contig ID	68369_1.R1011

5'-most EST	uC-zmflb73307a05b1
Method	BLASTX
NCBI GI	g2586082
BLAST score	338
E value	2.0e-31
Match length	191
% identity	38
NCBI Description	(U72725) retrofit [Oryza longistaminata]

Seq. No.	276577
Contig ID	68370_1.R1011
5'-most EST	ntr700072641.h1

Seq. No.	276578
Contig ID	68378_1.R1011
5'-most EST	LIB3062-018-Q1-K1-F9

Seq. No.	276579
Contig ID	68382_1.R1011
5'-most EST	dyk700102437.h1
Method	BLASTX
NCBI GI	g3786011
BLAST score	702
E value	4.0e-74
Match length	207
% identity	70
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	276580
Contig ID	68382_2.R1011
5'-most EST	LIB3062-018-Q1-K1-G12
Method	BLASTX
NCBI GI	g3786011
BLAST score	516
E value	2.0e-52
Match length	132
% identity	80
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	276581
Contig ID	68388_1.R1011
5'-most EST	uwc700155113.h1

Seq. No.	276582
Contig ID	68399_1.R1011
5'-most EST	LIB3062-019-Q1-K1-A10
Method	BLASTX
NCBI GI	g1706130
BLAST score	468
E value	2.0e-61
Match length	176
% identity	72
NCBI Description	CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052 calcium-dependent protein kinase homolog - carrot >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein

kinase [Daucus carota]

Seq. No.	276583
Contig ID	68413_1.R1011
5'-most EST	uC-zmflmo17187a10b1
Method	BLASTX
NCBI GI	g3880145
BLAST score	194
E value	2.0e-14
Match length	115
% identity	37
NCBI Description	(Z68319) similar to tyrosine specific protein phosphatase; cDNA EST yk460c9.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	276584
Contig ID	68419_1.R1011
5'-most EST	LIB3062-019-Q1-K1-B9

Seq. No.	276585
Contig ID	68420_1.R1011
5'-most EST	LIB3062-019-Q1-K1-C1

Seq. No.	276586
Contig ID	68424_1.R1011
5'-most EST	lhp700053469.r1

Seq. No.	276587
Contig ID	68428_1.R1011
5'-most EST	ntr700074124.h1
Method	BLASTX
NCBI GI	g2239260
BLAST score	843
E value	2.0e-96
Match length	274
% identity	61
NCBI Description	(Y13734) cinnamoyl CoA reductase [Zea mays]

Seq. No.	276588
Contig ID	68458_1.R1011
5'-most EST	uC-zmroteosinte115b12b1
Method	BLASTX
NCBI GI	g100226
BLAST score	454
E value	8.0e-45
Match length	258
% identity	37
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	276589
Contig ID	68467_1.R1011
5'-most EST	LIB3062-019-Q1-K1-G8
Method	BLASTX
NCBI GI	g4325354

BLAST score	339
E value	1.0e-31
Match length	164
% identity	46
NCBI Description	(AF128395) contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]

Seq. No.	276590
Contig ID	68473_1.R1011
5'-most EST	uC-zmroB73014c09b1
Method	BLASTX
NCBI GI	g4567269
BLAST score	757
E value	1.0e-80
Match length	217
% identity	68
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	276591
Contig ID	68481_1.R1011
5'-most EST	uC-zmflb73026d06b1
Method	BLASTX
NCBI GI	g4432814
BLAST score	379
E value	1.0e-35
Match length	312
% identity	30
NCBI Description	(AC006593) unknown protein [Arabidopsis thaliana]

Seq. No.	276592
Contig ID	68481_2.R1011
5'-most EST	uC-zmflb731215d04a1

Seq. No.	276593
Contig ID	68482_1.R1011
5'-most EST	uC-zmroteosinte047h03b1
Method	BLASTX
NCBI GI	g4056483
BLAST score	774
E value	2.0e-82
Match length	252
% identity	64
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276594
Contig ID	68492_1.R1011
5'-most EST	cat700018875.r1
Method	BLASTX
NCBI GI	g2894612
BLAST score	535
E value	2.0e-54
Match length	145
% identity	70
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	276595

Contig ID	68501_1.R1011
5'-most EST	wyr70_0239741.h1
Method	BLASTX
NCBI GI	g3600036
BLAST score	280
E value	4.0e-24
Match length	334
% identity	33
NCBI Description	(AF080119) contains similarity to protein kinase domains (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]

Seq. No.	276596
Contig ID	68501_2.R1011
5'-most EST	LIB3067-053-Q1-K1-F9
Method	BLASTX
NCBI GI	g3600036
BLAST score	204
E value	5.0e-16
Match length	85
% identity	54
NCBI Description	(AF080119) contains similarity to protein kinase domains (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]

Seq. No.	276597
Contig ID	68504_1.R1011
5'-most EST	uC-zmflmo17266e08b1
Method	BLASTX
NCBI GI	g2702277
BLAST score	908
E value	4.0e-98
Match length	291
% identity	63
NCBI Description	(AC003033) putative cyclin g-associated kinase [Arabidopsis thaliana] >gi_2914689 (AC003974) putative cyclin g-associated kinase [Arabidopsis thaliana]

Seq. No.	276598
Contig ID	68507_1.R1011
5'-most EST	LIB3062-031-Q1-K1-B9
Method	BLASTX
NCBI GI	g4539525
BLAST score	665
E value	2.0e-69
Match length	378
% identity	42
NCBI Description	(AJ012370) NAALADase II protein [Homo sapiens]

Seq. No.	276599
Contig ID	68510_1.R1011
5'-most EST	LIB3137-020-Q1-K1-H5
Method	BLASTX
NCBI GI	g3461842
BLAST score	321
E value	2.0e-29
Match length	197
% identity	37
NCBI Description	(AC005315) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No.	276600
Contig ID	68512_1.R1011
5'-most EST	pmx700091681.h1
Method	BLASTX
NCBI GI	g3668077
BLAST score	149
E value	3.0e-09
Match length	81
% identity	44
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276601
Contig ID	68512_2.R1011
5'-most EST	wyr700242546.h1
Method	BLASTX
NCBI GI	g3668077
BLAST score	152
E value	1.0e-09
Match length	86
% identity	42
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276602
Contig ID	68541_1.R1011
5'-most EST	uC-zmflmo17030d07b1

Seq. No.	276603
Contig ID	68544_1.R1011
5'-most EST	gwl700615478.h1
Method	BLASTX
NCBI GI	g1703105
BLAST score	248
E value	9.0e-21
Match length	166
% identity	41
NCBI Description	ACTIN, CYTOPLASMIC (ACTIN, MACRONUCLEAR) >gi_622989 (U18940) actin I [Oxytricha trifallax]

Seq. No.	276604
Contig ID	68552_1.R1011
5'-most EST	uC-zmroteosinte020g10b1
Method	BLASTX
NCBI GI	g3218521
BLAST score	197
E value	4.0e-15
Match length	122
% identity	40
NCBI Description	(AL023874) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=73.05; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P78381; 2-match_description=UDP-GALACTOSE TRANSLOCATOR (UDP-

Seq. No.	276605
Contig ID	68583_1.R1011

5'-most EST	dyk700102746.h1
Seq. No.	276606
Contig ID	68583_2.R1011
5'-most EST	pmx700090020.h1
Seq. No.	276607
Contig ID	68586_1.R1011
5'-most EST	LIB3062-021-Q1-K1-C11
Method	BLASTX
NCBI GI	g1930081
BLAST score	1140
E value	1.0e-125
Match length	337
% identity	65
NCBI Description	(U92878) acyl-ACP thioesterase [Garcinia mangostana]
Seq. No.	276608
Contig ID	68600_1.R1011
5'-most EST	kem700611004.h1
Seq. No.	276609
Contig ID	68600_2.R1011
5'-most EST	LIB3062-021-Q1-K1-D2
Seq. No.	276610
Contig ID	68603_1.R1011
5'-most EST	ymt700224819.h1
Method	BLASTX
NCBI GI	g2635765
BLAST score	156
E value	2.0e-14
Match length	74
% identity	58
NCBI Description	(Z99120) similar to NifS protein homolog [Bacillus subtilis]
Seq. No.	276611
Contig ID	68603_2.R1011
5'-most EST	uC-zmflb73128d04b1
Method	BLASTX
NCBI GI	g1001708
BLAST score	336
E value	2.0e-31
Match length	126
% identity	54
NCBI Description	(D64004) NifS [Synechocystis sp.]
Seq. No.	276612
Contig ID	68606_1.R1011
5'-most EST	LIB3062-021-Q1-K1-E10
Method	BLASTX
NCBI GI	g3337367
BLAST score	186
E value	1.0e-13
Match length	77
% identity	42

NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 276613
Contig ID 68610_1.R1011
5'-most EST uC-zmflmo17223d05a1
Method BLASTX
NCBI GI g1652057
BLAST score 155
E value 4.0e-10
Match length 82
% identity 41
NCBI Description (D90902) hypothetical protein [Synechocystis sp.]

Seq. No. 276614
Contig ID 68617_1.R1011
5'-most EST LIB3062-021-Q1-K1-F1

Seq. No. 276615
Contig ID 68619_1.R1011
5'-most EST uC-zmflb73272h12b1
Method BLASTX
NCBI GI g3367574
BLAST score 427
E value 1.0e-41
Match length 243
% identity 38
NCBI Description (AL031135) hypothetical protein [Arabidopsis thaliana]

Seq. No. 276616
Contig ID 68638_1.R1011
5'-most EST LIB3062-021-Q1-K1-G9

Seq. No. 276617
Contig ID 68645_1.R1011
5'-most EST ntr700074572.h1

Seq. No. 276618
Contig ID 68645_2.R1011
5'-most EST LIB3067-033-Q1-K1-A5
Method BLASTX
NCBI GI g3341694
BLAST score 248
E value 6.0e-21
Match length 100
% identity 47
NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No. 276619
Contig ID 68646_2.R1011
5'-most EST cat700017291.r1

Seq. No. 276620
Contig ID 68650_1.R1011
5'-most EST cyk700049035.f1

Seq. No. 276621
Contig ID 68653_1.R1011

5'-most EST	LIB83-006-Q1-E1-E5
Seq. No.	276622
Contig ID	68667_1.R1011
5'-most EST	cyk700049130.f1
Seq. No.	276623
Contig ID	68668_1.R1011
5'-most EST	LIB3062-022-Q1-K1-B4
Method	BLASTX
NCBI GI	g2463588
BLAST score	160
E value	5.0e-11
Match length	66
% identity	47
NCBI Description	(D38534) FB1035 precursor [Ananas comosus]
Seq. No.	276624
Contig ID	68670_1.R1011
5'-most EST	LIB3062-022-Q1-K1-B6
Method	BLASTX
NCBI GI	g2702280
BLAST score	396
E value	2.0e-38
Match length	97
% identity	77
NCBI Description	(AC003033) photomorphogenesis repressor COP1 [Arabidopsis thaliana]
Seq. No.	276625
Contig ID	68673_1.R1011
5'-most EST	wyr700240561.h1
Method	BLASTX
NCBI GI	g3860333
BLAST score	206
E value	2.0e-16
Match length	59
% identity	61
NCBI Description	(AJ012693) basic blue copper protein [Cicer arietinum]
Seq. No.	276626
Contig ID	68674_1.R1011
5'-most EST	LIB3062-022-Q1-K1-C11
Method	BLASTX
NCBI GI	g4185139
BLAST score	233
E value	3.0e-19
Match length	54
% identity	74
NCBI Description	(AC005724) putative diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.	276627
Contig ID	68682_1.R1011
5'-most EST	LIB3062-022-Q1-K1-D10
Seq. No.	276628

Contig ID	68683_1.R1011
5'-most EST	tzu700202546.h1
Method	BLASTX
NCBI GI	g3820531
BLAST score	779
E value	5.0e-83
Match length	260
% identity	57
NCBI Description	(AF072736) beta-glucosidase [Pinus contorta]

Seq. No.	276629
Contig ID	68688_1.R1011
5'-most EST	wyr700235374.h1
Method	BLASTX
NCBI GI	g2244970
BLAST score	839
E value	4.0e-90
Match length	242
% identity	62
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	276630
Contig ID	68691_1.R1011
5'-most EST	cjh700196477.h1
Method	BLASTX
NCBI GI	g3763933
BLAST score	636
E value	3.0e-66
Match length	174
% identity	76
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	276631
Contig ID	68691_2.R1011
5'-most EST	LIB3062-022-Q1-K1-D8
Method	BLASTX
NCBI GI	g3763933
BLAST score	280
E value	5.0e-27
Match length	95
% identity	71
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	276632
Contig ID	68691_4.R1011
5'-most EST	fdz701163022.h1

Seq. No.	276633
Contig ID	68694_1.R1011
5'-most EST	LIB3062-022-Q1-K1-E10

Seq. No.	276634
Contig ID	68699_1.R1011
5'-most EST	LIB3062-022-Q1-K1-E4
Method	BLASTX

NCBI GI	g3176709
BLAST score	290
E value	9.0e-26
Match length	175
% identity	34
NCBI Description	(AC002392) putative anthranilate N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana]

Seq. No.	276635
Contig ID	68701_1.R1011
5'-most EST	uC-zmflb73066g01b1
Method	BLASTX
NCBI GI	g3184283
BLAST score	1224
E value	1.0e-135
Match length	295
% identity	83
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	276636
Contig ID	68712_1.R1011
5'-most EST	xsy700209608.h1

Seq. No.	276637
Contig ID	68724_1.R1011
5'-most EST	uC-zmflmo17313g06b1

Seq. No.	276638
Contig ID	68725_1.R1011
5'-most EST	uC-zmflb73100h06b1
Method	BLASTX
NCBI GI	g2583120
BLAST score	306
E value	8.0e-28
Match length	142
% identity	45
NCBI Description	(AC002387) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	276639
Contig ID	68728_1.R1011
5'-most EST	LIB3062-022-Q1-K1-H11
Method	BLASTX
NCBI GI	g3641837
BLAST score	942
E value	1.0e-105
Match length	266
% identity	77
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	276640
Contig ID	68733_1.R1011
5'-most EST	LIB3068-003-Q1-K1-E7
Method	BLASTN

NCBI GI	g902200
BLAST score	563
E value	0.0e+00
Match length	631
% identity	98
NCBI Description	Z.mays complete chloroplast genome

Seq. No.	276641
Contig ID	68750_1.R1011
5'-most EST	uC-zmflb73301a04b2
Method	BLASTX
NCBI GI	g2961384
BLAST score	225
E value	2.0e-18
Match length	109
% identity	38
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	276642
Contig ID	68753_1.R1011
5'-most EST	LIB83-013-Q1-E1-H1
Method	BLASTX
NCBI GI	g3660548
BLAST score	265
E value	3.0e-23
Match length	78
% identity	63
NCBI Description	(AB013815) DREB1A [Arabidopsis thaliana]

Seq. No.	276643
Contig ID	68753_2.R1011
5'-most EST	LIB3062-023-Q1-K1-B6

Seq. No.	276644
Contig ID	68762_1.R1011
5'-most EST	wyr700237475.h1
Method	BLASTX
NCBI GI	g2832632
BLAST score	534
E value	3.0e-54
Match length	246
% identity	48
NCBI Description	(AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276645
Contig ID	68769_1.R1011
5'-most EST	uC-zmflmo17051f03b1

Seq. No.	276646
Contig ID	68777_1.R1011
5'-most EST	LIB3137-062-Q1-K1-G9

Seq. No.	276647
Contig ID	68782_1.R1011
5'-most EST	LIB3062-023-Q1-K1-E10

Seq. No.	276648
Contig ID	68791_1.R1011
5'-most EST	LIB3069-050-Q1-K1-G5
Method	BLASTX
NCBI GI	g3738334
BLAST score	231
E value	1.0e-18
Match length	126
% identity	38
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	276649
Contig ID	68800_1.R1011
5'-most EST	tfd700570294.h1
Method	BLASTX
NCBI GI	g2944417
BLAST score	169
E value	1.0e-11
Match length	82
% identity	48
NCBI Description	(AF049881) peroxidase FLXPER4 [Linum usitatissimum]

Seq. No.	276650
Contig ID	68802_1.R1011
5'-most EST	LIB3062-023-Q1-K1-G10

Seq. No.	276651
Contig ID	68802_2.R1011
5'-most EST	rvt700552428.h1

Seq. No.	276652
Contig ID	68818_1.R1011
5'-most EST	xdb700341749.h1
Method	BLASTX
NCBI GI	g3252807
BLAST score	415
E value	3.0e-40
Match length	182
% identity	49
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276653
Contig ID	68837_1.R1011
5'-most EST	xsy700213469.h1
Method	BLASTX
NCBI GI	g4126403
BLAST score	449
E value	2.0e-44
Match length	174
% identity	47
NCBI Description	(AB011796) flavonol synthase [Citrus unshiu]

Seq. No.	276654
Contig ID	68839_1.R1011
5'-most EST	ceu700429803.h1

Seq. No.	276655

Contig ID	68846_1.R1011
5'-most EST	LIB3066-035-Q1-K1-G3
Seq. No.	276656
Contig ID	68846_2.R1011
5'-most EST	uC-zmroteosinte017g08b1
Seq. No.	276657
Contig ID	68855_1.R1011
5'-most EST	LIB3062-024-Q1-K1-E6
Seq. No.	276658
Contig ID	68858_1.R1011
5'-most EST	hbs701184654.h1
Seq. No.	276659
Contig ID	68866_1.R1011
5'-most EST	hbs701183412.h1
Method	BLASTX
NCBI GI	g3184074
BLAST score	246
E value	1.0e-20
Match length	192
% identity	33
NCBI Description	(AL023779) coatomer beta' subunit (beta' coat protein) [Schizosaccharomyces pombe]
Seq. No.	276660
Contig ID	68867_1.R1011
5'-most EST	qmh700027972.f1
Method	BLASTX
NCBI GI	g4567205
BLAST score	359
E value	5.0e-50
Match length	171
% identity	65
NCBI Description	(AC007168) putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana]
Seq. No.	276661
Contig ID	68867_2.R1011
5'-most EST	uC-zmflmo17321e12b1
Method	BLASTX
NCBI GI	g4567205
BLAST score	841
E value	3.0e-90
Match length	227
% identity	71
NCBI Description	(AC007168) putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana]
Seq. No.	276662
Contig ID	68867_3.R1011
5'-most EST	cyk700049832.f1
Method	BLASTX
NCBI GI	g4567205
BLAST score	302

E value	2.0e-40
Match length	170
% identity	56
NCBI Description	(AC007168) putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	276663
Contig ID	68869_1.R1011
5'-most EST	dyk700104493.h1
Method	BLASTX
NCBI GI	g3047104
BLAST score	533
E value	3.0e-54
Match length	168
% identity	65
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	276664
Contig ID	68870_1.R1011
5'-most EST	LIB3136-014-Q1-K2-G6

Seq. No.	276665
Contig ID	68872_1.R1011
5'-most EST	uC-zmflb73239g10b2
Method	BLASTX
NCBI GI	g2739366
BLAST score	370
E value	7.0e-35
Match length	181
% identity	45
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	276666
Contig ID	68887_1.R1011
5'-most EST	bdu700382356.h1
Method	BLASTX
NCBI GI	g1706102
BLAST score	244
E value	2.0e-20
Match length	99
% identity	45
NCBI Description	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CPSF 160 KD SUBUNIT) >gi_1045574 (U37012) cleavage and polyadenylation specificity factor [Homo sapiens]

Seq. No.	276667
Contig ID	68888_1.R1011
5'-most EST	LIB3062-025-Q1-K1-A3
Method	BLASTX
NCBI GI	g4583652
BLAST score	162
E value	8.0e-11
Match length	55
% identity	49
NCBI Description	(AJ010346) RING-H2 [Homo sapiens] >gi_4583654_emb_CAB40414.1_ (AJ010347) RING-H2 [Homo sapiens]

Seq. No.	276668
Contig ID	68891_1.R1011
5'-most EST	LIB3062-025-Q1-K1-A6
Method	BLASTX
NCBI GI	g133314
BLAST score	203
E value	7.0e-16
Match length	114
% identity	46
NCBI Description	DNA-DIRECTED RNA POLYMERASE I LARGEST SUBUNIT >gi_479434_pir__S33884 DNA-directed RNA polymerase (EC 2.7.7.6) I largest chain - Euplotes octocarinatus (SGC9) >gi_2133433_pir__S73102 DNA-directed RNA polymerase (EC 2.7.7.6) I largest chain RPA1 - Euplotes octocarinatus (SGC9) (fragment) >gi_578406_emb_CAA47066_ (X66450) DNA-directed RNA polymerase I largest subunit [Euplotes octocarinatus]

Seq. No.	276669
Contig ID	68894_1.R1011
5'-most EST	LIB3062-025-Q1-K1-A9

Seq. No.	276670
Contig ID	68904_1.R1011
5'-most EST	LIB3062-025-Q1-K1-C1

Seq. No.	276671
Contig ID	68918_1.R1011
5'-most EST	cyk700051819.f1
Method	BLASTX
NCBI GI	g3068705
BLAST score	200
E value	2.0e-15
Match length	102
% identity	48
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	276672
Contig ID	68923_1.R1011
5'-most EST	dyk700102896.h1

Seq. No.	276673
Contig ID	68930_1.R1011
5'-most EST	LIB3137-027-Q1-K1-C1

Seq. No.	276674
Contig ID	68936_1.R1011
5'-most EST	LIB3062-025-Q1-K1-F1

Seq. No.	276675
Contig ID	68944_1.R1011
5'-most EST	uwc700152587.h1
Method	BLASTX
NCBI GI	g4006829
BLAST score	985
E value	1.0e-107

Match length	268
% identity	72
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	276676
Contig ID	68944_2.R1011
5'-most EST	uC-zmflmo170113g06b1

Seq. No.	276677
Contig ID	68955_1.R1011
5'-most EST	LIB3062-025-Q1-K1-G7

Seq. No.	276678
Contig ID	68963_1.R1011
5'-most EST	uC-zmflmo17118b06b1
Method	BLASTX
NCBI GI	g1800223
BLAST score	221
E value	9.0e-18
Match length	133
% identity	39
NCBI Description	(U65018) mannosyltransferase [Dictyostelium discoideum]

Seq. No.	276679
Contig ID	68968_1.R1011
5'-most EST	LIB3062-026-Q1-K1-A1
Method	BLASTX
NCBI GI	g2827555
BLAST score	265
E value	3.0e-23
Match length	92
% identity	58
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	276680
Contig ID	68977_1.R1011
5'-most EST	ntr700074812.h1
Method	BLASTX
NCBI GI	g4539305
BLAST score	661
E value	6.0e-96
Match length	257
% identity	62
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	276681
Contig ID	68978_1.R1011
5'-most EST	LIB3062-026-Q1-K1-B1
Method	BLASTX
NCBI GI	g3874271
BLAST score	292
E value	8.0e-26
Match length	74
% identity	70
NCBI Description	(Z81467) predicted using Genefinder; Similarity to Drosophila UDP-glucose:glycoprotein glucosyltransferase

(TR:Q09332); cDNA EST yk250b10.3 comes from this gene; cDNA EST yk250b10.5 comes from this gene [Caenorhabditis elegans] >gi_3876437_emb_CAB04207_ (Z81516) predicted using Genefinder; Similarity to Drosophila UDP-glucose:glycoprotein glucosyltransferase (TR:Q09332); cDNA EST yk250b10.3 comes from this gene; cDNA EST yk250b10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	276682
Contig ID	68978_2.R1011
5'-most EST	pwr700453268.h1

Seq. No.	276683
Contig ID	68998_1.R1011
5'-most EST	hbs701183211.h1
Method	BLASTX
NCBI GI	g4539314
BLAST score	483
E value	3.0e-48
Match length	212
% identity	47
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	276684
Contig ID	69004_1.R1011
5'-most EST	uC-zmflb73140d07b1
Method	BLASTX
NCBI GI	g122771
BLAST score	598
E value	7.0e-67
Match length	262
% identity	55
NCBI Description	TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR HBP1) >gi_100808_pir__S15346 transcription factor HBP-1a - wheat >gi_100838_pir__A41349 histone-specific transcription factor HBP1 - wheat >gi_21633_emb_CAA40101_ (X56781) HBP-1a [Triticum aestivum] >gi_170749 (M28704) DNA-binding protein [Triticum aestivum] >gi_1199790_dbj_BAA07289_ (D38111) transcription factor HBP-1a(17) [Triticum aestivum]

Seq. No.	276685
Contig ID	69008_1.R1011
5'-most EST	uC-zmroteosinte080h11b1

Seq. No.	276686
Contig ID	69012_1.R1011
5'-most EST	hbs701185619.h1

Seq. No.	276687
Contig ID	69019_1.R1011
5'-most EST	uC-zmflb73073d04b3
Method	BLASTX
NCBI GI	g2429288
BLAST score	314
E value	5.0e-29
Match length	82

% identity	71
NCBI Description	(AF014468) peroxidase [Oryza sativa]

Seq. No.	276688
Contig ID	69023_1.R1011
5'-most EST	LIB3062-026-Q1-K1-F6
Method	BLASTX
NCBI GI	g3702340
BLAST score	461
E value	6.0e-46
Match length	179
% identity	49
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276689
Contig ID	69029_1.R1011
5'-most EST	xmt700268040.h1

Seq. No.	276690
Contig ID	69039_1.R1011
5'-most EST	uC-zmflb73301d11b2
Method	BLASTX
NCBI GI	g4539305
BLAST score	1130
E value	1.0e-124
Match length	358
% identity	57
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	276691
Contig ID	69039_2.R1011
5'-most EST	LIB3062-026-Q1-K1-H3
Method	BLASTX
NCBI GI	g4539305
BLAST score	649
E value	7.0e-68
Match length	178
% identity	64
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	276692
Contig ID	69039_3.R1011
5'-most EST	afb700381978.h1
Method	BLASTX
NCBI GI	g4539305
BLAST score	149
E value	6.0e-16
Match length	64
% identity	59
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	276693
Contig ID	69041_1.R1011
5'-most EST	pmx700086081.h1
Method	BLASTX
NCBI GI	g3913811
BLAST score	1049

E value	1.0e-114
Match length	231
% identity	90
NCBI Description	GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR) >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA reductase [Oryza sativa]

Seq. No.	276694
Contig ID	69046_1.R1011
5'-most EST	LIB3062-027-Q1-K1-A5

Seq. No.	276695
Contig ID	69050_1.R1011
5'-most EST	xsy700214753.h1
Method	BLASTX
NCBI GI	g1360090
BLAST score	616
E value	4.0e-64
Match length	179
% identity	63
NCBI Description	(X95576) C1C-Nt1 [Nicotiana tabacum]

Seq. No.	276696
Contig ID	69055_1.R1011
5'-most EST	uC-zmflb73064a07b1

Seq. No.	276697
Contig ID	69089_1.R1011
5'-most EST	LIB84-010-Q1-E1-E9

Seq. No.	276698
Contig ID	69098_1.R1011
5'-most EST	pwr700449511.h1

Seq. No.	276699
Contig ID	69107_1.R1011
5'-most EST	pmx700091734.h1
Method	BLASTX
NCBI GI	g4539459
BLAST score	256
E value	4.0e-22
Match length	77
% identity	62
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	276700
Contig ID	69138_1.R1011
5'-most EST	qmh700029175.f1
Method	BLASTX
NCBI GI	g3668092
BLAST score	1309
E value	1.0e-150
Match length	532
% identity	52
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	276701

Contig ID	69139_1.R1011
5'-most EST	nbm700473240.h1

Seq. No.	276702
Contig ID	69142_1.R1011
5'-most EST	LIB3062-028-Q1-K1-A8
Method	BLASTX
NCBI GI	g1001379
BLAST score	219
E value	2.0e-17
Match length	79
% identity	54
NCBI Description	(D64006) aspartate beta-semialdehyde dehydrogenese [Synechocystis sp.]

Seq. No.	276703
Contig ID	69157_1.R1011
5'-most EST	LIB3062-028-Q1-K1-C7

Seq. No.	276704
Contig ID	69159_1.R1011
5'-most EST	LIB3062-028-Q1-K1-D1

Seq. No.	276705
Contig ID	69165_1.R1011
5'-most EST	uC-zmflmo17109g06a1
Method	BLASTX
NCBI GI	g4586062
BLAST score	392
E value	1.0e-37
Match length	223
% identity	40
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	276706
Contig ID	69193_1.R1011
5'-most EST	uC-zmflb73196f05b1
Method	BLASTX
NCBI GI	g349379
BLAST score	365
E value	1.0e-34
Match length	127
% identity	65
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]

Seq. No.	276707
Contig ID	69193_2.R1011
5'-most EST	wyr700239649.h1
Method	BLASTX
NCBI GI	g349379
BLAST score	232
E value	3.0e-19
Match length	98
% identity	55
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]

Seq. No.	276708

Contig ID	69204_1.R1011
5'-most EST	LIB3062-028-Q1-K1-H3

Seq. No.	276709
Contig ID	69205_1.R1011
5'-most EST	ntr700076352.h1
Method	BLASTN
NCBI GI	g3510347
BLAST score	34
E value	3.0e-09
Match length	102
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	276710
Contig ID	69206_1.R1011
5'-most EST	wty700164462.h1
Method	BLASTX
NCBI GI	g2708532
BLAST score	731
E value	3.0e-77
Match length	241
% identity	57
NCBI Description	(AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No.	276711
Contig ID	69213_1.R1011
5'-most EST	uC-zmroteosinte115f01b1

Seq. No.	276712
Contig ID	69217_1.R1011
5'-most EST	LIB3062-029-Q1-K1-A6
Method	BLASTX
NCBI GI	g279567
BLAST score	231
E value	1.0e-18
Match length	141
% identity	33
NCBI Description	insulinase (EC 3.4.99.45) - human

Seq. No.	276713
Contig ID	69226_1.R1011
5'-most EST	pmx700084447.h1

Seq. No.	276714
Contig ID	69239_1.R1011
5'-most EST	LIB3062-029-Q1-K1-C6
Method	BLASTX
NCBI GI	g2880047
BLAST score	385
E value	3.0e-37
Match length	129
% identity	60
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 276715

Contig ID	69242_1.R1011
5'-most EST	uC-zmflmo17248e10b1
Method	BLASTN
NCBI GI	g3851527
BLAST score	97
E value	1.0e-46
Match length	557
% identity	84
NCBI Description	Hordeum vulgare cultivar Bomi starch branching enzyme IIb (sbeIIb) gene, nuclear gene encoding plastid protein, partial cds

Seq. No.	276716
Contig ID	69243_1.R1011
5'-most EST	cjh700193458.h1
Method	BLASTX
NCBI GI	g4204281
BLAST score	177
E value	2.0e-12
Match length	111
% identity	38
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	276717
Contig ID	69267_1.R1011
5'-most EST	LIB84-001-Q1-E1-E1

Seq. No.	276718
Contig ID	69280_1.R1011
5'-most EST	LIB3062-029-Q1-K1-G6
Method	BLASTX
NCBI GI	g2191135
BLAST score	363
E value	2.0e-34
Match length	146
% identity	47
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	276719
Contig ID	69283_1.R1011
5'-most EST	LIB3062-029-Q1-K1-H2

Seq. No.	276720
Contig ID	69311_1.R1011
5'-most EST	xjt700094762.h1
Method	BLASTX
NCBI GI	g2243118
BLAST score	1487
E value	1.0e-166
Match length	406
% identity	69
NCBI Description	(Y10984) glutathione synthetase [Brassica juncea]

Seq. No.	276721
Contig ID	69367_1.R1011
5'-most EST	LIB3062-030-Q1-K1-H8

Seq. No.	276722
Contig ID	69368_1.R1011
5'-most EST	qmh700027873.f1

Seq. No.	276723
Contig ID	69369_1.R1011
5'-most EST	uC-zmflb73325f05a1
Method	BLASTN
NCBI GI	g793901
BLAST score	88
E value	9.0e-42
Match length	120
% identity	93
NCBI Description	Z.mays mRNA for ZEMa protein (ZEM1 gene)

Seq. No.	276724
Contig ID	69369_2.R1011
5'-most EST	LIB3062-031-Q1-K1-A1

Seq. No.	276725
Contig ID	69376_1.R1011
5'-most EST	ceu700432478.h1
Method	BLASTX
NCBI GI	g3449041
BLAST score	221
E value	6.0e-18
Match length	101
% identity	47
NCBI Description	(U73462) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	276726
Contig ID	69391_1.R1011
5'-most EST	ymt700223761.h1

Seq. No.	276727
Contig ID	69391_2.R1011
5'-most EST	uC-zmflb73080b08a1

Seq. No.	276728
Contig ID	69404_1.R1011
5'-most EST	uC-zmflmo17021b08b1
Method	BLASTX
NCBI GI	g3096947
BLAST score	438
E value	5.0e-43
Match length	270
% identity	38
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	276729
Contig ID	69412_1.R1011
5'-most EST	uC-zmrob73004c02b1
Method	BLASTX
NCBI GI	g3928088
BLAST score	224

E value	3.0e-18
Match length	82
% identity	51
NCBI Description	(AC005770) putative peroxidase [Arabidopsis thaliana]

Seq. No.	276730
Contig ID	69412_2.R1011
5'-most EST	xsy700213114.h1
Method	BLASTX
NCBI GI	g3928088
BLAST score	210
E value	2.0e-16
Match length	80
% identity	50
NCBI Description	(AC005770) putative peroxidase [Arabidopsis thaliana]

Seq. No.	276731
Contig ID	69413_1.R1011
5'-most EST	uC-zmflb73038f11b1
Method	BLASTX
NCBI GI	g2760839
BLAST score	293
E value	3.0e-31
Match length	351
% identity	34
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	276732
Contig ID	69423_1.R1011
5'-most EST	LIB83-001-Q1-E1-F8
Method	BLASTN
NCBI GI	g517257
BLAST score	346
E value	0.0e+00
Match length	636
% identity	99
NCBI Description	Z.mays MNB1a mRNA for DNA-binding protein

Seq. No.	276733
Contig ID	69429_1.R1011
5'-most EST	LIB3062-031-Q1-K1-F6

Seq. No.	276734
Contig ID	69430_1.R1011
5'-most EST	uC-zmflb73116e10a1

Seq. No.	276735
Contig ID	69437_1.R1011
5'-most EST	gwl700613877.h1
Method	BLASTX
NCBI GI	g4538987
BLAST score	554
E value	9.0e-86
Match length	249
% identity	67
NCBI Description	(AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]

Seq. No.	276736
Contig ID	69449_1.R1011
5'-most EST	uC-zmflm017205a07b1

Seq. No.	276737
Contig ID	69469_1.R1011
5'-most EST	LIB3068-032-Q1-K1-D2
Method	BLASTX
NCBI GI	g4220532
BLAST score	557
E value	4.0e-57
Match length	200
% identity	57
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	276738
Contig ID	69471_1.R1011
5'-most EST	ntr700076560.h1
Method	BLASTX
NCBI GI	g4539295
BLAST score	206
E value	1.0e-19
Match length	114
% identity	54
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	276739
Contig ID	69481_1.R1011
5'-most EST	LIB3062-032-Q1-K1-C8
Method	BLASTX
NCBI GI	g3426039
BLAST score	158
E value	1.0e-10
Match length	47
% identity	57
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	276740
Contig ID	69485_1.R1011
5'-most EST	LIB3066-033-Q1-K1-H3
Method	BLASTX
NCBI GI	g3935175
BLAST score	473
E value	3.0e-47
Match length	126
% identity	72
NCBI Description	(AC004557) F17L21.18 [Arabidopsis thaliana]

Seq. No.	276741
Contig ID	69486_1.R1011
5'-most EST	uC-zmflb73256c04b1

Seq. No.	276742
Contig ID	69487_1.R1011
5'-most EST	rvt700553103.h1
Method	BLASTX
NCBI GI	g112785

BLAST score	297
E value	8.0e-27
Match length	158
% identity	37
NCBI Description	DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1 3-methyladenine DNA glycosylase (EC 3.2.2.-) I - Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa 1-187) [Escherichia coli] >gi_147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432) 3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

Seq. No.	276743
Contig ID	69513_1.R1011
5'-most EST	LIB3062-032-Q1-K1-G12
Method	BLASTX
NCBI GI	g4126473
BLAST score	644
E value	2.0e-67
Match length	151
% identity	77
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	276744
Contig ID	69527_1.R1011
5'-most EST	ymt700221789.h1
Method	BLASTX
NCBI GI	g3157933
BLAST score	289
E value	2.0e-25
Match length	181
% identity	36
NCBI Description	(AC002131) Contains similarity to box helicases gb_U29097 from C. elegans and to the ENBP1 gene product gb_X95995 from Vicia sativa. [Arabidopsis thaliana]

Seq. No.	276745
Contig ID	69527_2.R1011
5'-most EST	uC-zmflb73238h11a1

Seq. No.	276746
Contig ID	69551_2.R1011
5'-most EST	nbm700477476.h1
Method	BLASTX
NCBI GI	g2739044
BLAST score	782
E value	1.0e-83
Match length	179
% identity	80
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No. 276747

Contig ID	69563_1.R1011
5'-most EST	uC-zmrob73005a04b1
Method	BLASTX
NCBI GI	g4206789
BLAST score	243
E value	2.0e-20
Match length	117
% identity	45
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	276748
Contig ID	69585_1.R1011
5'-most EST	LIB3136-037-P1-K1-B5
Method	BLASTX
NCBI GI	g3287693
BLAST score	315
E value	1.0e-28
Match length	87
% identity	72
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	276749
Contig ID	69602_1.R1011
5'-most EST	LIB3137-033-Q1-K1-D9
Method	BLASTX
NCBI GI	g1632822
BLAST score	511
E value	5.0e-52
Match length	105
% identity	91
NCBI Description	(Y08962) transmembrane protein [Oryza sativa] >gi_1667594 (U77297) transmembrane protein [Oryza sativa]

Seq. No.	276750
Contig ID	69611_1.R1011
5'-most EST	ymt700220593.h1
Method	BLASTX
NCBI GI	g230348
BLAST score	305
E value	2.0e-27
Match length	211
% identity	39
NCBI Description	Triacylglycerol Acylhydrolase (E.C.3.1.1.3)

Seq. No.	276751
Contig ID	69616_1.R1011
5'-most EST	LIB3062-034-Q1-K1-B1
Method	BLASTX
NCBI GI	g3080385
BLAST score	243
E value	2.0e-20
Match length	116
% identity	42
NCBI Description	(AL022603) serine/threonine protein kinase [Arabidopsis

thaliana] >gi_3402760_emb_CAA20206.1_ (AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	276752
Contig ID	69618_1.R1011
5'-most EST	uC-zmflb73261h04b3

Seq. No.	276753
Contig ID	69620_1.R1011
5'-most EST	gct701180596.h1

Seq. No.	276754
Contig ID	69639_1.R1011
5'-most EST	LIB3062-034-Q1-K1-D4

Seq. No.	276755
Contig ID	69640_1.R1011
5'-most EST	fdz701158328.h1
Method	BLASTX
NCBI GI	g2315981
BLAST score	276
E value	3.0e-24
Match length	93
% identity	56
NCBI Description	(U77911) 17-beta-hydroxysteroid dehydrogenase type IV [Gallus gallus]

Seq. No.	276756
Contig ID	69648_1.R1011
5'-most EST	uC-zmflmo17041f07b1
Method	BLASTX
NCBI GI	g3881448
BLAST score	153
E value	6.0e-12
Match length	88
% identity	50
NCBI Description	(Z47073) similar to man(9)-alpha-mannosidase; cDNA EST EMBL:D35441 comes from this gene; cDNA EST EMBL:D37263 comes from this gene; cDNA EST EMBL:C12591 comes from this gene; cDNA EST yk219b5.5 comes from this gene; cDNA EST yk

Seq. No.	276757
Contig ID	69659_1.R1011
5'-most EST	vux700156541.h1
Method	BLASTX
NCBI GI	g4160532
BLAST score	594
E value	2.0e-61
Match length	208
% identity	53
NCBI Description	(AJ011304) sphingosine-1-phosphate lyase [Homo sapiens]

Seq. No.	276758
Contig ID	69668_1.R1011
5'-most EST	jfc700968687.h1

Seq. No.	276759
Contig ID	69681_1.R1011
5'-most EST	tzu700202976.h1
Method	BLASTX
NCBI GI	g3355477
BLAST score	726
E value	8.0e-77
Match length	172
% identity	42
NCBI Description	(AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No.	276760
Contig ID	69681_2.R1011
5'-most EST	uC-zmromo17091f04a1

Seq. No.	276761
Contig ID	69687_1.R1011
5'-most EST	LIB3062-035-Q1-K1-A4
Method	BLASTX
NCBI GI	g2335096
BLAST score	243
E value	1.0e-20
Match length	81
% identity	67
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276762
Contig ID	69695_1.R1011
5'-most EST	LIB3062-035-Q1-K1-B2
Method	BLASTX
NCBI GI	g4469026
BLAST score	228
E value	1.0e-18
Match length	137
% identity	37
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276763
Contig ID	69698_1.R1011
5'-most EST	LIB3062-035-Q1-K1-B5

Seq. No.	276764
Contig ID	69701_1.R1011
5'-most EST	fC-zmst700336294a1
Method	BLASTX
NCBI GI	g2961358
BLAST score	979
E value	1.0e-106
Match length	318
% identity	63
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]

Seq. No.	276765
Contig ID	69701_2.R1011
5'-most EST	fC-zmst1700336294f1

Method	BLASTX
NCBI GI	g2961358
BLAST score	1047
E value	1.0e-115
Match length	282
% identity	75
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]

Seq. No.	276766
Contig ID	69701_3.R1011
5'-most EST	uC-zmrob73079d01b1
Method	BLASTX
NCBI GI	g2961358
BLAST score	410
E value	1.0e-84
Match length	272
% identity	66
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]

Seq. No.	276767
Contig ID	69713_1.R1011
5'-most EST	xjt700095878.h1

Seq. No.	276768
Contig ID	69713_2.R1011
5'-most EST	LIB84-030-Q1-E1-D1
Method	BLASTX
NCBI GI	g2435517
BLAST score	428
E value	6.0e-42
Match length	227
% identity	44
NCBI Description	(AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

Seq. No.	276769
Contig ID	69737_1.R1011
5'-most EST	rvt700553162.h1
Method	BLASTX
NCBI GI	g3746062
BLAST score	508
E value	4.0e-51
Match length	183
% identity	55
NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276770
Contig ID	69737_2.R1011
5'-most EST	ymt700223348.h1
Method	BLASTX
NCBI GI	g3746062
BLAST score	184
E value	2.0e-13
Match length	77
% identity	44

NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276771
Contig ID	69745_1.R1011
5'-most EST	uC-zmflmo17238a11b1

Seq. No.	276772
Contig ID	69782_1.R1011
5'-most EST	LIB3067-027-Q1-K1-G6

Seq. No.	276773
Contig ID	69785_1.R1011
5'-most EST	LIB3062-036-Q1-K1-B7

Seq. No.	276774
Contig ID	69786_1.R1011
5'-most EST	LIB3062-036-Q1-K1-B8

Seq. No.	276775
Contig ID	69788_1.R1011
5'-most EST	uC-zmflb73026e01b1
Method	BLASTX
NCBI GI	g678547
BLAST score	842
E value	3.0e-90
Match length	258
% identity	67
NCBI Description	(L13654) peroxidase [Lycopersicon esculentum]

Seq. No.	276776
Contig ID	69788_2.R1011
5'-most EST	ntr700074963.h1
Method	BLASTX
NCBI GI	g2956711
BLAST score	485
E value	8.0e-51
Match length	154
% identity	68
NCBI Description	(Y16776) peroxidase [Spinacia oleracea]

Seq. No.	276777
Contig ID	69788_3.R1011
5'-most EST	cyk700051487.f1

Seq. No.	276778
Contig ID	69808_1.R1011
5'-most EST	LIB3062-036-Q1-K1-E3
Method	BLASTX
NCBI GI	g3236254
BLAST score	334
E value	3.0e-31
Match length	151
% identity	47
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	276779
Contig ID	69810_1.R1011

5'-most EST	LIB3062-036-Q1-K1-E5
Method	BLASTX
NCBI GI	g3779218
BLAST score	792
E value	1.0e-84
Match length	196
% identity	77
NCBI Description	(AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No.	276780
Contig ID	69810_2.R1011
5'-most EST	gct701167631.h1
Method	BLASTX
NCBI GI	g3779218
BLAST score	457
E value	1.0e-45
Match length	125
% identity	73
NCBI Description	(AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No.	276781
Contig ID	69815_1.R1011
5'-most EST	wen700332530.h1
Method	BLASTX
NCBI GI	g117291
BLAST score	844
E value	1.0e-90
Match length	204
% identity	76
NCBI Description	CHLOROPLAST PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) (P36) (E29) >gi_81464_pir__S03638 triose phosphate/3-phosphoglycerate/phosphate translocator precursor - spinach >gi_21274_emb_CAA32016_ (X13754) phosphate translocator protein (AA 1 - 404) [Spinacia oleracea]

Seq. No.	276782
Contig ID	69830_1.R1011
5'-most EST	uC-zmf1b73040h11b1

Seq. No.	276783
Contig ID	69833_1.R1011
5'-most EST	LIB3062-036-Q1-K1-G8
Method	BLASTX
NCBI GI	g4567227
BLAST score	502
E value	6.0e-51
Match length	143
% identity	64
NCBI Description	(AC007119) putative transport protein [Arabidopsis thaliana]

Seq. No.	276784
Contig ID	69849_1.R1011
5'-most EST	uC-zmf1mo17282g11b1
Method	BLASTX
NCBI GI	g2182267

BLAST score	646
E value	2.0e-67
Match length	184
% identity	67
NCBI Description	(L37359) lipoxygenase [Hordeum vulgare]

Seq. No.	276785
Contig ID	69849_3.R1011
5'-most EST	wty700172106.h1
Method	BLASTN
NCBI GI	g2182266
BLAST score	82
E value	3.0e-38
Match length	150
% identity	89
NCBI Description	Hordeum vulgare lipoxygenase (LoxB) mRNA, complete cds

Seq. No.	276786
Contig ID	69855_1.R1011
5'-most EST	LIB3062-037-Q1-K1-A8
Method	BLASTX
NCBI GI	g1345132
BLAST score	345
E value	1.0e-32
Match length	115
% identity	23
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	276787
Contig ID	69874_1.R1011
5'-most EST	LIB3062-038-Q1-K1-C6
Method	BLASTX
NCBI GI	g3335060
BLAST score	981
E value	1.0e-106
Match length	268
% identity	73
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	276788
Contig ID	69876_1.R1011
5'-most EST	uC-zmflmo17011g05b1

Seq. No.	276789
Contig ID	69882_1.R1011
5'-most EST	rvt700549989.h1

Seq. No.	276790
Contig ID	69884_1.R1011
5'-most EST	LIB3136-047-Q1-K1-H2

Seq. No. 276791

Contig ID	69890_1.R1011
5'-most EST	uC-zmroteosinte046h09b1
Seq. No.	276792
Contig ID	69890_2.R1011
5'-most EST	ntr700075617.h1
Seq. No.	276793
Contig ID	69893_1.R1011
5'-most EST	wyr700238292.h1
Method	BLASTX
NCBI GI	g2253583
BLAST score	149
E value	1.0e-09
Match length	50
% identity	60
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276794
Contig ID	69902_1.R1011
5'-most EST	uC-zmroB73015d06b1
Seq. No.	276795
Contig ID	69909_1.R1011
5'-most EST	ntr700076025.h1
Method	BLASTX
NCBI GI	g2804278
BLAST score	819
E value	1.0e-87
Match length	197
% identity	79
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]
Seq. No.	276796
Contig ID	69916_1.R1011
5'-most EST	LIB3062-037-Q1-K1-G12
Seq. No.	276797
Contig ID	69922_1.R1011
5'-most EST	LIB3136-017-Q1-K1-E3
Method	BLASTX
NCBI GI	g3063459
BLAST score	182
E value	4.0e-13
Match length	223
% identity	30
NCBI Description	(AC003981) F22O13.21 [Arabidopsis thaliana]
Seq. No.	276798
Contig ID	69945_1.R1011
5'-most EST	LIB3062-038-Q1-K1-B12
Method	BLASTX
NCBI GI	g1703143
BLAST score	382
E value	7.0e-37
Match length	111
% identity	63

NCBI Description	ACTIN-LIKE PROTEIN 3 >gi_881635 (U29610) Arp3 [Acanthamoeba castellanii]
Seq. No.	276799
Contig ID	69947_1.R1011
5'-most EST	LIB3136-005-Q1-K1-H9
Seq. No.	276800
Contig ID	69975_1.R1011
5'-most EST	LIB3062-038-Q1-K1-E11
Seq. No.	276801
Contig ID	69979_1.R1011
5'-most EST	pmx700084382.h1
Method	BLASTX
NCBI GI	g3582333
BLAST score	329
E value	2.0e-30
Match length	183
% identity	40
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276802
Contig ID	69980_1.R1011
5'-most EST	uC-zmflmo17245a06b1
Seq. No.	276803
Contig ID	69985_1.R1011
5'-most EST	LIB3062-038-Q1-K1-F11
Seq. No.	276804
Contig ID	69989_1.R1011
5'-most EST	LIB3062-038-Q1-K1-F4
Method	BLASTX
NCBI GI	g2062405
BLAST score	300
E value	6.0e-27
Match length	106
% identity	49
NCBI Description	(U79011) cytochrome b5 [Borago officinalis]
Seq. No.	276805
Contig ID	69999_1.R1011
5'-most EST	LIB3062-038-Q1-K1-G3
Method	BLASTX
NCBI GI	g2341045
BLAST score	151
E value	6.0e-10
Match length	77
% identity	47
NCBI Description	(AC000104) F19P19.16 [Arabidopsis thaliana]
Seq. No.	276806
Contig ID	70033_1.R1011
5'-most EST	LIB3062-039-Q1-K1-C1
Seq. No.	276807

Contig ID	70037_1.R1011
5'-most EST	uC-zmflmo17317a05a1
Method	BLASTX
NCBI GI	g4204284
BLAST score	173
E value	2.0e-12
Match length	47
% identity	62
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	276808
Contig ID	70045_1.R1011
5'-most EST	LIB3062-039-Q1-K1-D12

Seq. No.	276809
Contig ID	70050_1.R1011
5'-most EST	LIB3062-052-Q1-K1-G12

Seq. No.	276810
Contig ID	70054_1.R1011
5'-most EST	xsy700217192.h1
Method	BLASTX
NCBI GI	g3924594
BLAST score	419
E value	4.0e-41
Match length	156
% identity	54
NCBI Description	(AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi_4262139_gb_AAD14439_ (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	276811
Contig ID	70059_1.R1011
5'-most EST	LIB3062-039-Q1-K1-E9
Method	BLASTX
NCBI GI	g3582336
BLAST score	146
E value	3.0e-09
Match length	97
% identity	40
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276812
Contig ID	70086_1.R1011
5'-most EST	fwa700100030.h1

Seq. No.	276813
Contig ID	70088_1.R1011
5'-most EST	wyr700239287.h1

Seq. No.	276814
Contig ID	70099_1.R1011
5'-most EST	LIB3069-024-Q1-K1-B6
Method	BLASTX
NCBI GI	g1209703
BLAST score	158

E value	3.0e-10
Match length	48
% identity	56
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	276815
Contig ID	70099_2.R1011
5'-most EST	uC-zmf1b73176b06b2
Method	BLASTX
NCBI GI	g1209703
BLAST score	1086
E value	1.0e-119
Match length	362
% identity	55
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	276816
Contig ID	70113_1.R1011
5'-most EST	LIB3062-040-Q1-K1-C4

Seq. No.	276817
Contig ID	70124_1.R1011
5'-most EST	LIB3069-036-Q1-K1-E2

Seq. No.	276818
Contig ID	70124_2.R1011
5'-most EST	pmx700088332.h1

Seq. No.	276819
Contig ID	70135_1.R1011
5'-most EST	LIB3062-040-Q1-K1-F6
Method	BLASTX
NCBI GI	g1654140
BLAST score	315
E value	7.0e-29
Match length	178
% identity	38
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	276820
Contig ID	70147_1.R1011
5'-most EST	LIB3062-040-Q1-K1-H4

Seq. No.	276821
Contig ID	70151_1.R1011
5'-most EST	LIB3069-044-Q1-K1-A1

Seq. No.	276822
Contig ID	70152_1.R1011
5'-most EST	uC-zmroteosinte072e02b2
Method	BLASTX
NCBI GI	g2213624
BLAST score	269
E value	1.0e-23
Match length	216
% identity	40
NCBI Description	(AC000103) F21J9.16 [Arabidopsis thaliana]

Seq. No.	276823
Contig ID	70152_2.R1011
5'-most EST	tfd700570072.h1

Seq. No.	276824
Contig ID	70156_1.R1011
5'-most EST	LIB3062-041-Q1-K1-A2
Method	BLASTX
NCBI GI	g457691
BLAST score	487
E value	4.0e-49
Match length	144
% identity	65
NCBI Description	(Z30331) Protein Kinase [Mesembryanthemum crystallinum]

Seq. No.	276825
Contig ID	70163_1.R1011
5'-most EST	pmx700088807.h1
Method	BLASTX
NCBI GI	g1143864
BLAST score	1112
E value	1.0e-122
Match length	274
% identity	73
NCBI Description	(U28047) beta glucosidase [Oryza sativa]

Seq. No.	276826
Contig ID	70173_1.R1011
5'-most EST	LIB3137-040-Q1-K1-A7

Seq. No.	276827
Contig ID	70173_2.R1011
5'-most EST	hbs701184293.h1

Seq. No.	276828
Contig ID	70184_1.R1011
5'-most EST	uC-zmflm017025a09b1
Method	BLASTX
NCBI GI	g1176658
BLAST score	584
E value	8.0e-60
Match length	256
% identity	50
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	276829
Contig ID	70199_1.R1011
5'-most EST	uC-zmflmo17073a06b1
Method	BLASTX
NCBI GI	g4490309
BLAST score	333
E value	6.0e-31
Match length	104
% identity	61

NCBI Description	(AL035678) peroxidase ATP17a-like protein [Arabidopsis thaliana]

Seq. No.	276830
Contig ID	70202_1.R1011
5'-most EST	LIB3062-041-Q1-K1-E7
Method	BLASTX
NCBI GI	g2655098
BLAST score	253
E value	2.0e-21
Match length	102
% identity	47
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	276831
Contig ID	70204_1.R1011
5'-most EST	uC-zmf1B73002f07b1
Method	BLASTX
NCBI GI	g544134
BLAST score	276
E value	2.0e-24
Match length	110
% identity	57
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	276832
Contig ID	70205_1.R1011
5'-most EST	dyk700102039.h1
Method	BLASTX
NCBI GI	g3341697
BLAST score	286
E value	2.0e-25
Match length	81
% identity	69
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276833
Contig ID	70214_1.R1011
5'-most EST	LIB3062-052-Q1-K1-E4
Method	BLASTX
NCBI GI	g4218120
BLAST score	275
E value	3.0e-35
Match length	126
% identity	59
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	276834
Contig ID	70215_1.R1011
5'-most EST	LIB3062-041-Q1-K1-F8

Seq. No.	276835
Contig ID	70217_1.R1011

5'-most EST	LIB3068-049-Q1-K1-H4
Method	BLASTX
NCBI GI	g131329
BLAST score	369
E value	5.0e-35
Match length	73
% identity	100
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72717_pir__F2ZMBH photosystem II phosphoprotein psbH - maize chloroplast >gi_12436_emb_CAA28998_ (X05422) psbF [Zea mays] >gi_902250_emb_CAA60314_ (X86563) PSII 10KDa phosphoprotein [Zea mays]

Seq. No.	276836
Contig ID	70227_1.R1011
5'-most EST	uC-zmflmo17362e05a1
Method	BLASTN
NCBI GI	g3289001
BLAST score	479
E value	0.0e+00
Match length	495
% identity	99
NCBI Description	Zea mays CRP1 (crp1) mRNA, nuclear gene encoding chloroplast protein, crp1-hcf111 allele, complete cds

Seq. No.	276837
Contig ID	70229_1.R1011
5'-most EST	uC-zmflb73173d03b1
Method	BLASTX
NCBI GI	g3036796
BLAST score	511
E value	1.0e-51
Match length	251
% identity	45
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805858_emb_CAA21478_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	276838
Contig ID	70229_2.R1011
5'-most EST	pmx700090772.h1

Seq. No.	276839
Contig ID	70230_1.R1011
5'-most EST	LIB3062-041-Q1-K1-H4

Seq. No.	276840
Contig ID	70237_1.R1011
5'-most EST	LIB3062-042-Q1-K1-A2
Method	BLASTX
NCBI GI	g2464914
BLAST score	258
E value	4.0e-22
Match length	120
% identity	47
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276841
Contig ID	70239_1.R1011
5'-most EST	wyr700239316.h1
Method	BLASTX
NCBI GI	g3738224
BLAST score	213
E value	4.0e-17
Match length	77
% identity	56
NCBI Description	(AB007787) DREB1A [Arabidopsis thaliana] >gi_3907539 (AF062924) transcriptional activator CBF1 homolog [Arabidopsis thaliana] >gi_4091983_gb_AAC99370_ (AF076155) CRT/DRE binding factor 3 [Arabidopsis thaliana] >gi_4322230_gb_AAD15977_ (AF074602) CRT/DRE binding factor 3 [Arabidopsis thaliana]

Seq. No.	276842
Contig ID	70244_1.R1011
5'-most EST	zuv700352761.h1
Method	BLASTX
NCBI GI	g120777
BLAST score	1160
E value	1.0e-127
Match length	418
% identity	53
NCBI Description	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH) >gi_147901 (M88334) succinic semialdehyde dehydrogenase [Escherichia coli] >gi_1789015 (AE000351) succinate-semialdehyde dehydrogenase, NADP-dependent activity [Escherichia coli]

Seq. No.	276843
Contig ID	70251_1.R1011
5'-most EST	uC-zmflmo17104d03b1

Seq. No.	276844
Contig ID	70252_1.R1011
5'-most EST	LIB3062-042-Q1-K1-C4
Method	BLASTX
NCBI GI	g3201617
BLAST score	309
E value	3.0e-28
Match length	93
% identity	59
NCBI Description	(AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276845
Contig ID	70278_1.R1011
5'-most EST	zla700379670.h1
Method	BLASTX
NCBI GI	g3941289
BLAST score	256
E value	5.0e-22
Match length	113
% identity	49
NCBI Description	(AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No.	276846
Contig ID	70298_1.R1011
5'-most EST	uC-zmflmo17286e12b1
Method	BLASTX
NCBI GI	g2980798
BLAST score	501
E value	1.0e-50
Match length	155
% identity	61
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	276847
Contig ID	70321_1.R1011
5'-most EST	nbm700474747.h1
Method	BLASTX
NCBI GI	g2735841
BLAST score	1545
E value	1.0e-172
Match length	353
% identity	90
NCBI Description	(AF010283) No definition line found [Sorghum bicolor]

Seq. No.	276848
Contig ID	70321_2.R1011
5'-most EST	uC-zmflB73042f11b1
Method	BLASTX
NCBI GI	g2735841
BLAST score	400
E value	1.0e-58
Match length	131
% identity	95
NCBI Description	(AF010283) No definition line found [Sorghum bicolor]

Seq. No.	276849
Contig ID	70325_1.R1011
5'-most EST	gct701167673.h1
Method	BLASTX
NCBI GI	g3242403
BLAST score	864
E value	6.0e-93
Match length	261
% identity	62
NCBI Description	(D83178) endonuclease [Hordeum vulgare]

Seq. No.	276850
Contig ID	70325_4.R1011
5'-most EST	tfd700576670.h1
Method	BLASTX
NCBI GI	g3242403
BLAST score	166
E value	6.0e-12
Match length	39
% identity	77
NCBI Description	(D83178) endonuclease [Hordeum vulgare]

Seq. No.	276851
Contig ID	70332_1.R1011

5'-most EST	uer700580705.h1
Seq. No.	276852
Contig ID	70366_1.R1011
5'-most EST	wyr700241607.h1
Method	BLASTX
NCBI GI	g2146742
BLAST score	769
E value	7.0e-82
Match length	257
% identity	62
NCBI Description	pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209631 (U36432) GNOM gene product [Arabidopsis thaliana]
Seq. No.	276853
Contig ID	70372_1.R1011
5'-most EST	gwl700613146.h1
Method	BLASTX
NCBI GI	g3831458
BLAST score	288
E value	8.0e-26
Match length	108
% identity	50
NCBI Description	(AC005700) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276854
Contig ID	70377_1.R1011
5'-most EST	LIB3062-043-Q1-K1-H7
Method	BLASTX
NCBI GI	g4204313
BLAST score	146
E value	6.0e-09
Match length	89
% identity	45
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	276855
Contig ID	70378_1.R1011
5'-most EST	uC-zmflb73216e03b2
Seq. No.	276856
Contig ID	70380_1.R1011
5'-most EST	LIB3062-044-Q1-K1-A10
Method	BLASTX
NCBI GI	g4337175
BLAST score	328
E value	2.0e-30
Match length	114
% identity	52
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.	276857

Contig ID	70386_1.R1011
5'-most EST	LIB3062-044-Q1-K1-A5

Seq. No.	276858
Contig ID	70392_1.R1011
5'-most EST	LIB3062-044-Q1-K1-B12
Method	BLASTX
NCBI GI	g4586249
BLAST score	265
E value	4.0e-23
Match length	120
% identity	45
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No.	276859
Contig ID	70398_1.R1011
5'-most EST	yyf700348116.h1
Method	BLASTX
NCBI GI	g1170949
BLAST score	554
E value	1.0e-56
Match length	276
% identity	64
NCBI Description	SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir__S38327 protein kinase - Arabidopsis thaliana >gi_166811 (L07249) protein kinase [Arabidopsis thaliana]

Seq. No.	276860
Contig ID	70416_1.R1011
5'-most EST	xsy700217984.h1
Method	BLASTX
NCBI GI	g2982459
BLAST score	151
E value	7.0e-13
Match length	106
% identity	40
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	276861
Contig ID	70432_2.R1011
5'-most EST	cyk700049541.f1
Method	BLASTX
NCBI GI	g2554675
BLAST score	300
E value	3.0e-27
Match length	113
% identity	52
NCBI Description	Three-Dimensional Structure Of Glycolate Oxidase With Bound Active-Site Inhibitors >gi_2624594_pdb_1AL7_ Three-Dimensional Structures Of Glycolate Oxidase With Bound Active-Site Inhibitors

Seq. No.	276862
Contig ID	70434_1.R1011
5'-most EST	LIB3070-013-Q1-N1-A11
Method	BLASTX

NCBI GI	g3402685
BLAST score	164
E value	1.0e-10
Match length	123
% identity	29
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	276863
Contig ID	70440_1.R1011
5'-most EST	fdz701165213.h1
Method	BLASTX
NCBI GI	g2462749
BLAST score	735
E value	7.0e-78
Match length	171
% identity	79
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	276864
Contig ID	70449_1.R1011
5'-most EST	xyt700344811.h1
Method	BLASTX
NCBI GI	g4587987
BLAST score	520
E value	1.0e-61
Match length	157
% identity	76
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No.	276865
Contig ID	70450_1.R1011
5'-most EST	LIB3062-044-Q1-K1-G4
Method	BLASTX
NCBI GI	g4587524
BLAST score	667
E value	5.0e-70
Match length	210
% identity	62
NCBI Description	(AC007060) T5I8.13 [Arabidopsis thaliana]

Seq. No.	276866
Contig ID	70454_1.R1011
5'-most EST	ntr700074663.h1
Method	BLASTX
NCBI GI	g3219267
BLAST score	988
E value	1.0e-107
Match length	321
% identity	62
NCBI Description	(AB015313) MAP kinase kinase 2 [Arabidopsis thaliana]

Seq. No.	276867
Contig ID	70454_2.R1011
5'-most EST	uC-zmromo17072b04a1

Seq. No.	276868
Contig ID	70462_1.R1011
5'-most EST	nbm700465815.h1
Seq. No.	276869
Contig ID	70471_1.R1011
5'-most EST	LIB3062-045-Q1-K1-A7
Seq. No.	276870
Contig ID	70473_1.R1011
5'-most EST	LIB3062-045-Q1-K1-A9
Seq. No.	276871
Contig ID	70489_1.R1011
5'-most EST	LIB3062-045-Q1-K1-C4
Seq. No.	276872
Contig ID	70489_2.R1011
5'-most EST	ntr700075893.h1
Seq. No.	276873
Contig ID	70491_1.R1011
5'-most EST	uC-zmroteosinte075f12b1
Method	BLASTX
NCBI GI	g4567271
BLAST score	284
E value	5.0e-25
Match length	205
% identity	41
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]
Seq. No.	276874
Contig ID	70498_1.R1011
5'-most EST	LIB3062-045-Q1-K1-D3
Seq. No.	276875
Contig ID	70531_1.R1011
5'-most EST	cyk700050481.f1
Method	BLASTX
NCBI GI	g2655291
BLAST score	509
E value	1.0e-51
Match length	168
% identity	59
NCBI Description	(AF032974) germin-like protein 4 [Oryza sativa]
Seq. No.	276876
Contig ID	70535_1.R1011
5'-most EST	LIB3137-030-Q1-K1-G3
Seq. No.	276877
Contig ID	70550_1.R1011
5'-most EST	LIB3069-031-Q1-K1-F10
Method	BLASTX
NCBI GI	g3608155
BLAST score	454
E value	1.0e-61

Match length	154
% identity	81
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	276878
Contig ID	70556_1.R1011
5'-most EST	uC-zmflb73167e11b2
Method	BLASTX
NCBI GI	g2832625
BLAST score	720
E value	4.0e-76
Match length	200
% identity	65
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	276879
Contig ID	70560_1.R1011
5'-most EST	uC-zmflb73198a04b1

Seq. No.	276880
Contig ID	70560_2.R1011
5'-most EST	uC-zmflb73063f03b1

Seq. No.	276881
Contig ID	70565_1.R1011
5'-most EST	LIB3062-046-Q1-K1-C4
Method	BLASTX
NCBI GI	g4335751
BLAST score	297
E value	6.0e-27
Match length	127
% identity	45
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	276882
Contig ID	70573_1.R1011
5'-most EST	LIB3062-046-Q1-K1-D11

Seq. No.	276883
Contig ID	70596_1.R1011
5'-most EST	uC-zmflb73067a02b1
Method	BLASTX
NCBI GI	g625509
BLAST score	533
E value	1.0e-54
Match length	111
% identity	25
NCBI Description	ubiquitin precursor - Arabidopsis thaliana (fragment)

Seq. No.	276884
Contig ID	70599_1.R1011
5'-most EST	LIB3069-048-Q1-K1-E12
Method	BLASTX
NCBI GI	g3033401
BLAST score	690
E value	8.0e-73

Match length	172
% identity	74
NCBI Description	(AC004238) putative potassium transporter [Arabidopsis thaliana]

Seq. No.	276885
Contig ID	70603_1.R1011
5'-most EST	xmt700262313.h1
Method	BLASTX
NCBI GI	g2497219
BLAST score	173
E value	4.0e-12
Match length	79
% identity	39
NCBI Description	HYPOTHETICAL 15.4 KD PROTEIN IN HAS1-JNM1 INTERGENIC REGION >gi_626266_pir__S47453 probable membrane protein YMR292w - yeast (Saccharomyces cerevisiae) >gi_530349_emb_CAA56801_ (X80836) len:138, CAI:0.12, potential spliced gene, hydropho bic composition [Saccharomyces cerevisiae]

Seq. No.	276886
Contig ID	70605_1.R1011
5'-most EST	uC-zmflb73027b02b1
Method	BLASTX
NCBI GI	g4262233
BLAST score	164
E value	3.0e-14
Match length	87
% identity	54
NCBI Description	(AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276887
Contig ID	70605_2.R1011
5'-most EST	xyt700342241.h1
Method	BLASTX
NCBI GI	g4206196
BLAST score	520
E value	1.0e-52
Match length	287
% identity	43
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276888
Contig ID	70614_1.R1011
5'-most EST	LIB3062-046-Q1-K1-G8

Seq. No.	276889
Contig ID	70626_1.R1011
5'-most EST	LIB3062-047-Q1-K1-A2
Method	BLASTX
NCBI GI	g224797
BLAST score	495
E value	4.0e-50
Match length	127
% identity	75
NCBI Description	urease [Canavalia ensiformis]

Seq. No.	276890
Contig ID	70638_1.R1011
5'-most EST	uC-zmflb73051b10b1
Method	BLASTX
NCBI GI	g2580499
BLAST score	1147
E value	1.0e-126
Match length	287
% identity	74
NCBI Description	(U67186) NADPH:ferrihemoprotein oxidoreductase [Eschscholzia californica]

Seq. No.	276891
Contig ID	70643_1.R1011
5'-most EST	LIB3062-047-Q1-K1-C2
Method	BLASTX
NCBI GI	g3252807
BLAST score	219
E value	7.0e-18
Match length	52
% identity	77
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276892
Contig ID	70647_1.R1011
5'-most EST	fwa700098014.h1
Method	BLASTX
NCBI GI	g4104457
BLAST score	446
E value	3.0e-44
Match length	87
% identity	99
NCBI Description	(AF036172) 2-oxoglutarate/malate translocator [Zea mays]

Seq. No.	276893
Contig ID	70649_1.R1011
5'-most EST	LIB3062-047-Q1-K1-D10
Method	BLASTX
NCBI GI	g4544369
BLAST score	235
E value	1.0e-19
Match length	84
% identity	55
NCBI Description	(AC006920) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276894
Contig ID	70656_1.R1011
5'-most EST	LIB3062-047-Q1-K1-D6

Seq. No.	276895
Contig ID	70658_1.R1011
5'-most EST	ceu700431893.h1
Method	BLASTX
NCBI GI	g836954
BLAST score	611
E value	3.0e-63
Match length	187

% identity	61
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]

Seq. No.	276896
Contig ID	70662_1.R1011
5'-most EST	uC-zmflmo17342b02b1
Method	BLASTX
NCBI GI	g3980412
BLAST score	423
E value	5.0e-41
Match length	280
% identity	41
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	276897
Contig ID	70662_4.R1011
5'-most EST	LIB3136-026-Q1-K1-F9

Seq. No.	276898
Contig ID	70665_1.R1011
5'-most EST	LIB3062-047-Q1-K1-E5
Method	BLASTX
NCBI GI	g3719215
BLAST score	174
E value	2.0e-12
Match length	76
% identity	47
NCBI Description	(AF005158) MADS-box Protein [Arabidopsis thaliana] >gi_3719217 (AF005159) MADS-box protein [Arabidopsis thaliana] >gi_4220536_emb_CAA23009_ (AL035356) MADS-box protein AGL24 [Arabidopsis thaliana]

Seq. No.	276899
Contig ID	70671_1.R1011
5'-most EST	pmx700086309.h1
Method	BLASTX
NCBI GI	g1669601
BLAST score	347
E value	7.0e-33
Match length	114
% identity	58
NCBI Description	(D88747) AR401 [Arabidopsis thaliana]

Seq. No.	276900
Contig ID	70672_1.R1011
5'-most EST	LIB3062-047-Q1-K1-G10

Seq. No.	276901
Contig ID	70700_1.R1011
5'-most EST	uC-zmflmo17218e11a1

Seq. No.	276902
Contig ID	70702_1.R1011
5'-most EST	LIB3062-048-Q1-K1-A5

Seq. No.	276903
Contig ID	70708_1.R1011

5'-most EST	xdb700339955.h1
Seq. No.	276904
Contig ID	70709_1.R1011
5'-most EST	LIB3062-048-Q1-K1-B11
Seq. No.	276905
Contig ID	70717_1.R1011
5'-most EST	LIB3062-048-Q1-K1-C1
Method	BLASTX
NCBI GI	g2541876
BLAST score	207
E value	2.0e-16
Match length	122
% identity	37
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
Seq. No.	276906
Contig ID	70744_1.R1011
5'-most EST	wty700165275.h1
Method	BLASTX
NCBI GI	g4218011
BLAST score	701
E value	7.0e-74
Match length	251
% identity	59
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	276907
Contig ID	70744_2.R1011
5'-most EST	fC-zmf1700352235f1
Method	BLASTX
NCBI GI	g4218011
BLAST score	841
E value	2.0e-90
Match length	227
% identity	70
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	276908
Contig ID	70756_1.R1011
5'-most EST	uC-zmf1mo17031d07b1
Method	BLASTN
NCBI GI	g22223
BLAST score	154
E value	8.0e-81
Match length	162
% identity	99
NCBI Description	Maize cab-1 gene for chlorophyll a/b-binding protein
Seq. No.	276909
Contig ID	70764_1.R1011

5'-most EST	LIB3062-049-Q1-K1-A6
Method	BLASTX
NCBI GI	g3702962
BLAST score	334
E value	6.0e-31
Match length	92
% identity	74
NCBI Description	(AF079484) rac GTP binding protein Arac7 [Arabidopsis thaliana]

Seq. No.	276910
Contig ID	70777_1.R1011
5'-most EST	LIB3067-019-Q1-K1-D4

Seq. No.	276911
Contig ID	70801_1.R1011
5'-most EST	LIB3062-049-Q1-K1-D9
Method	BLASTX
NCBI GI	g3024898
BLAST score	632
E value	5.0e-66
Match length	182
% identity	66
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) >gi_1504028_dbj_BAA13213_ (D86977) similar to putative ATP-dependent RNA helicase K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi_3123906 (AF038391) pre-mRNA splicing factor [Homo sapiens]

Seq. No.	276912
Contig ID	70817_1.R1011
5'-most EST	uC-zmroteosinte069f08b1

Seq. No.	276913
Contig ID	70820_1.R1011
5'-most EST	wyr700238283.h1

Seq. No.	276914
Contig ID	70823_1.R1011
5'-most EST	uC-zmroB73020f12b1
Method	BLASTX
NCBI GI	g2618696
BLAST score	189
E value	5.0e-14
Match length	98
% identity	38
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276915
Contig ID	70853_1.R1011
5'-most EST	uC-zmflMo17082e10b1
Method	BLASTX
NCBI GI	g3861382
BLAST score	145
E value	9.0e-09
Match length	66
% identity	44

NCBI Description	(AJ235273) PSEUDOURIDYLATE SYNTHASE I (truA) [Rickettsia prowazekii]
Seq. No.	276916
Contig ID	70859_1.R1011
5'-most EST	uC-zmflmo17187b06b1
Seq. No.	276917
Contig ID	70870_1.R1011
5'-most EST	LIB3062-050-Q1-K1-C8
Seq. No.	276918
Contig ID	70874_1.R1011
5'-most EST	LIB3062-050-Q1-K1-D11
Method	BLASTX
NCBI GI	g4586262
BLAST score	182
E value	3.0e-13
Match length	72
% identity	53
NCBI Description	(AL049640) putative calmodulin [Arabidopsis thaliana]
Seq. No.	276919
Contig ID	70890_1.R1011
5'-most EST	rv1700456578.h1
Method	BLASTX
NCBI GI	g3702331
BLAST score	545
E value	1.0e-63
Match length	255
% identity	55
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276920
Contig ID	70891_1.R1011
5'-most EST	dyk700106053.h1
Method	BLASTX
NCBI GI	g4512658
BLAST score	424
E value	2.0e-41
Match length	180
% identity	44
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]
Seq. No.	276921
Contig ID	70899_1.R1011
5'-most EST	pmx700083510.h1
Method	BLASTX
NCBI GI	g4582441
BLAST score	493
E value	1.0e-49
Match length	142
% identity	61
NCBI Description	(AC007142) unknown protein [Arabidopsis thaliana]
Seq. No.	276922
Contig ID	70905_1.R1011

5'-most EST	LIB3062-050-Q1-K1-G5
Seq. No.	276923
Contig ID	70912_1.R1011
5'-most EST	uC-zmflb73344g09a2
Method	BLASTX
NCBI GI	g4185507
BLAST score	673
E value	2.0e-70
Match length	208
% identity	60
NCBI Description	(AF100163) EZA1 [Arabidopsis thaliana]
Seq. No.	276924
Contig ID	70919_1.R1011
5'-most EST	LIB3062-050-Q1-K1-H7
Seq. No.	276925
Contig ID	70923_1.R1011
5'-most EST	uC-zmflmo17153h02a1
Seq. No.	276926
Contig ID	70923_2.R1011
5'-most EST	LIB3062-051-Q1-K1-A11
Seq. No.	276927
Contig ID	70929_1.R1011
5'-most EST	LIB3137-039-Q1-K1-A10
Seq. No.	276928
Contig ID	70935_1.R1011
5'-most EST	fwa700098572.h1
Seq. No.	276929
Contig ID	70944_1.R1011
5'-most EST	uC-zmflb73149c12b1
Method	BLASTX
NCBI GI	g2459435
BLAST score	201
E value	2.0e-32
Match length	119
% identity	61
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]
Seq. No.	276930
Contig ID	70944_2.R1011
5'-most EST	uC-zmflmo17068b10b2
Method	BLASTX
NCBI GI	g2459435
BLAST score	769
E value	4.0e-91
Match length	238
% identity	67
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	276931
Contig ID	70947_1.R1011
5'-most EST	LIB3062-051-Q1-K1-C7

Seq. No.	276932
Contig ID	70947_2.R1011
5'-most EST	uC-zmflmo17223a12a1

Seq. No.	276933
Contig ID	70949_1.R1011
5'-most EST	LIB3062-053-Q1-K1-A10

Seq. No.	276934
Contig ID	70952_1.R1011
5'-most EST	xmt700258334.h1
Method	BLASTX
NCBI GI	g3738316
BLAST score	257
E value	4.0e-22
Match length	76
% identity	67
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	276935
Contig ID	70970_1.R1011
5'-most EST	uwc700151290.h1
Method	BLASTX
NCBI GI	g1620371
BLAST score	830
E value	6.0e-89
Match length	239
% identity	62
NCBI Description	(Y08782) peroxidase ATP23a [Arabidopsis thaliana]

Seq. No.	276936
Contig ID	70993_1.R1011
5'-most EST	LIB3062-051-Q1-K1-H10

Seq. No.	276937
Contig ID	70996_1.R1011
5'-most EST	LIB3062-051-Q1-K1-H3
Method	BLASTX
NCBI GI	g4580394
BLAST score	374
E value	6.0e-36
Match length	118
% identity	58
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	276938
Contig ID	70997_1.R1011
5'-most EST	LIB3062-051-Q1-K1-H8
Method	BLASTX
NCBI GI	g4262167
BLAST score	497
E value	3.0e-50

Match length	169
% identity	60
NCBI Description	(AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No.	276939
Contig ID	71005_1.R1011
5'-most EST	uC-zmflb73180h08b1
Method	BLASTX
NCBI GI	g2154715
BLAST score	412
E value	5.0e-40
Match length	101
% identity	77
NCBI Description	(Y09418) CDPK-related protein kinase [Arabidopsis thaliana]

Seq. No.	276940
Contig ID	71029_1.R1011
5'-most EST	wty700169081.h1
Method	BLASTX
NCBI GI	g2829751
BLAST score	155
E value	1.0e-10
Match length	73
% identity	45
NCBI Description	MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) >gi_1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi_2190976 (AF002699) macrophage migration inhibitory factor [Brugia malayi]

Seq. No.	276941
Contig ID	71030_1.R1011
5'-most EST	LIB3062-052-Q1-K1-D11
Method	BLASTX
NCBI GI	g2673917
BLAST score	491
E value	1.0e-49
Match length	139
% identity	35
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	276942
Contig ID	71032_1.R1011
5'-most EST	qmh700026651.f1
Method	BLASTX
NCBI GI	g4432869
BLAST score	888
E value	1.0e-102
Match length	254
% identity	73
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276943
Contig ID	71036_1.R1011
5'-most EST	pmx700085384.h1
Method	BLASTX

NCBI GI	g4586061
BLAST score	994
E value	1.0e-108
Match length	257
% identity	68
NCBI Description	(AC007020) putative BOP1 protein [Arabidopsis thaliana]

Seq. No.	276944
Contig ID	71057_1.R1011
5'-most EST	uC-zmroteosinte016f10b1
Method	BLASTX
NCBI GI	g4455287
BLAST score	413
E value	3.0e-40
Match length	136
% identity	60
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	276945
Contig ID	71060_1.R1011
5'-most EST	LIB3062-052-Q1-K1-G6
Method	BLASTX
NCBI GI	g4490704
BLAST score	188
E value	7.0e-14
Match length	64
% identity	56
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	276946
Contig ID	71083_1.R1011
5'-most EST	xtj700377471.h1
Method	BLASTX
NCBI GI	g1143069
BLAST score	248
E value	4.0e-21
Match length	59
% identity	75
NCBI Description	(U30600) 3-ketoacyl carrier protein synthase III [Allium porrum]

Seq. No.	276947
Contig ID	71102_1.R1011
5'-most EST	uC-zmflMo17004h10b1
Method	BLASTX
NCBI GI	g2618687
BLAST score	461
E value	7.0e-46
Match length	170
% identity	59
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	276948
Contig ID	71105_1.R1011
5'-most EST	LIB3062-053-Q1-K1-D3

Seq. No.	276949

Contig ID	71110_1.R1011
5'-most EST	uC-zmflmo17270c03b1
Method	BLASTX
NCBI GI	g3420233
BLAST score	501
E value	1.0e-50
Match length	149
% identity	72
NCBI Description	(AF058763) uroporphyrinogen decarboxylase [Zea mays]

Seq. No.	276950
Contig ID	71112_1.R1011
5'-most EST	wyr700242338.h1
Method	BLASTX
NCBI GI	g1877221
BLAST score	411
E value	3.0e-40
Match length	147
% identity	58
NCBI Description	(Z83834) Mlo [Hordeum vulgare] >gi_2894377_emb_CAA74909.1_ (Y14573) Mlo protein [Hordeum vulgare]

Seq. No.	276951
Contig ID	71115_1.R1011
5'-most EST	LIB3062-053-Q1-K1-E4

Seq. No.	276952
Contig ID	71116_1.R1011
5'-most EST	uC-zmroB73028b02b1

Seq. No.	276953
Contig ID	71126_1.R1011
5'-most EST	xsy700211783.h1
Method	BLASTX
NCBI GI	g4539314
BLAST score	242
E value	7.0e-20
Match length	196
% identity	41
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	276954
Contig ID	71137_1.R1011
5'-most EST	uC-zmroB73015e05b1
Method	BLASTX
NCBI GI	g3367578
BLAST score	270
E value	4.0e-46
Match length	153
% identity	55
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	276955
Contig ID	71152_1.R1011
5'-most EST	pmx700091955.h1
Method	BLASTX

NCBI GI	g2664214
BLAST score	587
E value	1.0e-69
Match length	485
% identity	39
NCBI Description	(AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No.	276956
Contig ID	71152_2.R1011
5'-most EST	uC-zmflmo17103h08b1

Seq. No.	276957
Contig ID	71158_1.R1011
5'-most EST	wen700334123.h1
Method	BLASTX
NCBI GI	g337999
BLAST score	199
E value	2.0e-15
Match length	40
% identity	100
NCBI Description	(M63573) secreted cyclophilin-like protein [Homo sapiens]

Seq. No.	276958
Contig ID	71170_1.R1011
5'-most EST	LIB3062-056-Q1-K1-E9
Method	BLASTX
NCBI GI	g31397
BLAST score	239
E value	7.0e-20
Match length	46
% identity	96
NCBI Description	(X02761) fibronectin precursor [Homo sapiens]

Seq. No.	276959
Contig ID	71172_1.R1011
5'-most EST	yyf700351779.h1
Method	BLASTX
NCBI GI	g4504959
BLAST score	609
E value	2.0e-63
Match length	122
% identity	100
NCBI Description	laminin receptor 1 (67kD) >gi_1362848_pir__A56880 laminin receptor, 67K - human >gi_250127_bbs_105364 (S37431) 67 kda laminin receptor [human, lung cancer cell line SBC3, Peptide, 295 aa] [Homo sapiens]

Seq. No.	276960
Contig ID	71197_1.R1011
5'-most EST	LIB3062-057-Q1-K1-B3

Seq. No.	276961
Contig ID	71201_1.R1011
5'-most EST	xjt700093685.h1

Seq. No.	276962
Contig ID	71207_1.R1011

5'-most EST	uC-zmflmo17220e06b1
Method	BLASTX
NCBI GI	g2833469
BLAST score	160
E value	3.0e-10
Match length	147
% identity	29
NCBI Description	HYPOTHETICAL 22.2 KD PROTEIN SLR0305 >gi_1001792_dbj_BAA10672_ (D64005) hypothetical protein [Synechocystis sp.]

Seq. No.	276963
Contig ID	71208_1.R1011
5'-most EST	LIB3062-057-Q1-K1-C5

Seq. No.	276964
Contig ID	71217_1.R1011
5'-most EST	LIB3117-010-Q1-K1-E9

Seq. No.	276965
Contig ID	71225_1.R1011
5'-most EST	uC-zmflb73298g11b1
Method	BLASTX
NCBI GI	g1354362
BLAST score	164
E value	6.0e-11
Match length	237
% identity	25
NCBI Description	(U52008) Emm50 [Streptococcus pyogenes]

Seq. No.	276966
Contig ID	71226_1.R1011
5'-most EST	pmx700088702.h1
Method	BLASTX
NCBI GI	g399356
BLAST score	366
E value	1.0e-34
Match length	244
% identity	39
NCBI Description	PSEUDOURIDYLATE SYNTHASE 3 (PSEUDOURIDINE SYNTHASE 3) (DEPRESSED GROWTH-RATE PROTEIN DEG1) >gi_82981_pir__S14145 depressed growth-rate protein DEG1 - yeast (Saccharomyces cerevisiae) >gi_836755_dbj_BAA09239.1_ (D50617) depressed growth-rate protein [Saccharomyces cerevisiae] >gi_870819_dbj_BAA08034_ (D44600) DEPRESSED GROWTH-RATE PROTEIN DEG1 [Saccharomyces cerevisiae]

Seq. No.	276967
Contig ID	71228_1.R1011
5'-most EST	LIB3062-057-Q1-K1-E4
Method	BLASTX
NCBI GI	g2827699
BLAST score	170
E value	6.0e-12
Match length	95
% identity	44
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	276968
Contig ID	71241_1.R1011
5'-most EST	LIB3062-057-Q1-K1-F6
Method	BLASTX
NCBI GI	g2961358
BLAST score	264
E value	5.0e-23
Match length	111
% identity	48
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]

Seq. No.	276969
Contig ID	71242_1.R1011
5'-most EST	uC-zmrob73004f04b1
Method	BLASTX
NCBI GI	g3047104
BLAST score	540
E value	3.0e-55
Match length	195
% identity	56
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	276970
Contig ID	71245_1.R1011
5'-most EST	uC-zmflMo17019b09b1

Seq. No.	276971
Contig ID	71248_1.R1011
5'-most EST	LIB3062-057-Q1-K1-G3

Seq. No.	276972
Contig ID	71254_1.R1011
5'-most EST	LIB84-006-Q1-E1-D9
Method	BLASTX
NCBI GI	g4539403
BLAST score	257
E value	1.0e-21
Match length	81
% identity	56
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	276973
Contig ID	71273_1.R1011
5'-most EST	uC-zmrob73076c03b1

Seq. No.	276974
Contig ID	71273_2.R1011
5'-most EST	pmx700090705.h1

Seq. No.	276975
Contig ID	71280_1.R1011
5'-most EST	cyk700051683.f1
Method	BLASTX
NCBI GI	g1354849
BLAST score	463

E value	5.0e-46
Match length	158
% identity	54
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No.	276976
Contig ID	71292_1.R1011
5'-most EST	uC-zmf1b73096d11b1

Seq. No.	276977
Contig ID	71313_1.R1011
5'-most EST	pmx700086256.h1
Method	BLASTX
NCBI GI	g3850568
BLAST score	238
E value	8.0e-20
Match length	97
% identity	51
NCBI Description	(AC005278) Similar to hypothetical protein SPAC2F7.14c gi_1052797 from Schizosaccharomyces pombe cosmid gb_Z50142. [Arabidopsis thaliana]

Seq. No.	276978
Contig ID	71313_2.R1011
5'-most EST	nbm700466703.h1

Seq. No.	276979
Contig ID	71322_1.R1011
5'-most EST	uC-zmflmo17425f04a1

Seq. No.	276980
Contig ID	71323_1.R1011
5'-most EST	gct701173844.h1

Seq. No.	276981
Contig ID	71356_1.R1011
5'-most EST	wyr700241709.h1
Method	BLASTX
NCBI GI	g3540207
BLAST score	534
E value	2.0e-54
Match length	210
% identity	52
NCBI Description	(AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	276982
Contig ID	71372_1.R1011
5'-most EST	LIB3062-059-Q1-K1-E1
Method	BLASTX
NCBI GI	g1762945
BLAST score	147
E value	3.0e-09
Match length	55
% identity	53
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	276983
Contig ID	71373_1.R1011
5'-most EST	LIB3062-059-Q1-K1-E10

Seq. No.	276984
Contig ID	71374_1.R1011
5'-most EST	uC-zmrob73005f11b1
Method	BLASTX
NCBI GI	g3334667
BLAST score	217
E value	7.0e-19
Match length	136
% identity	41
NCBI Description	(Y10493) putative cytochrome P450 [Glycine max]

Seq. No.	276985
Contig ID	71394_1.R1011
5'-most EST	xyt700344287.h1
Method	BLASTX
NCBI GI	g1431629
BLAST score	234
E value	2.0e-19
Match length	95
% identity	44
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	276986
Contig ID	71406_1.R1011
5'-most EST	pmx700086566.h1
Method	BLASTX
NCBI GI	g3335060
BLAST score	1863
E value	0.0e+00
Match length	450
% identity	80
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	276987
Contig ID	71413_1.R1011
5'-most EST	LIB3066-001-Q1-K1-A11

Seq. No.	276988
Contig ID	71419_1.R1011
5'-most EST	LIB3066-001-Q1-K1-A7

Seq. No.	276989
Contig ID	71430_1.R1011
5'-most EST	LIB3066-001-Q1-K1-B8

Seq. No.	276990
Contig ID	71445_2.R1011
5'-most EST	uC-zmflb73361c08a2

Seq. No.	276991
Contig ID	71445_3.R1011

5'-most EST	uC-zmflmo17108f04b1
Method	BLASTX
NCBI GI	g4539463
BLAST score	145
E value	5.0e-09
Match length	40
% identity	65
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	276992
Contig ID	71445_4.R1011
5'-most EST	xmt700266082.h1

Seq. No.	276993
Contig ID	71452_1.R1011
5'-most EST	uC-zmroteosinte047c01b1
Method	BLASTX
NCBI GI	g1352679
BLAST score	373
E value	5.0e-35
Match length	111
% identity	66
NCBI Description	PROTEIN PHOSPHATASE 2C ABI1 (PP2C) >gi_2129699_pir__A54588 protein phosphatase ABI1 - Arabidopsis thaliana >gi_509419_emb_CAA55484_ (X78886) ABI1 [Arabidopsis thaliana]

Seq. No.	276994
Contig ID	71461_1.R1011
5'-most EST	LIB3066-032-Q1-K1-C7

Seq. No.	276995
Contig ID	71470_1.R1011
5'-most EST	LIB3067-036-Q1-K1-D6
Method	BLASTX
NCBI GI	g2270994
BLAST score	194
E value	1.0e-14
Match length	113
% identity	41
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	276996
Contig ID	71471_1.R1011
5'-most EST	LIB3066-003-Q1-K1-B6
Method	BLASTX
NCBI GI	g129535
BLAST score	211
E value	1.0e-16
Match length	82
% identity	54
NCBI Description	POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1) >gi_2119041_pir__I48718 poly(A) binding protein - mouse >gi_53754_emb_CAA46522_ (X65553) poly(A) binding protein [Mus musculus]

Seq. No.	276997

Contig ID	71484_1.R1011
5'-most EST	LIB3066-028-Q1-K1-C3

Seq. No.	276998
Contig ID	71494_1.R1011
5'-most EST	uC-zmroteosinte037h08b1
Method	BLASTX
NCBI GI	g4249418
BLAST score	328
E value	3.0e-30
Match length	90
% identity	61
NCBI Description	(AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H type domains), 5' partial [Arabidopsis thaliana]

Seq. No.	276999
Contig ID	71533_1.R1011
5'-most EST	tzu700202966.h1
Method	BLASTX
NCBI GI	g404688
BLAST score	345
E value	2.0e-32
Match length	98
% identity	55
NCBI Description	(L19074) cytochrome P450 [Catharanthus roseus]

Seq. No.	277000
Contig ID	71542_1.R1011
5'-most EST	LIB3066-002-Q1-K1-E9

Seq. No.	277001
Contig ID	71554_1.R1011
5'-most EST	uC-zmroteosinte013c09b1
Method	BLASTX
NCBI GI	g1644427
BLAST score	769
E value	7.0e-82
Match length	177
% identity	80
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	277002
Contig ID	71556_1.R1011
5'-most EST	LIB3066-002-Q1-K1-G2

Seq. No.	277003
Contig ID	71567_1.R1011
5'-most EST	LIB3066-002-Q1-K1-H4
Method	BLASTX
NCBI GI	g3297816
BLAST score	142
E value	9.0e-09
Match length	46
% identity	59
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	277004

Contig ID	71569_1.R1011
5'-most EST	LIB3066-002-Q1-K1-H6
Method	BLASTX
NCBI GI	g121446
BLAST score	721
E value	1.0e-76
Match length	141
% identity	99
NCBI Description	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR (FD-GOGAT) >gi_100877_pir__A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190) ferredoxin-dependent glutamate synthase [Zea mays]

Seq. No.	277005
Contig ID	71574_1.R1011
5'-most EST	LIB3066-004-Q1-K1-A11
Method	BLASTX
NCBI GI	g3236249
BLAST score	339
E value	7.0e-32
Match length	111
% identity	58
NCBI Description	(AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277006
Contig ID	71575_1.R1011
5'-most EST	tzu700203367.h1

Seq. No.	277007
Contig ID	71582_1.R1011
5'-most EST	LIB3066-003-Q1-K1-B1
Method	BLASTX
NCBI GI	g2832642
BLAST score	198
E value	5.0e-15
Match length	144
% identity	34
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	277008
Contig ID	71601_1.R1011
5'-most EST	LIB3066-009-Q1-K1-H6
Method	BLASTX
NCBI GI	g1657382
BLAST score	289
E value	6.0e-26
Match length	88
% identity	65
NCBI Description	(Y09101) cholinephosphate cytidylyltransferase [Pisum sativum]

Seq. No.	277009
Contig ID	71605_1.R1011
5'-most EST	LIB3066-003-Q1-K1-D3

Seq. No.	277010
Contig ID	71608_1.R1011

5'-most EST	LIB3066-055-Q1-K1-H1
Seq. No.	277011
Contig ID	71626_1.R1011
5'-most EST	wen700332631.h1
Method	BLASTX
NCBI GI	g3287695
BLAST score	764
E value	4.0e-81
Match length	298
% identity	54
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]
Seq. No.	277012
Contig ID	71626_2.R1011
5'-most EST	uC-zmflb73029c09a1
Seq. No.	277013
Contig ID	71628_1.R1011
5'-most EST	LIB3066-003-Q1-K1-F6
Method	BLASTX
NCBI GI	g134976
BLAST score	161
E value	6.0e-11
Match length	61
% identity	44
NCBI Description	GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042 glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter [Arabidopsis thaliana]
Seq. No.	277014
Contig ID	71629_1.R1011
5'-most EST	uC-zmflmo17163a08b1
Seq. No.	277015
Contig ID	71640_1.R1011
5'-most EST	LIB3066-048-Q1-K1-D11
Method	BLASTX
NCBI GI	g114217
BLAST score	1065
E value	1.0e-116
Match length	271
% identity	81
NCBI Description	ANTHOCYANIN REGULATORY R-S PROTEIN >gi_82721_pir__S06072 regulatory protein R-S - maize >gi_22472_emb_CAA33805_ (X15806) R-S protein (AA 1-612) [Zea mays]
Seq. No.	277016
Contig ID	71644_1.R1011
5'-most EST	LIB3066-003-Q1-K1-H12
Method	BLASTX
NCBI GI	g3641839
BLAST score	303
E value	2.0e-27

Match length	118
% identity	55
NCBI Description	(AL023094) isoflavone reductase - like protein [Arabidopsis thaliana]

Seq. No.	277017
Contig ID	71666_1.R1011
5'-most EST	xdb700341910.h1

Seq. No.	277018
Contig ID	71670_1.R1011
5'-most EST	LIB3066-004-Q1-K1-B9

Seq. No.	277019
Contig ID	71681_1.R1011
5'-most EST	LIB3066-004-Q1-K1-C9

Seq. No.	277020
Contig ID	71702_1.R1011
5'-most EST	uC-zmf1b73083g11b2
Method	BLASTX
NCBI GI	g4128133
BLAST score	612
E value	2.0e-63
Match length	228
% identity	52
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	277021
Contig ID	71711_1.R1011
5'-most EST	LIB3066-004-Q1-K1-F5

Seq. No.	277022
Contig ID	71738_1.R1011
5'-most EST	LIB3066-042-Q1-K1-A5
Method	BLASTX
NCBI GI	g2340108
BLAST score	363
E value	5.0e-62
Match length	142
% identity	89
NCBI Description	(U65948) starch branching enzyme IIa [Zea mays]

Seq. No.	277023
Contig ID	71753_1.R1011
5'-most EST	LIB3066-005-Q1-K1-D4

Seq. No.	277024
Contig ID	71761_1.R1011
5'-most EST	LIB36-005-Q1-E1-E5
Method	BLASTX
NCBI GI	g4586105
BLAST score	473
E value	3.0e-47
Match length	163
% identity	49
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	277025
Contig ID	71766_1.R1011
5'-most EST	LIB3066-005-Q1-K1-C2

Seq. No.	277026
Contig ID	71771_1.R1011
5'-most EST	fdz701159568.h1

Seq. No.	277027
Contig ID	71780_1.R1011
5'-most EST	uC-zmflmo17342e04b1

Seq. No.	277028
Contig ID	71793_1.R1011
5'-most EST	uC-zmroteosinte025d05b1
Method	BLASTX
NCBI GI	g2934902
BLAST score	1281
E value	1.0e-142
Match length	298
% identity	87
NCBI Description	(AF039304) cpSecY [Zea mays]

Seq. No.	277029
Contig ID	71826_1.R1011
5'-most EST	LIB3066-006-Q1-K1-A10

Seq. No.	277030
Contig ID	71826_2.R1011
5'-most EST	tzu700205982.h1

Seq. No.	277031
Contig ID	71827_1.R1011
5'-most EST	LIB3066-038-Q1-K1-C9

Seq. No.	277032
Contig ID	71827_2.R1011
5'-most EST	LIB3066-006-Q1-K1-A12

Seq. No.	277033
Contig ID	71842_1.R1011
5'-most EST	LIB3066-006-Q1-K1-B8
Method	BLASTX
NCBI GI	g2435518
BLAST score	216
E value	2.0e-26
Match length	123
% identity	50
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	277034
Contig ID	71864_1.R1011
5'-most EST	uC-zmflb73245g08b2

Seq. No.	277035

Contig ID	71897_1.R1011
5'-most EST	LIB3066-029-Q1-K1-F4

Seq. No.	277036
Contig ID	71899_1.R1011
5'-most EST	uC-zmflb73294c01b1
Method	BLASTX
NCBI GI	g4406780
BLAST score	1382
E value	1.0e-153
Match length	335
% identity	77
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	277037
Contig ID	71903_1.R1011
5'-most EST	LIB3066-006-Q1-K1-H5

Seq. No.	277038
Contig ID	71905_1.R1011
5'-most EST	uC-zmroteosinte014e03b1

Seq. No.	277039
Contig ID	71908_1.R1011
5'-most EST	LIB3067-053-Q1-K1-C4
Method	BLASTX
NCBI GI	g1497987
BLAST score	599
E value	5.0e-62
Match length	163
% identity	72
NCBI Description	(U62798) SCARECROW [Arabidopsis thaliana]

Seq. No.	277040
Contig ID	71922_1.R1011
5'-most EST	LIB3066-007-Q1-K1-B2

Seq. No.	277041
Contig ID	71932_1.R1011
5'-most EST	fwa700099414.h1

Seq. No.	277042
Contig ID	71932_2.R1011
5'-most EST	uC-zmflmo17097c08b1

Seq. No.	277043
Contig ID	71934_1.R1011
5'-most EST	LIB3066-007-Q1-K1-C4
Method	BLASTX
NCBI GI	g3482932
BLAST score	330
E value	1.0e-30
Match length	152
% identity	44
NCBI Description	(AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 277044
Contig ID 71937_1.R1011
5'-most EST LIB3066-032-Q1-K1-A5

Seq. No. 277045
Contig ID 72050_1.R1011
5'-most EST uC-zmflb73092c03a1

Seq. No. 277046
Contig ID 72072_1.R1011
5'-most EST LIB83-008-Q1-E1-D11

Seq. No. 277047
Contig ID 72095_1.R1011
5'-most EST fwa700098648.h1
Method BLASTX
NCBI GI g2500980
BLAST score 1154
E value 1.0e-138
Match length 347
% identity 72
NCBI Description GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS) >gi_1076718_pir__S51684 glutamate--tRNA ligase (EC 6.1.1.17) precursor - barley >gi_603849_emb_CAA58505_ (X83523) glutamate--tRNA ligase [Hordeum vulgare]

Seq. No. 277048
Contig ID 72108_1.R1011
5'-most EST LIB3066-040-Q1-K1-C4
Method BLASTX
NCBI GI g2505865
BLAST score 473
E value 2.0e-47
Match length 160
% identity 23
NCBI Description (Y12227) putative topoisomerase [Arabidopsis thaliana]

Seq. No. 277049
Contig ID 72112_1.R1011
5'-most EST LIB3066-009-Q1-K1-D3

Seq. No. 277050
Contig ID 72113_1.R1011
5'-most EST bdu700382170.h1
Method BLASTX
NCBI GI g3169171
BLAST score 433
E value 2.0e-42
Match length 149
% identity 51
NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445213 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No. 277051
Contig ID 72120_1.R1011
5'-most EST nwy700448008.h1

Seq. No.	277052
Contig ID	72127_1.R1011
5'-most EST	fwa700099813.h1

Seq. No.	277053
Contig ID	72139_1.R1011
5'-most EST	uC-zmflmo17262h09b1
Method	BLASTX
NCBI GI	g3024859
BLAST score	394
E value	6.0e-38
Match length	186
% identity	39
NCBI Description	HYPOTHETICAL PROTEIN AF0130 >gi_2650515 (AE001097) acetylpolyamine aminohydrolase (aphA) [Archaeoglobus fulgidus]

Seq. No.	277054
Contig ID	72142_1.R1011
5'-most EST	LIB3066-040-Q1-K1-E12

Seq. No.	277055
Contig ID	72161_1.R1011
5'-most EST	LIB3066-010-Q1-K1-A3
Method	BLASTX
NCBI GI	g4510373
BLAST score	203
E value	1.0e-15
Match length	130
% identity	35
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	277056
Contig ID	72161_2.R1011
5'-most EST	uC-zmflMo17010c05b1

Seq. No.	277057
Contig ID	72167_1.R1011
5'-most EST	uC-zmflb73065g01b1
Method	BLASTX
NCBI GI	g4325372
BLAST score	245
E value	3.0e-22
Match length	112
% identity	54
NCBI Description	(AF128396) contains similarity to protein disulfide isomerases [Arabidopsis thaliana]

Seq. No.	277058
Contig ID	72168_1.R1011
5'-most EST	uC-zmflB73042f01b1
Method	BLASTX
NCBI GI	g2129635
BLAST score	337
E value	2.0e-31

Match length	150
% identity	51
NCBI Description	light repressible receptor protein kinase - Arabidopsis thaliana >gi_1321686_emb_CAA66376_ (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No.	277059
Contig ID	72168_2.R1011
5'-most EST	LIB3136-020-Q1-K1-C9
Method	BLASTX
NCBI GI	g4587513
BLAST score	416
E value	1.0e-40
Match length	168
% identity	52
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	277060
Contig ID	72184_1.R1011
5'-most EST	vux700157381.h1
Method	BLASTX
NCBI GI	g3059129
BLAST score	335
E value	4.0e-31
Match length	192
% identity	39
NCBI Description	(AJ000477) cytochrome P450 [Helianthus tuberosus]

Seq. No.	277061
Contig ID	72200_1.R1011
5'-most EST	LIB3066-010-Q1-K1-F12
Method	BLASTX
NCBI GI	g3688209
BLAST score	335
E value	2.0e-31
Match length	109
% identity	65
NCBI Description	(AJ010093) MAP3K beta 1 protein kinase [Brassica napus]

Seq. No.	277062
Contig ID	72219_1.R1011
5'-most EST	LIB3066-010-Q1-K1-H3
Method	BLASTX
NCBI GI	g629792
BLAST score	285
E value	2.0e-25
Match length	143
% identity	44
NCBI Description	cysteine proteinase - rice >gi_530335_emb_CAA56844_ (X80876) cysteine protease [Oryza sativa]

Seq. No.	277063
Contig ID	72223_1.R1011
5'-most EST	uC-zmflmo17295a02b1

Seq. No.	277064

Contig ID 72245_1.R1011
5'-most EST LIB3066-011-Q1-K1-C2

Seq. No. 277065
Contig ID 72275_1.R1011
5'-most EST LIB3066-011-Q1-K1-F12
Method BLASTX
NCBI GI g4539335
BLAST score 862
E value 2.0e-92
Match length 407
% identity 41
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 277066
Contig ID 72293_1.R1011
5'-most EST LIB3066-032-Q1-K1-G3
Method BLASTX
NCBI GI g3548808
BLAST score 409
E value 4.0e-40
Match length 96
% identity 74
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 277067
Contig ID 72303_1.R1011
5'-most EST LIB3066-012-Q1-K1-A1

Seq. No. 277068
Contig ID 72304_2.R1011
5'-most EST LIB84-017-Q1-E1-A7
Method BLASTX
NCBI GI g2980762
BLAST score 468
E value 1.0e-46
Match length 183
% identity 52
NCBI Description (AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No. 277069
Contig ID 72312_1.R1011
5'-most EST LIB3066-016-Q1-K1-F7

Seq. No. 277070
Contig ID 72312_2.R1011
5'-most EST pmx700085541.h1

Seq. No. 277071
Contig ID 72312_3.R1011
5'-most EST LIB3066-030-Q1-E1-E2

Seq. No. 277072
Contig ID 72319_1.R1011
5'-most EST LIB3066-012-Q1-K1-B2
Method BLASTX
NCBI GI g4490311

BLAST score	513
E value	3.0e-52
Match length	136
% identity	67
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	277073
Contig ID	72320_1.R1011
5'-most EST	bdu700382829.h1

Seq. No.	277074
Contig ID	72323_1.R1011
5'-most EST	nwy700443606.h1
Method	BLASTX
NCBI GI	g4584545
BLAST score	435
E value	1.0e-42
Match length	249
% identity	41
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	277075
Contig ID	72356_1.R1011
5'-most EST	LIB3066-012-Q1-K1-E9

Seq. No.	277076
Contig ID	72370_1.R1011
5'-most EST	uC-zmf1b73177f01b1
Method	BLASTX
NCBI GI	g541824
BLAST score	432
E value	2.0e-42
Match length	182
% identity	51
NCBI Description	protein kinase - spinach >gi_457709_emb_CAA82991_ (Z30330) protein kinase [Spinacia oleracea]

Seq. No.	277077
Contig ID	72388_1.R1011
5'-most EST	uC-zmflmo17105h12b1

Seq. No.	277078
Contig ID	72400_1.R1011
5'-most EST	LIB3066-013-Q1-K1-H9

Seq. No.	277079
Contig ID	72400_2.R1011
5'-most EST	LIB3069-012-Q1-K1-A4

Seq. No.	277080
Contig ID	72400_3.R1011
5'-most EST	LIB3066-049-Q1-K1-D6

Seq. No.	277081
Contig ID	72459_1.R1011
5'-most EST	uC-zmflmo17076c10b1
Method	BLASTX

NCBI GI	g4210504
BLAST score	526
E value	2.0e-58
Match length	227
% identity	52
NCBI Description	(AC002392) putative cadmium-transporting ATPase [Arabidopsis thaliana]

Seq. No.	277082
Contig ID	72490_1.R1011
5'-most EST	LIB3136-002-P1-K1-G4
Method	BLASTX
NCBI GI	g3258575
BLAST score	181
E value	4.0e-21
Match length	72
% identity	75
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	277083
Contig ID	72493_1.R1011
5'-most EST	ymt700224433.h1

Seq. No.	277084
Contig ID	72493_3.R1011
5'-most EST	ceu700430163.h1

Seq. No.	277085
Contig ID	72495_1.R1011
5'-most EST	LIB3066-014-Q1-K1-C2

Seq. No.	277086
Contig ID	72515_1.R1011
5'-most EST	uC-zmflb73183h11b1
Method	BLASTX
NCBI GI	g4455272
BLAST score	309
E value	6.0e-28
Match length	142
% identity	48
NCBI Description	(AL035527) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	277087
Contig ID	72515_2.R1011
5'-most EST	uC-zmflb73051c12a2

Seq. No.	277088
Contig ID	72534_1.R1011
5'-most EST	LIB3066-014-Q1-K1-G1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	277089
Contig ID	72542_1.R1011
5'-most EST	LIB3066-042-Q1-K1-F2
Method	BLASTX
NCBI GI	g3212865
BLAST score	518
E value	1.0e-52
Match length	202
% identity	56
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	277090
Contig ID	72546_1.R1011
5'-most EST	uC-zmflmo17204a10b1
Method	BLASTX
NCBI GI	g2104535
BLAST score	268
E value	3.0e-23
Match length	96
% identity	58
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	277091
Contig ID	72555_1.R1011
5'-most EST	xyt700344275.h1

Seq. No.	277092
Contig ID	72612_1.R1011
5'-most EST	uwc700155282.h1

Seq. No.	277093
Contig ID	72619_1.R1011
5'-most EST	LIB3066-015-Q1-K1-F6
Method	BLASTX
NCBI GI	g3046815
BLAST score	485
E value	6.0e-75
Match length	226
% identity	65
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	277094
Contig ID	72629_1.R1011
5'-most EST	LIB3066-029-Q1-K1-E7

Seq. No.	277095
Contig ID	72635_1.R1011
5'-most EST	LIB3066-015-Q1-K1-H11

Seq. No.	277096
Contig ID	72644_1.R1011
5'-most EST	yyf700349863.h1

Seq. No.	277097
Contig ID	72654_1.R1011
5'-most EST	LIB3066-016-Q1-K1-B2

Seq. No.	277098
Contig ID	72672_1.R1011
5'-most EST	LIB3066-016-Q1-K1-C7
Method	BLASTX
NCBI GI	g2498731
BLAST score	395
E value	3.0e-38
Match length	116
% identity	63
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	277099
Contig ID	72683_1.R1011
5'-most EST	LIB3066-016-Q1-K1-D7
Method	BLASTX
NCBI GI	g3297815
BLAST score	388
E value	3.0e-37
Match length	113
% identity	64
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	277100
Contig ID	72697_1.R1011
5'-most EST	xsy700212418.h1
Method	BLASTX
NCBI GI	g2344887
BLAST score	517
E value	3.0e-52
Match length	227
% identity	49
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	277101
Contig ID	72701_1.R1011
5'-most EST	LIB3066-016-Q1-K1-F5

Seq. No.	277102
Contig ID	72701_3.R1011
5'-most EST	rvl700457252.h1

Seq. No.	277103
Contig ID	72741_1.R1011
5'-most EST	LIB3066-017-Q1-K1-B9

Seq. No.	277104
Contig ID	72752_1.R1011
5'-most EST	xmt700266517.h1
Method	BLASTX
NCBI GI	g3548815
BLAST score	470
E value	8.0e-47
Match length	161
% identity	56

NCBI Description	(AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]

Seq. No.	277105
Contig ID	72752_2.R1011
5'-most EST	LIB3067-043-Q1-K1-B5
Method	BLASTX
NCBI GI	g3702343
BLAST score	521
E value	9.0e-53
Match length	135
% identity	76
NCBI Description	(AC005397) putative homeotic gene regulator [Arabidopsis thaliana]

Seq. No.	277106
Contig ID	72796_1.R1011
5'-most EST	uC-zmflmo17257e12b1
Method	BLASTX
NCBI GI	g2804278
BLAST score	793
E value	1.0e-113
Match length	240
% identity	82
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	277107
Contig ID	72796_2.R1011
5'-most EST	LIB3068-060-Q1-K1-E8
Method	BLASTX
NCBI GI	g2804278
BLAST score	305
E value	1.0e-27
Match length	70
% identity	89
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	277108
Contig ID	72813_1.R1011
5'-most EST	ypc700805379.h1

Seq. No.	277109
Contig ID	72815_1.R1011
5'-most EST	bdu700382305.h1

Seq. No.	277110
Contig ID	72830_1.R1011
5'-most EST	uC-zmflmo17289f01b1

Seq. No.	277111
Contig ID	72837_1.R1011
5'-most EST	LIB3066-018-Q1-K1-D9
Method	BLASTN
NCBI GI	g473185
BLAST score	69
E value	2.0e-30
Match length	101

% identity	92
NCBI Description	Z.mays U3snRNA pseudogene

Seq. No.	277112
Contig ID	72852_1.R1011
5'-most EST	uC-zmflmo17258c09b1

Seq. No.	277113
Contig ID	72925_1.R1011
5'-most EST	uC-zmflmo17113d12a1

Seq. No.	277114
Contig ID	72926_1.R1011
5'-most EST	bdu700382955.h1
Method	BLASTX
NCBI GI	g3287683
BLAST score	177
E value	1.0e-18
Match length	104
% identity	50
NCBI Description	(AC003979) Similar to apoptosis protein MA-3 gb_D50465 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	277115
Contig ID	72932_1.R1011
5'-most EST	xjt700092721.h1
Method	BLASTX
NCBI GI	g1946366
BLAST score	145
E value	6.0e-09
Match length	53
% identity	55
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	277116
Contig ID	72938_1.R1011
5'-most EST	LIB84-014-Q1-E1-E12
Method	BLASTX
NCBI GI	g1800219
BLAST score	1011
E value	1.0e-110
Match length	214
% identity	92
NCBI Description	(U56731) phytochrome C [Sorghum bicolor]

Seq. No.	277117
Contig ID	72960_1.R1011
5'-most EST	LIB3066-019-Q1-K1-H7
Method	BLASTX
NCBI GI	g4510340
BLAST score	207
E value	2.0e-16
Match length	119
% identity	42
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 277118

Contig ID	72964_1.R1011
5'-most EST	LIB3066-020-Q1-K1-A9

Seq. No.	277119
Contig ID	73007_1.R1011
5'-most EST	ymy700282548.h2
Method	BLASTX
NCBI GI	g1323748
BLAST score	219
E value	9.0e-18
Match length	70
% identity	59
NCBI Description	(U32430) thiol protease [Triticum aestivum]

Seq. No.	277120
Contig ID	73018_1.R1011
5'-most EST	uwc700152030.h1
Method	BLASTX
NCBI GI	g4512651
BLAST score	926
E value	1.0e-102
Match length	321
% identity	54
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	277121
Contig ID	73020_1.R1011
5'-most EST	LIB3066-020-Q1-K1-F11

Seq. No.	277122
Contig ID	73038_1.R1011
5'-most EST	uC-zmflb73264h11b1
Method	BLASTX
NCBI GI	g125606
BLAST score	218
E value	1.0e-17
Match length	89
% identity	54
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No.	277123
Contig ID	73060_1.R1011
5'-most EST	LIB3066-021-Q1-K1-B12
Method	BLASTX
NCBI GI	g4586056
BLAST score	221
E value	6.0e-18
Match length	121
% identity	46
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	277124
Contig ID	73066_1.R1011

5'-most EST	LIB3066-021-Q1-K1-B7
Seq. No.	277125
Contig ID	73077_1.R1011
5'-most EST	uC-zmflb73208h07b1
Seq. No.	277126
Contig ID	73093_1.R1011
5'-most EST	uC-zmflmo17070h04b1
Method	BLASTX
NCBI GI	g1076498
BLAST score	334
E value	1.0e-30
Match length	148
% identity	46
NCBI Description	zinc-finger protein (C-terminal) - soybean >gi_558543_emb_CAA85320_ (Z36749) C-terminal zinc-finger [Glycine max]
Seq. No.	277127
Contig ID	73104_1.R1011
5'-most EST	LIB3066-021-Q1-K1-F3
Method	BLASTX
NCBI GI	g2827709
BLAST score	695
E value	2.0e-73
Match length	173
% identity	75
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	277128
Contig ID	73158_1.R1011
5'-most EST	LIB3066-023-Q1-K1-A4
Method	BLASTX
NCBI GI	g2264373
BLAST score	490
E value	2.0e-49
Match length	160
% identity	58
NCBI Description	(AC002354) putative NAM/no apical meristem protein [Arabidopsis thaliana]
Seq. No.	277129
Contig ID	73170_1.R1011
5'-most EST	pmx700082243.h1
Seq. No.	277130
Contig ID	73178_1.R1011
5'-most EST	LIB3066-023-Q1-K1-C11
Method	BLASTX
NCBI GI	g1673366
BLAST score	340
E value	1.0e-31
Match length	141
% identity	52
NCBI Description	(Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis thaliana]

Seq. No.	277131
Contig ID	73180_1.R1011
5'-most EST	ypc700799080.h1
Method	BLASTX
NCBI GI	g32709
BLAST score	1292
E value	1.0e-143
Match length	379
% identity	63
NCBI Description	(X62570) IFP53 [Homo sapiens]

Seq. No.	277132
Contig ID	73180_3.R1011
5'-most EST	yyf700351995.h1
Method	BLASTX
NCBI GI	g2982724
BLAST score	193
E value	7.0e-15
Match length	54
% identity	70
NCBI Description	(AB012222) tryptophan-tRNA synthetase [Cavia porcellus]

Seq. No.	277133
Contig ID	73183_1.R1011
5'-most EST	LIB3066-023-Q1-K1-C5
Method	BLASTX
NCBI GI	g4417289
BLAST score	179
E value	5.0e-13
Match length	83
% identity	41
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	277134
Contig ID	73185_1.R1011
5'-most EST	nbm700467854.h1

Seq. No.	277135
Contig ID	73186_1.R1011
5'-most EST	wty700166327.h1

Seq. No.	277136
Contig ID	73194_1.R1011
5'-most EST	LIB3066-023-Q1-K1-D7

Seq. No.	277137
Contig ID	73249_1.R1011
5'-most EST	LIB3066-024-Q1-K1-A6

Seq. No.	277138
Contig ID	73256_1.R1011
5'-most EST	uC-zmflmo17155a08b1

Seq. No.	277139
Contig ID	73270_1.R1011
5'-most EST	LIB3066-024-Q1-K1-C6

Method	BLASTX
NCBI GI	g4454484
BLAST score	571
E value	7.0e-59
Match length	159
% identity	72
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	277140
Contig ID	73275_1.R1011
5'-most EST	LIB3066-049-Q1-K1-F3

Seq. No.	277141
Contig ID	73280_1.R1011
5'-most EST	LIB3066-037-Q1-K1-B1

Seq. No.	277142
Contig ID	73291_1.R1011
5'-most EST	LIB3066-024-Q1-K1-E6
Method	BLASTX
NCBI GI	g2781347
BLAST score	1088
E value	1.0e-119
Match length	294
% identity	71
NCBI Description	(AC003113) F24O1.3 [Arabidopsis thaliana]

Seq. No.	277143
Contig ID	73310_1.R1011
5'-most EST	LIB3066-024-Q1-K1-G2
Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	277144
Contig ID	73328_1.R1011
5'-most EST	hvj700618712.h1
Method	BLASTX
NCBI GI	g4587550
BLAST score	174
E value	4.0e-12
Match length	84
% identity	39
NCBI Description	(AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No.	277145
Contig ID	73352_1.R1011
5'-most EST	LIB3066-025-Q1-K1-C5

Seq. No.	277146
Contig ID	73372_1.R1011

5'-most EST	yyf700350967.h1
Seq. No.	277147
Contig ID	73375_1.R1011
5'-most EST	LIB3066-025-Q1-K1-E9
Seq. No.	277148
Contig ID	73385_1.R1011
5'-most EST	gct701167421.h1
Method	BLASTX
NCBI GI	g2245020
BLAST score	488
E value	4.0e-57
Match length	156
% identity	65
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]
Seq. No.	277149
Contig ID	73393_1.R1011
5'-most EST	uC-zmroteosinte002h11b1
Method	BLASTX
NCBI GI	g2245125
BLAST score	168
E value	2.0e-11
Match length	72
% identity	50
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	277150
Contig ID	73393_2.R1011
5'-most EST	uC-zmflmo17180b05b1
Method	BLASTX
NCBI GI	g2245125
BLAST score	150
E value	3.0e-09
Match length	39
% identity	69
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	277151
Contig ID	73413_1.R1011
5'-most EST	uC-zmflb73183g05b1
Method	BLASTX
NCBI GI	g4469024
BLAST score	753
E value	1.0e-106
Match length	265
% identity	68
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	277152
Contig ID	73417_1.R1011
5'-most EST	LIB3066-038-Q1-K1-D7
Seq. No.	277153
Contig ID	73421_1.R1011
5'-most EST	kem700611159.h1

Seq. No.	277154
Contig ID	73423_1.R1011
5'-most EST	LIB3066-026-Q1-K1-C1
Method	BLASTX
NCBI GI	g2673914
BLAST score	1159
E value	1.0e-127
Match length	394
% identity	55
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277155
Contig ID	73423_2.R1011
5'-most EST	wty700166662.h1
Method	BLASTX
NCBI GI	g2673914
BLAST score	201
E value	2.0e-15
Match length	57
% identity	65
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277156
Contig ID	73425_1.R1011
5'-most EST	LIB3066-026-Q1-K1-C12

Seq. No.	277157
Contig ID	73438_1.R1011
5'-most EST	pmx700088991.h1
Method	BLASTX
NCBI GI	g4646202
BLAST score	195
E value	5.0e-15
Match length	50
% identity	72
NCBI Description	(AC007230) ESTs gb_H76289 and gb_H76537 come from this gene. [Arabidopsis thaliana]

Seq. No.	277158
Contig ID	73449_1.R1011
5'-most EST	LIB3066-026-Q1-K1-E5
Method	BLASTX
NCBI GI	g1617270
BLAST score	738
E value	2.0e-78
Match length	204
% identity	67
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	277159
Contig ID	73463_1.R1011
5'-most EST	uC-zmf1b73045d11a2

Seq. No.	277160
Contig ID	73465_1.R1011
5'-most EST	LIB3066-050-Q1-K1-H7

Method	BLASTX
NCBI GI	g4581150
BLAST score	205
E value	4.0e-16
Match length	92
% identity	45
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277161
Contig ID	73474_1.R1011
5'-most EST	LIB3066-026-Q1-K1-G8

Seq. No.	277162
Contig ID	73489_1.R1011
5'-most EST	cyk700050293.f1
Method	BLASTX
NCBI GI	g2130024
BLAST score	249
E value	4.0e-21
Match length	130
% identity	48
NCBI Description	DNA-binding protein ABF2 - wild oat >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No.	277163
Contig ID	73489_2.R1011
5'-most EST	dyk700103579.h1
Method	BLASTX
NCBI GI	g2130024
BLAST score	248
E value	5.0e-21
Match length	92
% identity	58
NCBI Description	DNA-binding protein ABF2 - wild oat >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No.	277164
Contig ID	73509_1.R1011
5'-most EST	LIB3066-027-Q1-K1-C2

Seq. No.	277165
Contig ID	73511_1.R1011
5'-most EST	LIB3066-051-Q1-K1-G2
Method	BLASTX
NCBI GI	g4567279
BLAST score	484
E value	1.0e-48
Match length	173
% identity	54
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	277166
Contig ID	73516_1.R1011
5'-most EST	LIB3066-027-Q1-K1-D1

Method	BLASTX
NCBI GI	g1001499
BLAST score	426
E value	3.0e-44
Match length	214
% identity	47
NCBI Description	(D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	277167
Contig ID	73519_1.R1011
5'-most EST	uC-zmflmo17067b05b1

Seq. No.	277168
Contig ID	73535_1.R1011
5'-most EST	uC-zmflb73058e03b1
Method	BLASTX
NCBI GI	g2160185
BLAST score	613
E value	1.0e-63
Match length	213
% identity	54
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	277169
Contig ID	73549_1.R1011
5'-most EST	hvj700619204.h1
Method	BLASTX
NCBI GI	g1652860
BLAST score	198
E value	5.0e-15
Match length	142
% identity	37
NCBI Description	(D90909) hypothetical protein [Synechocystis sp.]

Seq. No.	277170
Contig ID	73556_1.R1011
5'-most EST	uC-zmflb73236g11b1

Seq. No.	277171
Contig ID	73562_1.R1011
5'-most EST	LIB3066-027-Q1-K1-H2
Method	BLASTX
NCBI GI	g3150415
BLAST score	475
E value	2.0e-47
Match length	104
% identity	81
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	277172
Contig ID	73562_2.R1011
5'-most EST	uC-zmflmo17078c05a1
Method	BLASTX
NCBI GI	g3150415

BLAST score	202
E value	7.0e-16
Match length	44
% identity	80
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	277173
Contig ID	73566_1.R1011
5'-most EST	uC-zmflb73236f08b1
Method	BLASTX
NCBI GI	g404690
BLAST score	213
E value	5.0e-17
Match length	110
% identity	37
NCBI Description	(L19075) cytochrome P450 [Catharanthus roseus]

Seq. No.	277174
Contig ID	73590_1.R1011
5'-most EST	dyk700104111.h1

Seq. No.	277175
Contig ID	73592_1.R1011
5'-most EST	LIB3066-028-Q1-K1-C4
Method	BLASTX
NCBI GI	g2944385
BLAST score	480
E value	3.0e-48
Match length	123
% identity	75
NCBI Description	(AF048691) calcium dependent protein kinase [Oryza sativa]

Seq. No.	277176
Contig ID	73599_1.R1011
5'-most EST	LIB3068-002-Q1-K1-B9

Seq. No.	277177
Contig ID	73603_1.R1011
5'-most EST	LIB3066-028-Q1-K1-D5
Method	BLASTX
NCBI GI	g3738285
BLAST score	194
E value	7.0e-15
Match length	79
% identity	49
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	277178
Contig ID	73610_1.R1011
5'-most EST	LIB3066-028-Q1-K1-E2
Method	BLASTX
NCBI GI	g4559380
BLAST score	613
E value	1.0e-63
Match length	186

% identity	61
NCBI Description	(AC006526) putative auxin-responsive GH3 protein [Arabidopsis thaliana]
Seq. No.	277179
Contig ID	73613_1.R1011
5'-most EST	nbm700477544.h1
Seq. No.	277180
Contig ID	73614_1.R1011
5'-most EST	pmx700089222.h1
Seq. No.	277181
Contig ID	73618_1.R1011
5'-most EST	LIB3066-028-Q1-K1-F10
Method	BLASTX
NCBI GI	g3157927
BLAST score	231
E value	4.0e-19
Match length	70
% identity	70
NCBI Description	(AC002131) Contains similarity to GDP-dissociation inhibitor gb_L07918 from Mus musculus. [Arabidopsis thaliana]
Seq. No.	277182
Contig ID	73643_1.R1011
5'-most EST	wuj700282108.h1
Seq. No.	277183
Contig ID	73645_1.R1011
5'-most EST	rvl700457051.h1
Method	BLASTX
NCBI GI	g3128173
BLAST score	658
E value	5.0e-69
Match length	145
% identity	85
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.	277184
Contig ID	73651_1.R1011
5'-most EST	LIB3068-043-Q1-K1-F2
Seq. No.	277185
Contig ID	73667_1.R1011
5'-most EST	uC-zmflmo17020c07b1
Seq. No.	277186
Contig ID	73668_1.R1011
5'-most EST	LIB3066-029-Q1-K1-B6
Seq. No.	277187
Contig ID	73674_1.R1011
5'-most EST	uC-zmrob73011d10b1
Seq. No.	277188

Contig ID 73674_2.R1011
5'-most EST LIB3066-029-Q1-K1-C11

Seq. No. 277189
Contig ID 73687_1.R1011
5'-most EST fdz70l161736.h1
Method BLASTX
NCBI GI g3292826
BLAST score 274
E value 1.0e-23
Match length 120
% identity 62
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 277190
Contig ID 73697_1.R1011
5'-most EST LIB3066-029-Q1-K1-E11

Seq. No. 277191
Contig ID 73730_1.R1011
5'-most EST uC-zmf1b73065d10b1
Method BLASTX
NCBI GI g2499115
BLAST score 1021
E value 1.0e-111
Match length 250
% identity 74
NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1835788 (U86662) VPS41 [Lycopersicon esculentum]

Seq. No. 277192
Contig ID 73744_1.R1011
5'-most EST LIB3066-030-Q1-E1-A5
Method BLASTX
NCBI GI g4490311
BLAST score 332
E value 5.0e-31
Match length 113
% identity 57
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 277193
Contig ID 73746_1.R1011
5'-most EST LIB3066-030-Q1-K1-H6

Seq. No. 277194
Contig ID 73753_1.R1011
5'-most EST LIB3066-030-Q1-E1-B4

Seq. No. 277195
Contig ID 73757_1.R1011
5'-most EST LIB3066-030-Q1-E1-B8

Seq. No. 277196
Contig ID 73759_1.R1011
5'-most EST LIB3066-030-Q1-E1-C1

Seq. No.	277197
Contig ID	73764_1.R1011
5'-most EST	LIB3066-030-Q1-K1-F10
Method	BLASTX
NCBI GI	g3056725
BLAST score	260
E value	1.0e-22
Match length	133
% identity	42
NCBI Description	(AF034774) ent-kaurene synthase [Arabidopsis thaliana]

Seq. No.	277198
Contig ID	73770_1.R1011
5'-most EST	LIB3066-030-Q1-K1-E1

Seq. No.	277199
Contig ID	73772_1.R1011
5'-most EST	LIB3066-035-Q1-K1-D1
Method	BLASTX
NCBI GI	g2894598
BLAST score	370
E value	4.0e-35
Match length	121
% identity	61
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	277200
Contig ID	73780_1.R1011
5'-most EST	LIB3066-030-Q1-E1-E12

Seq. No.	277201
Contig ID	73784_1.R1011
5'-most EST	LIB3066-030-Q1-K1-D8

Seq. No.	277202
Contig ID	73791_1.R1011
5'-most EST	LIB3066-030-Q1-E1-F11

Seq. No.	277203
Contig ID	73805_1.R1011
5'-most EST	LIB3066-030-Q1-E1-G4
Method	BLASTX
NCBI GI	g2979545
BLAST score	193
E value	1.0e-14
Match length	121
% identity	40
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	277204
Contig ID	73805_2.R1011
5'-most EST	LIB3136-019-Q1-K1-C8
Method	BLASTX
NCBI GI	g2979545
BLAST score	479
E value	5.0e-48
Match length	135

% identity	65
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	277205
Contig ID	73806_1.R1011
5'-most EST	LIB3066-030-Q1-K1-B8
Method	BLASTX
NCBI GI	g4056490
BLAST score	165
E value	2.0e-11
Match length	127
% identity	40
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277206
Contig ID	73895_1.R1011
5'-most EST	LIB3066-030-Q1-K1-H11

Seq. No.	277207
Contig ID	73913_1.R1011
5'-most EST	LIB3066-033-Q1-E1-G8
Method	BLASTX
NCBI GI	g629852
BLAST score	218
E value	3.0e-17
Match length	190
% identity	34
NCBI Description	polygalacturonase - maize >gi_288367_emb_CAA46680_ (X65845) polygalacturonase [Zea mays]

Seq. No.	277208
Contig ID	73913_2.R1011
5'-most EST	LIB3066-032-Q1-E1-G5
Method	BLASTX
NCBI GI	g629852
BLAST score	204
E value	3.0e-29
Match length	259
% identity	39
NCBI Description	polygalacturonase - maize >gi_288367_emb_CAA46680_ (X65845) polygalacturonase [Zea mays]

Seq. No.	277209
Contig ID	73946_1.R1011
5'-most EST	LIB3066-031-Q1-E1-D7
Method	BLASTX
NCBI GI	g548597
BLAST score	145
E value	5.0e-09
Match length	103
% identity	39
NCBI Description	PROFILIN

Seq. No.	277210
Contig ID	73954_1.R1011
5'-most EST	LIB3066-031-Q1-E1-E12

Seq. No.	277211
Contig ID	73982_1.R1011
5'-most EST	LIB3066-032-Q1-E1-H12

Seq. No.	277212
Contig ID	73991_1.R1011
5'-most EST	pwr700450516.h1
Method	BLASTX
NCBI GI	g3395938
BLAST score	359
E value	5.0e-34
Match length	96
% identity	41
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	277213
Contig ID	74001_1.R1011
5'-most EST	LIB3066-031-Q1-K1-B1
Method	BLASTX
NCBI GI	g3785987
BLAST score	161
E value	6.0e-11
Match length	62
% identity	58
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277214
Contig ID	74007_1.R1011
5'-most EST	uC-zmflmo17039d02a1
Method	BLASTX
NCBI GI	g3643607
BLAST score	1203
E value	1.0e-132
Match length	272
% identity	79
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	277215
Contig ID	74171_1.R1011
5'-most EST	LIB3069-050-Q1-K1-H8
Method	BLASTX
NCBI GI	g2842486
BLAST score	360
E value	7.0e-34
Match length	114
% identity	62
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]

Seq. No.	277216
Contig ID	74171_2.R1011
5'-most EST	LIB3066-043-Q1-K1-C7
Method	BLASTX
NCBI GI	g4056457
BLAST score	358
E value	1.0e-33
Match length	121

% identity	56
NCBI Description	(AC005990) ESTs gb_234051 and gb_F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	277217
Contig ID	74171_3.R1011
5'-most EST	uC-zmflmo17078b07b1
Method	BLASTX
NCBI GI	g4056457
BLAST score	192
E value	2.0e-14
Match length	59
% identity	66
NCBI Description	(AC005990) ESTs gb_234051 and gb_F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	277218
Contig ID	74180_1.R1011
5'-most EST	LIB3066-032-Q1-K1-C2
Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	277219
Contig ID	74183_1.R1011
5'-most EST	uC-zmflmo17155d04b1

Seq. No.	277220
Contig ID	74183_2.R1011
5'-most EST	uC-zmroteosinte017f02b1

Seq. No.	277221
Contig ID	74183_5.R1011
5'-most EST	cyk700050510.f1

Seq. No.	277222
Contig ID	74199_1.R1011
5'-most EST	uC-zmflmo17001d10b1
Method	BLASTX
NCBI GI	g2492782
BLAST score	906
E value	9.0e-98
Match length	261
% identity	65
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992) alpha-galactosidase [Coffea arabica]

Seq. No.	277223
Contig ID	74208_1.R1011
5'-most EST	wyr700238129.h1

Seq. No.	277224

Contig ID 74211_1.R1011
5'-most EST uC-zmflmo17025c03a1

Seq. No. 277225
Contig ID 74215_1.R1011
5'-most EST uC-zmroteosinte115g04b1

Seq. No. 277226
Contig ID 74249_1.R1011
5'-most EST LIB3066-033-Q1-E1-A3

Seq. No. 277227
Contig ID 74250_1.R1011
5'-most EST LIB3066-033-Q1-E1-A5

Seq. No. 277228
Contig ID 74253_1.R1011
5'-most EST LIB3066-033-Q1-E1-A8

Seq. No. 277229
Contig ID 74272_1.R1011
5'-most EST LIB3066-033-Q1-E1-G10

Seq. No. 277230
Contig ID 74277_1.R1011
5'-most EST LIB3066-033-Q1-E1-F12

Seq. No. 277231
Contig ID 74324_1.R1011
5'-most EST wyr700242195.h1

Seq. No. 277232
Contig ID 74330_1.R1011
5'-most EST LIB3066-033-Q1-K1-A4

Seq. No. 277233
Contig ID 74346_1.R1011
5'-most EST uC-zmflmo17174d01b1

Seq. No. 277234
Contig ID 74347_1.R1011
5'-most EST LIB3066-033-Q1-K1-C1
Method BLASTX
NCBI GI g3297818
BLAST score 237
E value 1.0e-19
Match length 93
% identity 40
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 277235
Contig ID 74347_2.R1011
5'-most EST hbs701182767.h1

Seq. No. 277236
Contig ID 74349_1.R1011
5'-most EST uC-zmflmo17339b08b1

Method	BLASTX
NCBI GI	g2352084
BLAST score	229
E value	2.0e-18
Match length	52
% identity	85
NCBI Description	(U96613) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	277237
Contig ID	74349_2.R1011
5'-most EST	LIB3066-033-Q1-K1-C11
Method	BLASTX
NCBI GI	g2352084
BLAST score	367
E value	4.0e-35
Match length	118
% identity	63
NCBI Description	(U96613) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	277238
Contig ID	74351_1.R1011
5'-most EST	uC-zmflmo17044h02a1
Method	BLASTX
NCBI GI	g133918
BLAST score	329
E value	2.0e-30
Match length	62
% identity	98
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 >gi_70861_pir__R3WT2 ribosomal protein S2 - wheat chloroplast >gi_552977 (M35396) ribosomal protein S2 [Triticum aestivum]

Seq. No.	277239
Contig ID	74379_1.R1011
5'-most EST	LIB3066-033-Q1-K1-F1
Method	BLASTX
NCBI GI	g4138581
BLAST score	613
E value	9.0e-64
Match length	193
% identity	41
NCBI Description	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No.	277240
Contig ID	74390_1.R1011
5'-most EST	pwr700453152.h1
Method	BLASTX
NCBI GI	g3341686
BLAST score	247
E value	4.0e-21
Match length	69
% identity	62
NCBI Description	(AC003672) putative glycosyl transferase [Arabidopsis thaliana]

Seq. No. 277241

Contig ID	74402_1.R1011
5'-most EST	mwy700440369.h1
Method	BLASTX
NCBI GI	g4646208
BLAST score	295
E value	1.0e-26
Match length	235
% identity	33
NCBI Description	(AC007230) Contains similarity to F13P17.8 gi_3337355 hypothetical protein from Arabidopsis thaliana BAC gb_AC004481

Seq. No.	277242
Contig ID	74411_1.R1011
5'-most EST	LIB3066-033-Q1-K1-H9

Seq. No.	277243
Contig ID	74430_1.R1011
5'-most EST	LIB3066-034-Q1-K1-B5
Method	BLASTX
NCBI GI	g2262111
BLAST score	556
E value	4.0e-57
Match length	163
% identity	64
NCBI Description	(AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]

Seq. No.	277244
Contig ID	74434_1.R1011
5'-most EST	LIB3066-055-Q1-K1-H4
Method	BLASTX
NCBI GI	g3763916
BLAST score	169
E value	7.0e-12
Match length	86
% identity	42
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	277245
Contig ID	74466_1.R1011
5'-most EST	wyr700239189.h1
Method	BLASTX
NCBI GI	g3292831
BLAST score	594
E value	3.0e-61
Match length	153
% identity	69
NCBI Description	(AL031018) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	277246
Contig ID	74472_1.R1011
5'-most EST	LIB3066-034-Q1-K1-F6
Method	BLASTX

NCBI GI	g4417293
BLAST score	322
E value	7.0e-30
Match length	86
% identity	72
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	277247
Contig ID	74507_1.R1011
5'-most EST	LIB3066-035-Q1-K1-B10

Seq. No.	277248
Contig ID	74543_1.R1011
5'-most EST	uC-zmflb73241h10b2
Method	BLASTX
NCBI GI	g4263821
BLAST score	430
E value	2.0e-42
Match length	123
% identity	72
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277249
Contig ID	74594_1.R1011
5'-most EST	LIB3066-036-Q1-K1-C1

Seq. No.	277250
Contig ID	74601_1.R1011
5'-most EST	uC-zmroteosinte084c03b1
Method	BLASTX
NCBI GI	g4539369
BLAST score	262
E value	1.0e-22
Match length	86
% identity	60
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	277251
Contig ID	74611_1.R1011
5'-most EST	LIB3066-036-Q1-K1-E5

Seq. No.	277252
Contig ID	74629_1.R1011
5'-most EST	cyk700048231.f1

Seq. No.	277253
Contig ID	74634_1.R1011
5'-most EST	LIB3066-036-Q1-K1-H4
Method	BLASTX
NCBI GI	g3643608
BLAST score	212
E value	7.0e-17
Match length	62
% identity	56
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277254

Contig ID	74649_1.R1011
5'-most EST	fwa700098728.h1
Method	BLASTX
NCBI GI	g2582822
BLAST score	496
E value	4.0e-59
Match length	147
% identity	78
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	277255
Contig ID	74676_1.R1011
5'-most EST	LIB3066-037-Q1-K1-D7
Method	BLASTX
NCBI GI	g4138722
BLAST score	402
E value	3.0e-39
Match length	106
% identity	74
NCBI Description	(Y09590) hexose transporter [Vitis vinifera]

Seq. No.	277256
Contig ID	74684_1.R1011
5'-most EST	uC-zmflmo17297g02b1
Method	BLASTX
NCBI GI	g2688824
BLAST score	145
E value	6.0e-09
Match length	62
% identity	53
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	277257
Contig ID	74688_1.R1011
5'-most EST	LIB3066-037-Q1-K1-E8
Method	BLASTX
NCBI GI	g3047065
BLAST score	216
E value	5.0e-17
Match length	58
% identity	60
NCBI Description	(AF058825) contains similarity to human OS-9 precurosor (GB:U41635) [Arabidopsis thaliana]

Seq. No.	277258
Contig ID	74698_1.R1011
5'-most EST	LIB3066-037-Q1-K1-F6

Seq. No.	277259
Contig ID	74704_1.R1011
5'-most EST	LIB3066-037-Q1-K1-G12
Method	BLASTX
NCBI GI	g2809263
BLAST score	196
E value	5.0e-15

Match length	119
% identity	34
NCBI Description	(AC002560) F21B7.32 [Arabidopsis thaliana]

Seq. No.	277260
Contig ID	74730_1.R1011
5'-most EST	LIB3066-038-Q1-K1-B6

Seq. No.	277261
Contig ID	74760_1.R1011
5'-most EST	LIB3066-038-Q1-K1-E2
Method	BLASTX
NCBI GI	g3548815
BLAST score	195
E value	7.0e-15
Match length	152
% identity	38
NCBI Description	(AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]

Seq. No.	277262
Contig ID	74767_1.R1011
5'-most EST	LIB3067-021-Q1-K1-E9
Method	BLASTX
NCBI GI	g4165323
BLAST score	198
E value	3.0e-15
Match length	59
% identity	63
NCBI Description	(AB022442) p-type H+-ATPase [Vicia faba]

Seq. No.	277263
Contig ID	74786_1.R1011
5'-most EST	fwa700099972.h1
Method	BLASTX
NCBI GI	g4490719
BLAST score	186
E value	7.0e-14
Match length	62
% identity	52
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	277264
Contig ID	74799_2.R1011
5'-most EST	gct701176129.h1

Seq. No.	277265
Contig ID	74804_1.R1011
5'-most EST	uC-zmflmo17059e10a1

Seq. No.	277266
Contig ID	74822_1.R1011
5'-most EST	LIB3066-040-Q1-K1-D2
Method	BLASTX
NCBI GI	g3395439
BLAST score	261
E value	1.0e-22

Match length 94
% identity 59
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 277267
Contig ID 74860_1.R1011
5'-most EST LIB3066-042-Q1-K1-A11

Seq. No. 277268
Contig ID 74860_2.R1011
5'-most EST cyk700049245.f1
Method BLASTX
NCBI GI g3879167
BLAST score 189
E value 3.0e-14
Match length 103
% identity 35
NCBI Description (Z66515) similar to FAD-1 like protein; cDNA EST yk313h1.5 comes from this gene; cDNA EST yk457a9.3 comes from this gene; cDNA EST yk457a9.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 277269
Contig ID 74861_1.R1011
5'-most EST LIB3066-042-Q1-K1-A12
Method BLASTX
NCBI GI g4063748
BLAST score 355
E value 2.0e-33
Match length 116
% identity 56
NCBI Description (AC005851) unknown protein [Arabidopsis thaliana]

Seq. No. 277270
Contig ID 74866_1.R1011
5'-most EST LIB84-029-Q1-E1-F4
Method BLASTX
NCBI GI g4263704
BLAST score 510
E value 3.0e-51
Match length 234
% identity 41
NCBI Description (AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No. 277271
Contig ID 74866_2.R1011
5'-most EST xsy700207331.h1

Seq. No. 277272
Contig ID 74879_1.R1011
5'-most EST LIB3066-042-Q1-K1-B9
Method BLASTX
NCBI GI g3367523
BLAST score 179
E value 6.0e-13
Match length 76

% identity	47
NCBI Description	(AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No.	277273
Contig ID	74894_1.R1011
5'-most EST	LIB3066-042-Q1-K1-D12
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	277274
Contig ID	74910_1.R1011
5'-most EST	xsy700213777.h1
Method	BLASTX
NCBI GI	g2980781
BLAST score	285
E value	3.0e-25
Match length	186
% identity	35
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	277275
Contig ID	74913_1.R1011
5'-most EST	dyk700106511.h1
Method	BLASTX
NCBI GI	g4103635
BLAST score	253
E value	2.0e-21
Match length	148
% identity	36
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	277276
Contig ID	74923_1.R1011
5'-most EST	gwl700613493.h1

Seq. No.	277277
Contig ID	74929_1.R1011
5'-most EST	LIB3066-042-Q1-K1-G3

Seq. No.	277278
Contig ID	74938_1.R1011
5'-most EST	LIB3069-032-Q1-K1-H12
Method	BLASTX
NCBI GI	g1510135
BLAST score	592
E value	4.0e-61
Match length	167
% identity	63
NCBI Description	(D86574) iron-sulfur subunit of succinate dehydrogenase [Plasmodium falciparum]

Seq. No.	277279
Contig ID	74938_2.R1011
5'-most EST	tzu700205706.h1
Method	BLASTX
NCBI GI	g3860614
BLAST score	399
E value	1.0e-38
Match length	113
% identity	64
NCBI Description	(AJ235270) SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (sdhB) [Rickettsia prowazekii]

Seq. No.	277280
Contig ID	74983_1.R1011
5'-most EST	rvt700549584.h1
Method	BLASTX
NCBI GI	g3041758
BLAST score	172
E value	6.0e-12
Match length	173
% identity	33
NCBI Description	(D85081) unnamed protein product [Escherichia coli]

Seq. No.	277281
Contig ID	74993_1.R1011
5'-most EST	uC-zmf1b73134b02b1
Method	BLASTX
NCBI GI	g2246376
BLAST score	466
E value	1.0e-46
Match length	178
% identity	59
NCBI Description	(Z86093) b-Zip DNA binding protein [Arabidopsis thaliana]

Seq. No.	277282
Contig ID	75000_1.R1011
5'-most EST	uC-zmrob73079a05b1

Seq. No.	277283
Contig ID	75011_1.R1011
5'-most EST	LIB3066-043-Q1-K1-G4
Method	BLASTX
NCBI GI	g4455275
BLAST score	227
E value	4.0e-18
Match length	156
% identity	41
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	277284
Contig ID	75038_1.R1011
5'-most EST	LIB3066-044-Q1-K1-A9
Method	BLASTX
NCBI GI	g2239089
BLAST score	262
E value	2.0e-22
Match length	180

% identity	41
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	277285
Contig ID	75046_1.R1011
5'-most EST	xyt700346575.h1
Method	BLASTX
NCBI GI	g3608412
BLAST score	449
E value	1.0e-44
Match length	152
% identity	60
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No.	277286
Contig ID	75072_1.R1011
5'-most EST	LIB3066-044-Q1-K1-E12

Seq. No.	277287
Contig ID	75087_1.R1011
5'-most EST	LIB3066-044-Q1-K1-F5
Method	BLASTX
NCBI GI	g4510383
BLAST score	468
E value	7.0e-47
Match length	152
% identity	61
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	277288
Contig ID	75097_1.R1011
5'-most EST	fwa700099117.h1
Method	BLASTX
NCBI GI	g4538624
BLAST score	208
E value	5.0e-16
Match length	178
% identity	30
NCBI Description	(AJ133502) hypothetical protein [Nicotiana tabacum]

Seq. No.	277289
Contig ID	75101_1.R1011
5'-most EST	LIB3066-044-Q1-K1-H10
Method	BLASTX
NCBI GI	g3292902
BLAST score	169
E value	9.0e-12
Match length	82
% identity	40
NCBI Description	(AL031027) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=67.72; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P98174;

2-match_description=PUTATIVE RHO/RAC GUANINE NUCLEOT

Seq. No.	277290
Contig ID	75130_1.R1011
5'-most EST	LIB3066-045-Q1-K1-B4

Seq. No.	277291
Contig ID	75148_1.R1011
5'-most EST	uC-zmflMo17006b02b1

Seq. No.	277292
Contig ID	75151_1.R1011
5'-most EST	LIB3066-045-Q1-K1-D5
Method	BLASTX
NCBI GI	g478809
BLAST score	590
E value	4.0e-61
Match length	178
% identity	60
NCBI Description	protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449) protein kinase [Glycine max] >gi_444789_prf__1908223A protein kinase [Glycine max]

Seq. No.	277293
Contig ID	75158_1.R1011
5'-most EST	LIB3066-045-Q1-K1-E12
Method	BLASTX
NCBI GI	g4249388
BLAST score	248
E value	5.0e-21
Match length	88
% identity	58
NCBI Description	(AC005966) Similar to gb_AF025438 Opa-interacting protein (OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	277294
Contig ID	75174_1.R1011
5'-most EST	LIB3066-045-Q1-K1-F7

Seq. No.	277295
Contig ID	75207_1.R1011
5'-most EST	uC-zmflmo17248f12b1
Method	BLASTX
NCBI GI	g4455225
BLAST score	1897
E value	0.0e+00
Match length	499
% identity	67
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	277296
Contig ID	75216_1.R1011
5'-most EST	LIB3066-046-Q1-K1-C3
Method	BLASTX
NCBI GI	g3850575
BLAST score	266
E value	5.0e-23

Match length	154
% identity	42
NCBI Description	(AC005278) F15k9.21 [Arabidopsis thaliana]

Seq. No.	277297
Contig ID	75235_1.R1011
5'-most EST	LIB3066-046-Q1-K1-E6

Seq. No.	277298
Contig ID	75242_1.R1011
5'-most EST	hvj700622893.h1
Method	BLASTX
NCBI GI	g3643600
BLAST score	232
E value	4.0e-19
Match length	62
% identity	71
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277299
Contig ID	75251_1.R1011
5'-most EST	uC-zmflmo17134e11b1

Seq. No.	277300
Contig ID	75256_1.R1011
5'-most EST	uC-zmflm017205c05b1
Method	BLASTX
NCBI GI	g2760321
BLAST score	182
E value	2.0e-13
Match length	75
% identity	44
NCBI Description	(AC002130) F1N21.6 [Arabidopsis thaliana]

Seq. No.	277301
Contig ID	75268_1.R1011
5'-most EST	LIB3066-047-Q1-K1-A6

Seq. No.	277302
Contig ID	75285_1.R1011
5'-most EST	LIB3066-047-Q1-K1-C10

Seq. No.	277303
Contig ID	75315_1.R1011
5'-most EST	LIB3066-047-Q1-K1-E8

Seq. No.	277304
Contig ID	75322_1.R1011
5'-most EST	uC-zmflmo17073e03b1

Seq. No.	277305
Contig ID	75346_1.R1011
5'-most EST	gwl700612687.h1
Method	BLASTX
NCBI GI	g2792297
BLAST score	270
E value	2.0e-23

Match length	61
% identity	69
NCBI Description	(AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No.	277306
Contig ID	75370_1.R1011
5'-most EST	xjt700093652.h1

Seq. No.	277307
Contig ID	75370_2.R1011
5'-most EST	uC-zmflmo17057e07b1

Seq. No.	277308
Contig ID	75382_1.R1011
5'-most EST	uC-zmflmo17330h04b1

Seq. No.	277309
Contig ID	75394_1.R1011
5'-most EST	LIB3066-048-Q1-K1-E2
Method	BLASTX
NCBI GI	g2262176
BLAST score	207
E value	5.0e-16
Match length	97
% identity	45
NCBI Description	(AC002329) putative RING zinc-finger protein [Arabidopsis thaliana] >gi_3790573 (AF078824) RING-H2 finger protein RHA3a [Arabidopsis thaliana]

Seq. No.	277310
Contig ID	75403_1.R1011
5'-most EST	LIB3117-009-Q1-K1-E4

Seq. No.	277311
Contig ID	75429_1.R1011
5'-most EST	LIB3066-048-Q1-K1-H6

Seq. No.	277312
Contig ID	75462_1.R1011
5'-most EST	LIB3066-049-Q1-K1-D8

Seq. No.	277313
Contig ID	75471_1.R1011
5'-most EST	uwc700155144.h1

Seq. No.	277314
Contig ID	75484_1.R1011
5'-most EST	LIB3066-049-Q1-K1-G8
Method	BLASTX
NCBI GI	g4007792
BLAST score	448
E value	3.0e-44
Match length	163
% identity	60
NCBI Description	(AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]

Seq. No.	277315
Contig ID	75489_1.R1011
5'-most EST	cyk700051889.f1

Seq. No.	277316
Contig ID	75497_1.R1011
5'-most EST	LIB3066-050-Q1-K1-A4
Method	BLASTX
NCBI GI	g3128185
BLAST score	145
E value	5.0e-09
Match length	104
% identity	37
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	277317
Contig ID	75503_1.R1011
5'-most EST	LIB3066-055-Q1-K1-D10
Method	BLASTX
NCBI GI	g100396
BLAST score	155
E value	3.0e-10
Match length	74
% identity	53
NCBI Description	DNA-binding protein - garden petunia >gi_20546_emb_CAA43111_ (X60700) DNA-binding protein [Petunia x hybrida]

Seq. No.	277318
Contig ID	75509_1.R1011
5'-most EST	ntr700073148.h1
Method	BLASTX
NCBI GI	g3377806
BLAST score	160
E value	2.0e-10
Match length	107
% identity	31
NCBI Description	(AF075597) contains similarity to Arabidopsis thaliana drought-induced protein Di19 (GB:X78584) [Arabidopsis thaliana]

Seq. No.	277319
Contig ID	75527_1.R1011
5'-most EST	gct701180140.h1
Method	BLASTX
NCBI GI	g4204263
BLAST score	320
E value	2.0e-29
Match length	125
% identity	54
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	277320
Contig ID	75530_1.R1011
5'-most EST	LIB3066-050-Q1-K1-D6
Method	BLASTX
NCBI GI	g2104535

BLAST score	451
E value	7.0e-45
Match length	117
% identity	75
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	277321
Contig ID	75564_1.R1011
5'-most EST	LIB3066-050-Q1-K1-H10

Seq. No.	277322
Contig ID	75577_1.R1011
5'-most EST	uC-zmflb73404c12a1

Seq. No.	277323
Contig ID	75597_1.R1011
5'-most EST	LIB3066-051-Q1-K1-C12
Method	BLASTX
NCBI GI	g1619300
BLAST score	537
E value	1.0e-54
Match length	178
% identity	57
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	277324
Contig ID	75603_1.R1011
5'-most EST	uer700583980.h1

Seq. No.	277325
Contig ID	75606_1.R1011
5'-most EST	LIB3066-051-Q1-K1-D10

Seq. No.	277326
Contig ID	75611_1.R1011
5'-most EST	hbs701183270.h1

Seq. No.	277327
Contig ID	75628_1.R1011
5'-most EST	cyk700052405.f1

Seq. No.	277328
Contig ID	75628_2.R1011
5'-most EST	uC-zmflb73189c12a1

Seq. No.	277329
Contig ID	75628_3.R1011
5'-most EST	LIB3066-051-Q1-K1-F11

Seq. No.	277330
Contig ID	75638_1.R1011
5'-most EST	LIB3066-051-Q1-K1-G11
Method	BLASTX
NCBI GI	g3170178
BLAST score	175
E value	1.0e-12
Match length	115

% identity	38
NCBI Description	(AF039689) antigen NY-CO-7 [Homo sapiens]
Seq. No.	277331
Contig ID	75653_1.R1011
5'-most EST	xjt700094483.h1
Seq. No.	277332
Contig ID	75700_1.R1011
5'-most EST	LIB3067-026-Q1-K1-F6
Seq. No.	277333
Contig ID	75729_1.R1011
5'-most EST	ceu700432687.h1
Method	BLASTX
NCBI GI	g3287691
BLAST score	375
E value	9.0e-36
Match length	226
% identity	42
NCBI Description	(AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]
Seq. No.	277334
Contig ID	75747_1.R1011
5'-most EST	LIB3066-054-Q1-K1-C7
Method	BLASTN
NCBI GI	g311238
BLAST score	47
E value	3.0e-17
Match length	102
% identity	87
NCBI Description	Z.mays cat1 gene for catalase
Seq. No.	277335
Contig ID	75753_1.R1011
5'-most EST	xmt700266543.h1
Method	BLASTX
NCBI GI	g2116759
BLAST score	378
E value	3.0e-36
Match length	189
% identity	39
NCBI Description	(D86418) YfnA [Bacillus subtilis]
Seq. No.	277336
Contig ID	75806_1.R1011
5'-most EST	uC-zmflmo17127c07a1
Method	BLASTX
NCBI GI	g2827649
BLAST score	310
E value	4.0e-28
Match length	138
% identity	49
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]
Seq. No.	277337

Contig ID	75806_2.R1011
5'-most EST	LIB3066-053-Q1-K1-G7
Method	BLASTX
NCBI GI	g2660664
BLAST score	385
E value	7.0e-37
Match length	151
% identity	53
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	277338
Contig ID	75811_1.R1011
5'-most EST	LIB3066-054-Q1-K1-H11
Method	BLASTX
NCBI GI	g4249391
BLAST score	520
E value	8.0e-53
Match length	150
% identity	63
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	277339
Contig ID	75815_1.R1011
5'-most EST	uC-zmromo17119e11a1
Method	BLASTX
NCBI GI	g4185312
BLAST score	807
E value	1.0e-86
Match length	156
% identity	97
NCBI Description	(AF090446) copia protein [Zea mays]

Seq. No.	277340
Contig ID	75851_1.R1011
5'-most EST	LIB3066-054-Q1-K1-D11
Method	BLASTX
NCBI GI	g2464901
BLAST score	421
E value	2.0e-41
Match length	125
% identity	63
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	277341
Contig ID	75853_1.R1011
5'-most EST	xsy700209134.h1

Seq. No.	277342
Contig ID	75873_1.R1011
5'-most EST	uC-zmflb73061f07b1
Method	BLASTX
NCBI GI	g4587515
BLAST score	462
E value	6.0e-46
Match length	212

% identity	50
NCBI Description	(AC007060) EST gb_Z37678 comes from this gene. [Arabidopsis thaliana]
Seq. No.	277343
Contig ID	75918_1.R1011
5'-most EST	uC-zmflmo17332b09a1
Seq. No.	277344
Contig ID	75918_2.R1011
5'-most EST	uC-zmroteosinte092c05b2
Seq. No.	277345
Contig ID	75924_1.R1011
5'-most EST	LIB3066-055-Q1-K1-C11
Method	BLASTX
NCBI GI	g3287693
BLAST score	200
E value	2.0e-15
Match length	68
% identity	62
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]
Seq. No.	277346
Contig ID	75930_1.R1011
5'-most EST	uC-zmflb73303g11b1
Method	BLASTX
NCBI GI	g728880
BLAST score	548
E value	7.0e-56
Match length	186
% identity	60
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]
Seq. No.	277347
Contig ID	75930_2.R1011
5'-most EST	LIB3137-038-Q1-K1-H8
Method	BLASTN
NCBI GI	g1906603
BLAST score	45
E value	4.0e-16
Match length	72
% identity	92
NCBI Description	Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence
Seq. No.	277348
Contig ID	75934_1.R1011
5'-most EST	zuv700355546.h1
Seq. No.	277349

Contig ID	75946_1.R1011
5'-most EST	uC-zmflb73091b02b2
Method	BLASTX
NCBI GI	g4006902
BLAST score	201
E value	3.0e-15
Match length	160
% identity	31
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	277350
Contig ID	75947_1.R1011
5'-most EST	LIB3066-055-Q1-K1-E3
Method	BLASTX
NCBI GI	g4531442
BLAST score	415
E value	1.0e-40
Match length	140
% identity	60
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277351
Contig ID	75968_1.R1011
5'-most EST	yyf700349573.h1
Method	BLASTX
NCBI GI	g1857256
BLAST score	279
E value	9.0e-25
Match length	107
% identity	50
NCBI Description	(U75360) MURAZC [Zea mays]

Seq. No.	277352
Contig ID	75976_1.R1011
5'-most EST	uC-zmflb73146h06b1

Seq. No.	277353
Contig ID	75979_1.R1011
5'-most EST	uC-zmroB73015c07b1
Method	BLASTX
NCBI GI	g2183223
BLAST score	765
E value	2.0e-81
Match length	227
% identity	65
NCBI Description	(AF002017) arginine decarboxylase [Dianthus caryophyllus]

Seq. No.	277354
Contig ID	76004_1.R1011
5'-most EST	LIB3066-056-Q1-K1-B5
Method	BLASTX
NCBI GI	g2832677
BLAST score	281
E value	3.0e-25
Match length	145
% identity	46
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277355
Contig ID	76008_1.R1011
5'-most EST	LIB3066-056-Q1-K1-B9
Method	BLASTX
NCBI GI	g2828293
BLAST score	264
E value	5.0e-23
Match length	76
% identity	68
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	277356
Contig ID	76011_1.R1011
5'-most EST	LIB3066-056-Q1-K1-C12
Method	BLASTX
NCBI GI	g2245108
BLAST score	241
E value	4.0e-20
Match length	70
% identity	59
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	277357
Contig ID	76014_1.R1011
5'-most EST	pmx700087437.h1
Method	BLASTX
NCBI GI	g4584539
BLAST score	506
E value	2.0e-51
Match length	160
% identity	62
NCBI Description	(AL049608) extensin-like protein [Arabidopsis thaliana]

Seq. No.	277358
Contig ID	76025_1.R1011
5'-most EST	xmt700260770.h1
Method	BLASTX
NCBI GI	g1669341
BLAST score	345
E value	4.0e-32
Match length	201
% identity	38
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	277359
Contig ID	76026_1.R1011
5'-most EST	wty700170921.h1
Method	BLASTX
NCBI GI	g2880057
BLAST score	220
E value	9.0e-18
Match length	157
% identity	38
NCBI Description	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]

Seq. No.	277360
Contig ID	76038_1.R1011
5'-most EST	uC-zmroB73001a10b1
Method	BLASTX
NCBI GI	g585452
BLAST score	859
E value	1.0e-92
Match length	181
% identity	88
NCBI Description	MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi_1076666_pir__A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor, mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002) precursor of the 59kDa subunit of the mitochondrial NAD+-dependent malic enzyme [Solanum tuberosum]

Seq. No.	277361
Contig ID	76044_1.R1011
5'-most EST	LIB3066-056-Q1-K1-F11

Seq. No.	277362
Contig ID	76071_1.R1011
5'-most EST	LIB3066-056-Q1-K1-H4
Method	BLASTX
NCBI GI	g3337367
BLAST score	290
E value	4.0e-26
Match length	128
% identity	46
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277363
Contig ID	76084_1.R1011
5'-most EST	LIB3137-062-Q1-K1-E12

Seq. No.	277364
Contig ID	76084_2.R1011
5'-most EST	uC-zmflmo17323g05a1

Seq. No.	277365
Contig ID	76099_1.R1011
5'-most EST	qmh700029519.f1
Method	BLASTX
NCBI GI	g2739044
BLAST score	1164
E value	1.0e-128
Match length	312
% identity	69
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No.	277366
Contig ID	76101_1.R1011
5'-most EST	uC-zmflmo17340g08a1

Seq. No.	277367
Contig ID	76110_1.R1011
5'-most EST	tfd700572963.h1

Seq. No.	277368
Contig ID	76118_1.R1011
5'-most EST	uC-zmflb73196b07a2
Method	BLASTX
NCBI GI	g3913804
BLAST score	251
E value	3.0e-21
Match length	62
% identity	85
NCBI Description	HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone [Zea mays]

Seq. No.	277369
Contig ID	76126_1.R1011
5'-most EST	fC-zmfl700343201a5
Method	BLASTX
NCBI GI	g2864613
BLAST score	467
E value	1.0e-46
Match length	188
% identity	49
NCBI Description	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	277370
Contig ID	76143_1.R1011
5'-most EST	LIB3067-027-Q1-K1-E6

Seq. No.	277371
Contig ID	76143_2.R1011
5'-most EST	LIB3069-036-Q1-K1-E4

Seq. No.	277372
Contig ID	76146_1.R1011
5'-most EST	LIB3067-001-Q1-K1-H10

Seq. No.	277373
Contig ID	76149_1.R1011
5'-most EST	uC-zmflmo17099e08b1

Seq. No.	277374
Contig ID	76172_1.R1011
5'-most EST	uC-zmflmo17270a12b1
Method	BLASTX
NCBI GI	g4416302
BLAST score	180
E value	2.0e-28
Match length	81
% identity	76
NCBI Description	(AF105716) copia-type pol polyprotein [Zea mays]

Seq. No. 277375

Contig ID	76178_1.R1011
5'-most EST	LIB3067-002-Q1-K1-C10
Method	BLASTX
NCBI GI	g2829903
BLAST score	378
E value	2.0e-36
Match length	83
% identity	83
NCBI Description	(AC002311) unknown protein [Arabidopsis thaliana]

Seq. No.	277376
Contig ID	76182_1.R1011
5'-most EST	ypc700799447.h1
Method	BLASTX
NCBI GI	g4263722
BLAST score	1302
E value	1.0e-144
Match length	347
% identity	68
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	277377
Contig ID	76185_1.R1011
5'-most EST	LIB3136-013-Q1-K1-D12

Seq. No.	277378
Contig ID	76187_1.R1011
5'-most EST	uC-zmflb73257g05a2

Seq. No.	277379
Contig ID	76190_1.R1011
5'-most EST	dyk700102806.h1
Method	BLASTX
NCBI GI	g2444178
BLAST score	635
E value	1.0e-132
Match length	363
% identity	69
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	277380
Contig ID	76193_1.R1011
5'-most EST	uC-zmflb73008g05b1
Method	BLASTX
NCBI GI	g4567310
BLAST score	303
E value	5.0e-27
Match length	89
% identity	75
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	277381
Contig ID	76209_1.R1011
5'-most EST	LIB3067-002-Q1-K1-F10
Method	BLASTX
NCBI GI	g2651303
BLAST score	293

E value	4.0e-26
Match length	80
% identity	71
NCBI Description	(AC002336) putative potassium transporter [Arabidopsis thaliana]

Seq. No.	277382
Contig ID	76212_1.R1011
5'-most EST	uC-zmflmo17259h11b1

Seq. No.	277383
Contig ID	76264_1.R1011
5'-most EST	LIB3067-058-Q1-K1-D10

Seq. No.	277384
Contig ID	76264_3.R1011
5'-most EST	uC-zmflb73116d09b2

Seq. No.	277385
Contig ID	76280_1.R1011
5'-most EST	ymt700224368.h1

Seq. No.	277386
Contig ID	76300_1.R1011
5'-most EST	LIB3067-005-Q1-K1-E10
Method	BLASTX
NCBI GI	g2583128
BLAST score	260
E value	1.0e-22
Match length	133
% identity	43
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277387
Contig ID	76303_1.R1011
5'-most EST	LIB3067-048-Q1-K1-G7
Method	BLASTX
NCBI GI	g4218120
BLAST score	355
E value	1.0e-33
Match length	103
% identity	59
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	277388
Contig ID	76315_1.R1011
5'-most EST	uC-zmflb73129d04b1

Seq. No.	277389
Contig ID	76341_1.R1011
5'-most EST	LIB3067-005-Q1-K1-A7
Method	BLASTN
NCBI GI	g296593
BLAST score	53
E value	8.0e-21
Match length	182

% identity	89
NCBI Description	H. vulgare pZE40 gene

Seq. No.	277390
Contig ID	76351_1.R1011
5'-most EST	ceu700422546.h1
Method	BLASTX
NCBI GI	g2245086
BLAST score	373
E value	1.0e-35
Match length	173
% identity	42
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277391
Contig ID	76374_1.R1011
5'-most EST	xyt700346286.h1
Method	BLASTX
NCBI GI	g1168493
BLAST score	848
E value	4.0e-91
Match length	212
% identity	78
NCBI Description	ARGINASE >gi_602422 (U15019) arginase [Arabidopsis thaliana] >gi_4325373_gb_AAD17369_ (AF128396) Arabidopsis thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6, E=3.7e-142 N=1) [Arabidopsis thaliana]

Seq. No.	277392
Contig ID	76378_1.R1011
5'-most EST	uC-zmflmo17132e11b1
Method	BLASTX
NCBI GI	g2244840
BLAST score	210
E value	3.0e-16
Match length	126
% identity	41
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277393
Contig ID	76404_1.R1011
5'-most EST	dyk700106178.h1

Seq. No.	277394
Contig ID	76407_1.R1011
5'-most EST	LIB36-021-Q1-E1-E6
Method	BLASTX
NCBI GI	g2281092
BLAST score	202
E value	2.0e-15
Match length	53
% identity	75
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277395
Contig ID	76407_2.R1011
5'-most EST	LIB3069-036-Q1-K1-E3

Method	BLASTX
NCBI GI	g2281092
BLAST score	201
E value	1.0e-15
Match length	53
% identity	75
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277396
Contig ID	76413_1.R1011
5'-most EST	LIB3067-006-Q1-K1-A3

Seq. No.	277397
Contig ID	76422_1.R1011
5'-most EST	uC-zmflb73256f09b1

Seq. No.	277398
Contig ID	76426_1.R1011
5'-most EST	uC-zmflb73098e01b1
Method	BLASTX
NCBI GI	g2213597
BLAST score	841
E value	3.0e-90
Match length	301
% identity	51
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No.	277399
Contig ID	76439_1.R1011
5'-most EST	tzu700203880.h1

Seq. No.	277400
Contig ID	76445_1.R1011
5'-most EST	LIB3067-006-Q1-K1-E2
Method	BLASTX
NCBI GI	g3128185
BLAST score	157
E value	2.0e-10
Match length	103
% identity	42
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	277401
Contig ID	76455_1.R1011
5'-most EST	LIB3067-006-Q1-K1-F12

Seq. No.	277402
Contig ID	76458_1.R1011
5'-most EST	ceu700431476.h1
Method	BLASTX
NCBI GI	g2129825
BLAST score	516
E value	2.0e-52
Match length	113
% identity	89
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	277403
Contig ID	76462_1.R1011
5'-most EST	wty700170214.h1
Method	BLASTX
NCBI GI	g2766448
BLAST score	928
E value	1.0e-100
Match length	215
% identity	81
NCBI Description	(AF029856) cytochrome P450 CYP98A1 [Sorghum bicolor]

Seq. No.	277404
Contig ID	76470_1.R1011
5'-most EST	ntr700073092.h1
Method	BLASTX
NCBI GI	g2982463
BLAST score	413
E value	2.0e-40
Match length	122
% identity	66
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	277405
Contig ID	76475_1.R1011
5'-most EST	fC-zmf1700338620a5
Method	BLASTX
NCBI GI	g1402894
BLAST score	316
E value	6.0e-29
Match length	92
% identity	71
NCBI Description	(X96867) adenine phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	277406
Contig ID	76488_1.R1011
5'-most EST	nbm700476392.h1
Method	BLASTX
NCBI GI	g4567197
BLAST score	230
E value	8.0e-19
Match length	200
% identity	35
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	277407
Contig ID	76502_2.R1011
5'-most EST	LIB3067-007-Q1-K1-C3
Method	BLASTX
NCBI GI	g4262236
BLAST score	203
E value	3.0e-16
Match length	58
% identity	72
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	277408
Contig ID	76539_1.R1011
5'-most EST	uwc700156247.h1

Seq. No.	277409
Contig ID	76539_3.R1011
5'-most EST	LIB3067-007-Q1-K1-H3
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	277410
Contig ID	76540_1.R1011
5'-most EST	LIB3067-007-Q1-K1-H4
Method	BLASTX
NCBI GI	g2894596
BLAST score	256
E value	4.0e-22
Match length	94
% identity	54
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	277411
Contig ID	76543_1.R1011
5'-most EST	LIB3067-007-Q1-K1-H8
Method	BLASTX
NCBI GI	g2618699
BLAST score	345
E value	2.0e-32
Match length	170
% identity	42
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	277412
Contig ID	76582_1.R1011
5'-most EST	mwy700441604.h1

Seq. No.	277413
Contig ID	76583_1.R1011
5'-most EST	uC-zmflmo17171c06b1

Seq. No.	277414
Contig ID	76589_1.R1011
5'-most EST	ymt700223191.h1
Method	BLASTX
NCBI GI	g1931655
BLAST score	395
E value	3.0e-38
Match length	175
% identity	51
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	277415
Contig ID	76590_1.R1011
5'-most EST	LIB3067-008-Q1-K1-E6

Seq. No.	277416
Contig ID	76610_1.R1011
5'-most EST	LIB3067-008-Q1-K1-G4

Seq. No.	277417
Contig ID	76619_1.R1011
5'-most EST	uC-zmflmo17139e09a1

Seq. No.	277418
Contig ID	76619_2.R1011
5'-most EST	LIB3068-051-Q1-K1-H9

Seq. No.	277419
Contig ID	76621_1.R1011
5'-most EST	LIB3067-008-Q1-K1-H4
Method	BLASTX
NCBI GI	g4586053
BLAST score	542
E value	2.0e-55
Match length	144
% identity	61
NCBI Description	(AC007020) putative lacasse [Arabidopsis thaliana]

Seq. No.	277420
Contig ID	76624_1.R1011
5'-most EST	LIB3117-014-Q1-K1-B8
Method	BLASTX
NCBI GI	g1871187
BLAST score	495
E value	5.0e-50
Match length	155
% identity	60
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	277421
Contig ID	76635_1.R1011
5'-most EST	LIB3136-032-Q1-K1-C1
Method	BLASTX
NCBI GI	g1588281
BLAST score	215
E value	8.0e-17
Match length	201
% identity	32
NCBI Description	RING3 protein [Homo sapiens]

Seq. No.	277422
Contig ID	76635_2.R1011
5'-most EST	uC-zmflb73380a04a1

Seq. No.	277423
Contig ID	76635_3.R1011
5'-most EST	yyf700349057.h1

Seq. No.	277424
Contig ID	76639_1.R1011
5'-most EST	dyk700102553.h1
Method	BLASTX
NCBI GI	g2459442
BLAST score	563
E value	1.0e-57
Match length	200
% identity	65
NCBI Description	(AC002332) putative DNA-binding protein PD1 [Arabidopsis thaliana]

Seq. No.	277425
Contig ID	76648_1.R1011
5'-most EST	pmx700090183.h1
Method	BLASTX
NCBI GI	g2707336
BLAST score	947
E value	1.0e-102
Match length	258
% identity	69
NCBI Description	(AF037442) histone acetyltransferase [Arabidopsis thaliana]

Seq. No.	277426
Contig ID	76668_1.R1011
5'-most EST	LIB3067-009-Q1-K1-F8

Seq. No.	277427
Contig ID	76670_1.R1011
5'-most EST	LIB3067-009-Q1-K1-G4

Seq. No.	277428
Contig ID	76671_1.R1011
5'-most EST	LIB3067-009-Q1-K1-G3
Method	BLASTX
NCBI GI	g3360289
BLAST score	1120
E value	1.0e-123
Match length	320
% identity	67
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	277429
Contig ID	76671_2.R1011
5'-most EST	uC-zmf1b73252d06b3
Method	BLASTX
NCBI GI	g3360289
BLAST score	810
E value	8.0e-87
Match length	195
% identity	77
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	277430
Contig ID	76683_1.R1011

5'-most EST	LIB3067-009-Q1-K1-H8
Seq. No.	277431
Contig ID	76684_1.R1011
5'-most EST	LIB3069-040-Q1-K1-E6
Method	BLASTX
NCBI GI	g951166
BLAST score	1473
E value	1.0e-164
Match length	290
% identity	99
NCBI Description	(U31451) invertase [Zea mays]
Seq. No.	277432
Contig ID	76687_1.R1011
5'-most EST	hvj700620216.h1
Method	BLASTX
NCBI GI	g4512713
BLAST score	311
E value	2.0e-28
Match length	158
% identity	45
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.	277433
Contig ID	76691_1.R1011
5'-most EST	LIB3067-010-Q1-K1-A6
Method	BLASTX
NCBI GI	g4490316
BLAST score	283
E value	3.0e-25
Match length	79
% identity	61
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.	277434
Contig ID	76698_1.R1011
5'-most EST	uC-zmflmo17201e07a1
Seq. No.	277435
Contig ID	76700_1.R1011
5'-most EST	wty700164490.h1
Method	BLASTX
NCBI GI	g3834307
BLAST score	514
E value	3.0e-82
Match length	283
% identity	62
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]
Seq. No.	277436
Contig ID	76704_1.R1011
5'-most EST	wyr700237838.h1
Method	BLASTX

NCBI GI	g3121836
BLAST score	222
E value	5.0e-18
Match length	75
% identity	53
NCBI Description	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_2181182_emb_CAA63969_ (X94306) CDP-diacylglycerol synthetase [Arabidopsis thaliana]

Seq. No.	277437
Contig ID	76707_1.R1011
5'-most EST	uC-zmroteosinte053d08b2

Seq. No.	277438
Contig ID	76708_1.R1011
5'-most EST	uC-zmflmo17057f07b1
Method	BLASTX
NCBI GI	g117586
BLAST score	147
E value	5.0e-09
Match length	141
% identity	26
NCBI Description	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS) >gi_627051_pir__A54533 circumsporozoite protein - Plasmodium falciparum (strain T4, Thailand) >gi_160217 (M19752) circumsporozoite protein [Plasmodium falciparum]

Seq. No.	277439
Contig ID	76716_1.R1011
5'-most EST	xsy700213408.h1

Seq. No.	277440
Contig ID	76718_1.R1011
5'-most EST	uC-zmflmo17137g11b1

Seq. No.	277441
Contig ID	76727_1.R1011
5'-most EST	LIB3067-010-Q1-K1-E3
Method	BLASTX
NCBI GI	g4455335
BLAST score	442
E value	7.0e-44
Match length	142
% identity	58
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	277442
Contig ID	76731_1.R1011
5'-most EST	LIB3067-010-Q1-K1-F10

Seq. No.	277443
Contig ID	76738_1.R1011
5'-most EST	LIB3067-011-Q1-K1-F5

Seq. No.	277444
Contig ID	76740_2.R1011
5'-most EST	LIB3067-010-Q1-K1-F9

Seq. No.	277445
Contig ID	76741_1.R1011
5'-most EST	ceu700429954.h1
Method	BLASTX
NCBI GI	g4056468
BLAST score	354
E value	3.0e-33
Match length	154
% identity	44
NCBI Description	(AC005990) Contains similarity to gb_X66426 polygalacturonase from Persea americana and is a member of the signal peptidase family PF_00461 and polygalacturonase family PF_00295. [Arabidopsis thaliana]

Seq. No.	277446
Contig ID	76755_1.R1011
5'-most EST	gct701168807.h1

Seq. No.	277447
Contig ID	76813_1.R1011
5'-most EST	uC-zmflmo17e02b1
Method	BLASTX
NCBI GI	g4249662
BLAST score	1201
E value	1.0e-132
Match length	316
% identity	80
NCBI Description	(AF089810) Altered Response to Gravity [Arabidopsis thaliana]

Seq. No.	277448
Contig ID	76840_1.R1011
5'-most EST	xmt700258740.h1
Method	BLASTX
NCBI GI	g4512618
BLAST score	219
E value	9.0e-18
Match length	75
% identity	52
NCBI Description	(AC004793) Strong similarity to gi_3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb_AF080119 and is a member of the reverse transcriptase family PF_00078

Seq. No.	277449
Contig ID	76841_1.R1011
5'-most EST	LIB3067-013-Q1-K1-D4

Seq. No.	277450
Contig ID	76856_1.R1011
5'-most EST	uwc700155066.h1

Seq. No.	277451

Contig ID	76884_1.R1011
5'-most EST	uC-zmflmo17103h03b1
Method	BLASTX
NCBI GI	g3928097
BLAST score	321
E value	2.0e-29
Match length	157
% identity	46
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	277452
Contig ID	76885_1.R1011
5'-most EST	LIB3067-014-Q1-K1-A1

Seq. No.	277453
Contig ID	76897_1.R1011
5'-most EST	LIB3067-014-Q1-K1-B11

Seq. No.	277454
Contig ID	76900_1.R1011
5'-most EST	gct701173003.h2
Method	BLASTX
NCBI GI	g3757522
BLAST score	361
E value	3.0e-34
Match length	90
% identity	72
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	277455
Contig ID	76908_1.R1011
5'-most EST	uC-zmflB73005c10b1
Method	BLASTX
NCBI GI	g2969887
BLAST score	300
E value	2.0e-27
Match length	65
% identity	83
NCBI Description	(Y16766) sucrose/H+ symporter [Daucus carota] >gi_2969889_emb_CAA76368_ (Y16767) sucrose/H+ symporter [Daucus carota]

Seq. No.	277456
Contig ID	76910_1.R1011
5'-most EST	yyf700350602.h1
Method	BLASTX
NCBI GI	g4544412
BLAST score	266
E value	1.0e-22
Match length	138
% identity	39
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277457
Contig ID	76916_1.R1011
5'-most EST	LIB3067-014-Q1-K1-D4

Method	BLASTX
NCBI GI	g283051
BLAST score	410
E value	3.0e-40
Match length	128
% identity	65
NCBI Description	RNA-directed DNA polymerase (EC 2.7.7.49) - maize transposon (fragment)

Seq. No.	277458
Contig ID	76919_1.R1011
5'-most EST	uC-zmroteosinte062e10b1

Seq. No.	277459
Contig ID	76951_1.R1011
5'-most EST	afb700380910.h1
Method	BLASTX
NCBI GI	g2275213
BLAST score	164
E value	3.0e-11
Match length	33
% identity	85
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277460
Contig ID	76954_1.R1011
5'-most EST	uC-zmflB73010a05b1

Seq. No.	277461
Contig ID	76975_2.R1011
5'-most EST	LIB3067-016-Q1-K1-C4

Seq. No.	277462
Contig ID	76987_1.R1011
5'-most EST	LIB3067-016-Q1-K1-E12

Seq. No.	277463
Contig ID	76995_1.R1011
5'-most EST	LIB3067-016-Q1-K1-F1

Seq. No.	277464
Contig ID	76998_1.R1011
5'-most EST	LIB3067-016-Q1-K1-F3

Seq. No.	277465
Contig ID	77001_1.R1011
5'-most EST	rv1700456019.h1
Method	BLASTX
NCBI GI	g4454031
BLAST score	774
E value	3.0e-82
Match length	219
% identity	68
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	277466
Contig ID	77002_1.R1011

5'-most EST	uC-zmroteosinte077g12b1
Seq. No.	277467
Contig ID	77003_1.R1011
5'-most EST	uC-zmflb73119c09a1
Seq. No.	277468
Contig ID	77032_1.R1011
5'-most EST	LIB3067-017-Q1-K1-B7
Method	BLASTX
NCBI GI	g4206155
BLAST score	152
E value	1.0e-09
Match length	73
% identity	36
NCBI Description	(AF109219) Mcd4p homolog [Homo sapiens]
Seq. No.	277469
Contig ID	77033_1.R1011
5'-most EST	ymt700220981.h1
Method	BLASTX
NCBI GI	g1771162
BLAST score	1507
E value	0.0e+00
Match length	503
% identity	68
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]
Seq. No.	277470
Contig ID	77033_2.R1011
5'-most EST	uC-zmroteosinte030a11b1
Method	BLASTX
NCBI GI	g4219092
BLAST score	491
E value	1.0e-49
Match length	133
% identity	74
NCBI Description	(AF117707) putative copper/zinc superoxide dismutase copper chaperone precursor [Lycopersicon esculentum]
Seq. No.	277471
Contig ID	77062_2.R1011
5'-most EST	LIB3067-038-Q1-K1-E4
Method	BLASTX
NCBI GI	g3337350
BLAST score	240
E value	3.0e-32
Match length	120
% identity	61
NCBI Description	(AC004481) putative permease [Arabidopsis thaliana]
Seq. No.	277472
Contig ID	77069_1.R1011
5'-most EST	xmt700257624.h1
Method	BLASTX

NCBI GI	g3913952
BLAST score	275
E value	3.0e-24
Match length	102
% identity	54
NCBI Description	ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi_2351578 (U82330) adenylate kinase homolog [Prunus armeniaca]

Seq. No.	277473
Contig ID	77071_1.R1011
5'-most EST	uC-zmroteosinte060f09b1
Method	BLASTX
NCBI GI	g2252866
BLAST score	219
E value	3.0e-17
Match length	91
% identity	58
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	277474
Contig ID	77074_1.R1011
5'-most EST	yyf700351868.h1
Method	BLASTX
NCBI GI	g3914191
BLAST score	435
E value	9.0e-43
Match length	214
% identity	11
NCBI Description	UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT) >gi_1931579 (U76557) O-GlcNAc transferase, p110 subunit [Rattus norvegicus]

Seq. No.	277475
Contig ID	77084_1.R1011
5'-most EST	uC-zmflmo17129g04b1

Seq. No.	277476
Contig ID	77099_1.R1011
5'-most EST	uer700579327.h1

Seq. No.	277477
Contig ID	77103_1.R1011
5'-most EST	yyf700350269.h1

Seq. No.	277478
Contig ID	77110_1.R1011
5'-most EST	LIB3067-018-Q1-K1-C3

Seq. No.	277479
Contig ID	77124_1.R1011
5'-most EST	LIB3067-018-Q1-K1-E4
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	7.0e-11

Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	277480
Contig ID	77136_1.R1011
5'-most EST	uC-zmflmo17037g05b1

Seq. No.	277481
Contig ID	77137_1.R1011
5'-most EST	uC-zmroteosinte004a03b1
Method	BLASTX
NCBI GI	g4314388
BLAST score	476
E value	1.0e-47
Match length	183
% identity	55
NCBI Description	(AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277482
Contig ID	77144_1.R1011
5'-most EST	nbm700478055.h1
Method	BLASTX
NCBI GI	g2626753
BLAST score	665
E value	2.0e-82
Match length	254
% identity	64
NCBI Description	(AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No.	277483
Contig ID	77149_1.R1011
5'-most EST	xmt700261310.h1

Seq. No.	277484
Contig ID	77165_1.R1011
5'-most EST	xsy700208767.h1

Seq. No.	277485
Contig ID	77172_1.R1011
5'-most EST	uwc700156106.h2

Seq. No.	277486
Contig ID	77193_1.R1011
5'-most EST	LIB3067-051-Q1-K1-E1

Seq. No.	277487
Contig ID	77203_1.R1011
5'-most EST	LIB3136-025-Q1-K1-E7

Seq. No.	277488
Contig ID	77214_1.R1011
5'-most EST	rvt700552663.h1

Seq. No.	277489
Contig ID	77224_1.R1011
5'-most EST	xsy700208517.h1

Method	BLASTX
NCBI GI	g4008006
BLAST score	257
E value	4.0e-22
Match length	127
% identity	46
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	277490
Contig ID	77238_1.R1011
5'-most EST	LIB3067-020-Q1-K1-B9

Seq. No.	277491
Contig ID	77241_1.R1011
5'-most EST	LIB3067-025-Q1-K1-B12
Method	BLASTN
NCBI GI	g4185305
BLAST score	122
E value	5.0e-62
Match length	308
% identity	89
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	277492
Contig ID	77247_1.R1011
5'-most EST	kem700610883.h1
Method	BLASTX
NCBI GI	g3702121
BLAST score	698
E value	1.0e-73
Match length	221
% identity	68
NCBI Description	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]

Seq. No.	277493
Contig ID	77265_1.R1011
5'-most EST	tzu700201295.h1
Method	BLASTX
NCBI GI	g2829612
BLAST score	289
E value	7.0e-26
Match length	96
% identity	56
NCBI Description	HYPOTHETICAL 30.8 KD PROTEIN SLL0818 >gi_1653197_dbj_BAA18113_ (D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	277494
Contig ID	77270_1.R1011
5'-most EST	LIB3067-021-Q1-K1-F11

Seq. No.	277495

Contig ID	77279_1.R1011
5'-most EST	LIB3067-022-Q1-K1-A1
Method	BLASTX
NCBI GI	g3152587
BLAST score	1038
E value	1.0e-113
Match length	223
% identity	86
NCBI Description	(AC002986) Similar to CREB-binding protein homolog gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No.	277496
Contig ID	77280_1.R1011
5'-most EST	LIB3067-022-Q1-K1-A11

Seq. No.	277497
Contig ID	77283_1.R1011
5'-most EST	uC-zmflMo17002c02b1
Method	BLASTX
NCBI GI	g478740
BLAST score	211
E value	6.0e-17
Match length	67
% identity	69
NCBI Description	phenylalanine ammonia-lyase (EC 4.1.3.5) - rice

Seq. No.	277498
Contig ID	77285_1.R1011
5'-most EST	uC-zmflmo17285b07b1
Method	BLASTX
NCBI GI	g4538973
BLAST score	282
E value	6.0e-25
Match length	109
% identity	56
NCBI Description	(AL049487) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277499
Contig ID	77291_1.R1011
5'-most EST	LIB3067-022-Q1-K1-B12
Method	BLASTX
NCBI GI	g3319342
BLAST score	175
E value	6.0e-22
Match length	104
% identity	56
NCBI Description	(AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

Seq. No.	277500
Contig ID	77295_1.R1011
5'-most EST	uC-zmroteosinte017e10b1
Method	BLASTX
NCBI GI	g134792

BLAST score	313
E value	1.0e-28
Match length	124
% identity	52
NCBI Description	MICROSOMAL SIGNAL PEPTIDASE 21 KD SUBUNIT (SPC21) >gi_89064_pir__A34229 signal peptidase (EC 3.4.99.-) 21K chain - dog >gi_164084 (J05069) signal peptidase 21 kDa subunit [Canis familiaris]

Seq. No.	277501
Contig ID	77295_3.R1011
5'-most EST	dyk700103108.h1
Method	BLASTX
NCBI GI	g3320104
BLAST score	431
E value	2.0e-45
Match length	104
% identity	87
NCBI Description	(AJ007366) calcium-dependent protein kinase [Zea mays]

Seq. No.	277502
Contig ID	77299_1.R1011
5'-most EST	tzu700204672.h1
Method	BLASTX
NCBI GI	g1769907
BLAST score	462
E value	3.0e-46
Match length	134
% identity	60
NCBI Description	(X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]

Seq. No.	277503
Contig ID	77306_1.R1011
5'-most EST	LIB3067-022-Q1-K1-C6
Method	BLASTX
NCBI GI	g115504
BLAST score	291
E value	6.0e-26
Match length	149
% identity	43
NCBI Description	CALMODULIN >gi_71691_pir__MCAS calmodulin - Emericella nidulans >gi_1363900_pir__JC4216 calmodulin - Aspergillus oryzae >gi_168031 (J05545) calmodulin [Emericella nidulans] >gi_521146 (U12505) calmodulin [Ajellomyces capsulatus] >gi_541650_dbj_BAA07920_ (D44468) calmodulin [Aspergillus oryzae] >gi_3342062 (AF072882) calmodulin [Ajellomyces capsulatus]

Seq. No.	277504
Contig ID	77312_1.R1011
5'-most EST	uC-zmflmo17041h09b1
Method	BLASTX
NCBI GI	g2444178
BLAST score	652
E value	2.0e-68
Match length	168

% identity	75
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	277505
Contig ID	77318_1.R1011
5'-most EST	gwl700613139.h1

Seq. No.	277506
Contig ID	77342_1.R1011
5'-most EST	xdb700340187.h1

Seq. No.	277507
Contig ID	77343_1.R1011
5'-most EST	uC-zmflb73174b03b1
Method	BLASTN
NCBI GI	g6598431
BLAST score	36
E value	2.0e-10
Match length	68
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	277508
Contig ID	77343_2.R1011
5'-most EST	uC-zmflb73006a04a1

Seq. No.	277509
Contig ID	77343_3.R1011
5'-most EST	LIB3067-022-Q1-K1-G11

Seq. No.	277510
Contig ID	77360_1.R1011
5'-most EST	uC-zmflmo17307e10b1

Seq. No.	277511
Contig ID	77377_1.R1011
5'-most EST	uC-zmflb73278d03a2
Method	BLASTX
NCBI GI	g3269296
BLAST score	173
E value	2.0e-12
Match length	58
% identity	53
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	277512
Contig ID	77379_1.R1011
5'-most EST	uC-zmflmo17421g08a1

Seq. No.	277513
Contig ID	77386_1.R1011
5'-most EST	LIB3067-023-Q1-K1-C4
Method	BLASTX
NCBI GI	g2598227
BLAST score	361
E value	3.0e-34

Match length	119
% identity	64
NCBI Description	(AJ222585) AT-hook protein 1 [Arabidopsis thaliana]

Seq. No.	277514
Contig ID	77392_1.R1011
5'-most EST	hbs701182009.h1
Method	BLASTX
NCBI GI	g4337192
BLAST score	223
E value	7.0e-18
Match length	46
% identity	80
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277515
Contig ID	77398_1.R1011
5'-most EST	LIB3069-006-Q1-K1-F3
Method	BLASTX
NCBI GI	g4507805
BLAST score	275
E value	3.0e-28
Match length	217
% identity	36
NCBI Description	uncoupling protein 2 (mitochondrial, proton carrier) >gi_1857278 (U76367) uncoupling protein-2 [Homo sapiens]

Seq. No.	277516
Contig ID	77405_1.R1011
5'-most EST	uC-zmroteosinte040d10b1

Seq. No.	277517
Contig ID	77417_1.R1011
5'-most EST	LIB3117-015-Q1-K1-C6
Method	BLASTN
NCBI GI	g2826899
BLAST score	78
E value	1.0e-35
Match length	230
% identity	83
NCBI Description	Oryza sativa mRNA for DNA polymerase alpha catalytic subunit, complete cds

Seq. No.	277518
Contig ID	77418_1.R1011
5'-most EST	LIB3067-023-Q1-K1-F3
Method	BLASTX
NCBI GI	g2129753
BLAST score	368
E value	1.0e-38
Match length	124
% identity	67
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	277519

Contig ID	77421_1.R1011
5'-most EST	fdz701162939.h1
Seq. No.	277520
Contig ID	77425_1.R1011
5'-most EST	LIB83-009-Q1-E1-A9
Seq. No.	277521
Contig ID	77427_1.R1011
5'-most EST	hbs701183568.h1
Seq. No.	277522
Contig ID	77427_2.R1011
5'-most EST	hvj700619926.h1
Seq. No.	277523
Contig ID	77435_1.R1011
5'-most EST	LIB3069-043-Q1-K1-E11
Method	BLASTX
NCBI GI	g2961384
BLAST score	451
E value	1.0e-44
Match length	144
% identity	56
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]
Seq. No.	277524
Contig ID	77435_2.R1011
5'-most EST	uC-zmflb73004f12a1
Method	BLASTX
NCBI GI	g2961384
BLAST score	162
E value	4.0e-11
Match length	60
% identity	47
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]
Seq. No.	277525
Contig ID	77442_1.R1011
5'-most EST	uC-zmflb73221f04a2
Seq. No.	277526
Contig ID	77442_2.R1011
5'-most EST	uC-zmflb73217f04b2
Seq. No.	277527
Contig ID	77454_1.R1011
5'-most EST	LIB3067-025-Q1-K1-A9
Seq. No.	277528
Contig ID	77460_1.R1011
5'-most EST	LIB3069-015-Q1-K1-F1
Seq. No.	277529
Contig ID	77460_2.R1011

5'-most EST	nbm700476843.h1
Seq. No.	277530
Contig ID	77462_1.R1011
5'-most EST	LIB3067-025-Q1-K1-B5
Method	BLASTX
NCBI GI	g2827621
BLAST score	323
E value	9.0e-30
Match length	113
% identity	50
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]
Seq. No.	277531
Contig ID	77493_1.R1011
5'-most EST	cat700019972.r1
Method	BLASTX
NCBI GI	g3193290
BLAST score	563
E value	1.0e-57
Match length	212
% identity	53
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido
Seq. No.	277532
Contig ID	77512_1.R1011
5'-most EST	uC-zmrob73017d08a1
Seq. No.	277533
Contig ID	77512_3.R1011
5'-most EST	LIB3067-025-Q1-K1-G11
Seq. No.	277534
Contig ID	77523_1.R1011
5'-most EST	wty700171946.h1
Seq. No.	277535
Contig ID	77537_1.R1011
5'-most EST	LIB83-014-Q1-E1-E10
Seq. No.	277536
Contig ID	77542_1.R1011
5'-most EST	LIB3067-026-Q1-K1-A8
Method	BLASTX
NCBI GI	g1019946
BLAST score	472
E value	4.0e-47
Match length	98
% identity	88
NCBI Description	(U37060) ascorbate peroxidase [Gossypium hirsutum]
Seq. No.	277537
Contig ID	77544_1.R1011

5'-most EST	LIB3067-026-Q1-K1-B1
Seq. No.	277538
Contig ID	77545_1.R1011
5'-most EST	uC-zmroteosinte036h04b1
Method	BLASTX
NCBI GI	g4388717
BLAST score	404
E value	3.0e-39
Match length	172
% identity	48
NCBI Description	(AC006413) putative nuclear phosphoprotein (contains multiple TPR repeats prosite:QDOC50005) [Arabidopsis thaliana]
Seq. No.	277539
Contig ID	77549_1.R1011
5'-most EST	LIB3067-026-Q1-K1-B3
Seq. No.	277540
Contig ID	77556_1.R1011
5'-most EST	uC-zmflb73305f12a1
Seq. No.	277541
Contig ID	77601_1.R1011
5'-most EST	LIB3067-026-Q1-K1-G8
Seq. No.	277542
Contig ID	77602_1.R1011
5'-most EST	LIB3067-026-Q1-K1-H1
Method	BLASTX
NCBI GI	g3292824
BLAST score	256
E value	2.0e-42
Match length	172
% identity	56
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	277543
Contig ID	77619_1.R1011
5'-most EST	xsy700208320.h1
Seq. No.	277544
Contig ID	77626_1.R1011
5'-most EST	LIB3067-027-Q1-K1-B4
Method	BLASTX
NCBI GI	g3482975
BLAST score	299
E value	1.0e-26
Match length	266
% identity	30
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]
Seq. No.	277545
Contig ID	77635_1.R1011
5'-most EST	uC-zmflb73003c10b1

Seq. No.	277546
Contig ID	77636_1.R1011
5'-most EST	nbm700475570.h1
Method	BLASTX
NCBI GI	g4539291
BLAST score	155
E value	4.0e-10
Match length	102
% identity	37
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	277547
Contig ID	77641_1.R1011
5'-most EST	clt700043709.f1
Method	BLASTX
NCBI GI	g2660677
BLAST score	517
E value	2.0e-52
Match length	181
% identity	54
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	277548
Contig ID	77647_1.R1011
5'-most EST	LIB3136-034-Q1-K1-B10
Method	BLASTX
NCBI GI	g4510342
BLAST score	573
E value	7.0e-59
Match length	163
% identity	69
NCBI Description	(AC006921) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	277549
Contig ID	77653_1.R1011
5'-most EST	LIB3069-026-Q1-K1-F10

Seq. No.	277550
Contig ID	77664_1.R1011
5'-most EST	rvt700548836.h1
Method	BLASTX
NCBI GI	g1091678
BLAST score	221
E value	1.0e-17
Match length	84
% identity	45
NCBI Description	activator-like transposable element [Pennisetum glaucum]

Seq. No.	277551
Contig ID	77668_1.R1011
5'-most EST	LIB3067-027-Q1-K1-F6
Method	BLASTX
NCBI GI	g1717871
BLAST score	230
E value	7.0e-27
Match length	136

% identity	53
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15) >gi_1078006_pir__S53974 hypothetical protein YMR304w - yeast (Saccharomyces cerevisiae) >gi_798946_emb_CAA89137_ (Z49212) unknown [Saccharomyces cerevisiae]

Seq. No.	277552
Contig ID	77684_1.R1011
5'-most EST	LIB3069-003-Q1-K1-C6
Method	BLASTX
NCBI GI	g3834306
BLAST score	173
E value	4.0e-12
Match length	44
% identity	68
NCBI Description	(AC005679) EST gb_R65024 comes from this gene. [Arabidopsis thaliana]

Seq. No.	277553
Contig ID	77685_1.R1011
5'-most EST	LIB3067-027-Q1-K1-H2

Seq. No.	277554
Contig ID	77710_1.R1011
5'-most EST	LIB3067-028-Q1-K1-B9

Seq. No.	277555
Contig ID	77712_1.R1011
5'-most EST	wty700170628.h1

Seq. No.	277556
Contig ID	77715_1.R1011
5'-most EST	LIB3067-028-Q1-K1-C2
Method	BLASTX
NCBI GI	g3252870
BLAST score	352
E value	2.0e-33
Match length	119
% identity	57
NCBI Description	(AF033537) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	277557
Contig ID	77717_1.R1011
5'-most EST	yyf700350014.h1
Method	BLASTX
NCBI GI	g4455294
BLAST score	164
E value	3.0e-23
Match length	163
% identity	21
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	277558
Contig ID	77727_1.R1011
5'-most EST	LIB3067-028-Q1-K1-D2

Method	BLASTX
NCBI GI	g4249386
BLAST score	283
E value	3.0e-25
Match length	150
% identity	45
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	277559
Contig ID	77734_1.R1011
5'-most EST	LIB3067-028-Q1-K1-E1

Seq. No.	277560
Contig ID	77735_1.R1011
5'-most EST	LIB3067-028-Q1-K1-E10

Seq. No.	277561
Contig ID	77751_1.R1011
5'-most EST	LIB3067-028-Q1-K1-F8
Method	BLASTX
NCBI GI	g4309741
BLAST score	572
E value	6.0e-59
Match length	161
% identity	67
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277562
Contig ID	77761_1.R1011
5'-most EST	LIB3067-028-Q1-K1-G6

Seq. No.	277563
Contig ID	77766_1.R1011
5'-most EST	wyr700241259.h1
Method	BLASTX
NCBI GI	g625973
BLAST score	162
E value	1.0e-10
Match length	103
% identity	42
NCBI Description	disease resistance protein RPS2 - Arabidopsis thaliana >gi_548086 (U14158) RPS2 [Arabidopsis thaliana] >gi_549979 (U12860) RPS2 [Arabidopsis thaliana] >gi_4538938_emb_CAB39674.1_ (AL049483) disease resistance protein RPS2 [Arabidopsis thaliana]

Seq. No.	277564
Contig ID	77768_1.R1011
5'-most EST	qmh700026975.f1
Method	BLASTX
NCBI GI	g2618699
BLAST score	253
E value	2.0e-21
Match length	122
% identity	38

NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.	277565
Contig ID	77796_1.R1011
5'-most EST	cjh700194364.h1
Seq. No.	277566
Contig ID	77802_1.R1011
5'-most EST	LIB3070-009-Q1-N1-A4
Seq. No.	277567
Contig ID	77806_1.R1011
5'-most EST	LIB3067-029-Q1-K1-D12
Method	BLASTX
NCBI GI	g138603
BLAST score	687
E value	1.0e-72
Match length	142
% identity	93
NCBI Description	REGULATORY PROTEIN VIVIPAROUS-1 >gi_100922_pir__A40024 regulatory protein Viviparous-1 - maize >gi_168605 (M60214) viviparous-1 [Zea mays]
Seq. No.	277568
Contig ID	77808_1.R1011
5'-most EST	LIB3069-049-Q1-K1-A7
Seq. No.	277569
Contig ID	77815_1.R1011
5'-most EST	uC-zmflmo17321a10b1
Seq. No.	277570
Contig ID	77818_1.R1011
5'-most EST	hbs701182986.h1
Seq. No.	277571
Contig ID	77837_1.R1011
5'-most EST	LIB3067-029-Q1-K1-G11
Seq. No.	277572
Contig ID	77841_1.R1011
5'-most EST	clt700042003.f1
Method	BLASTX
NCBI GI	g4006881
BLAST score	644
E value	5.0e-67
Match length	226
% identity	60
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]
Seq. No.	277573
Contig ID	77855_1.R1011
5'-most EST	LIB3067-029-Q1-K1-H6
Method	BLASTX
NCBI GI	g2454182
BLAST score	520
E value	6.0e-53

Match length	111
% identity	86
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	277574
Contig ID	77871_1.R1011
5'-most EST	uC-zmflMo17084b08b1
Method	BLASTX
NCBI GI	g4559358
BLAST score	171
E value	6.0e-12
Match length	55
% identity	55
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	277575
Contig ID	77872_1.R1011
5'-most EST	LIB3067-030-Q1-K1-B4

Seq. No.	277576
Contig ID	77882_1.R1011
5'-most EST	wty700163884.h1
Method	BLASTX
NCBI GI	g1843628
BLAST score	748
E value	3.0e-79
Match length	231
% identity	62
NCBI Description	(U88061) SNF5 homolog BSH [Arabidopsis thaliana]

Seq. No.	277577
Contig ID	77891_1.R1011
5'-most EST	LIB3067-030-Q1-K1-D4

Seq. No.	277578
Contig ID	77900_1.R1011
5'-most EST	xyt700345088.h1
Method	BLASTX
NCBI GI	g4467126
BLAST score	255
E value	8.0e-22
Match length	173
% identity	31
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	277579
Contig ID	77906_1.R1011
5'-most EST	xdb700339218.h1
Method	BLASTX
NCBI GI	g4469023
BLAST score	859
E value	2.0e-92
Match length	248
% identity	70

NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	277580
Contig ID	77908_1.R1011
5'-most EST	LIB3067-030-Q1-K1-F1
Method	BLASTX
NCBI GI	g4587570
BLAST score	190
E value	3.0e-14
Match length	176
% identity	30
NCBI Description	(AC006550) Strong similarity to gi_2244833 centromere protein homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from this gene
Seq. No.	277581
Contig ID	77927_1.R1011
5'-most EST	uC-zmflMo17082d03b1
Seq. No.	277582
Contig ID	77935_1.R1011
5'-most EST	uC-zmflb73051a02b1
Method	BLASTX
NCBI GI	g3075397
BLAST score	156
E value	5.0e-10
Match length	111
% identity	38
NCBI Description	(AC004484) hypothetical protein [Arabidopsis thaliana]
Seq. No.	277583
Contig ID	77935_5.R1011
5'-most EST	nbm700475701.h1
Seq. No.	277584
Contig ID	77941_1.R1011
5'-most EST	dyk700106668.h1
Method	BLASTX
NCBI GI	g4056483
BLAST score	145
E value	5.0e-09
Match length	91
% identity	40
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.	277585
Contig ID	77942_1.R1011
5'-most EST	LIB3117-012-Q1-K1-A11
Seq. No.	277586
Contig ID	77943_1.R1011
5'-most EST	uC-zmflb73137d05b1
Method	BLASTX
NCBI GI	g3228666
BLAST score	310
E value	2.0e-28

Match length	102
% identity	56
NCBI Description	(AF069987) nitrilase 1 [Homo sapiens] >gi_3242978 (AF069984) nitrilase homolog 1 [Homo sapiens]

Seq. No.	277587
Contig ID	77944_1.R1011
5'-most EST	wyr700243546.h1
Method	BLASTX
NCBI GI	g3341695
BLAST score	232
E value	5.0e-19
Match length	146
% identity	41
NCBI Description	(AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	277588
Contig ID	77944_2.R1011
5'-most EST	LIB3067-031-Q1-K1-A7
Method	BLASTX
NCBI GI	g3341695
BLAST score	352
E value	4.0e-33
Match length	87
% identity	69
NCBI Description	(AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	277589
Contig ID	77944_3.R1011
5'-most EST	pwr700452650.h1
Method	BLASTX
NCBI GI	g3341695
BLAST score	158
E value	1.0e-19
Match length	105
% identity	56
NCBI Description	(AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	277590
Contig ID	77973_2.R1011
5'-most EST	cjh700193746.h1

Seq. No.	277591
Contig ID	77999_1.R1011
5'-most EST	uC-zmflmo17198e11b1
Method	BLASTX
NCBI GI	g3063698
BLAST score	609
E value	5.0e-63
Match length	285
% identity	49
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 277592

Contig ID 78010_1.R1011
5'-most EST LIB3067-031-Q1-K1-H4

Seq. No. 277593
Contig ID 78016_1.R1011
5'-most EST uC-zmflmo17067d12b1
Method BLASTX
NCBI GI g4584429
BLAST score 282
E value 7.0e-25
Match length 167
% identity 41
NCBI Description (AJ237751) aquaglyceroporin [Nicotiana tabacum]

Seq. No. 277594
Contig ID 78023_1.R1011
5'-most EST ymt700221029.h1
Method BLASTX
NCBI GI g2677836
BLAST score 177
E value 2.0e-12
Match length 187
% identity 29
NCBI Description (AF020788) SEL-10 [Caenorhabditis elegans]

Seq. No. 277595
Contig ID 78024_1.R1011
5'-most EST uC-zmflb73013c10b1

Seq. No. 277596
Contig ID 78026_1.R1011
5'-most EST wty700168484.h1

Seq. No. 277597
Contig ID 78026_2.R1011
5'-most EST cat700021222.r1

Seq. No. 277598
Contig ID 78037_1.R1011
5'-most EST LIB3067-032-Q1-K1-C10

Seq. No. 277599
Contig ID 78038_1.R1011
5'-most EST LIB3067-032-Q1-K1-C11

Seq. No. 277600
Contig ID 78041_1.R1011
5'-most EST LIB3067-032-Q1-K1-C3

Seq. No. 277601
Contig ID 78047_1.R1011
5'-most EST kem700612280.h1

Seq. No. 277602
Contig ID 78081_1.R1011
5'-most EST clt700045352.f1
Method BLASTX

NCBI GI	g4646233
BLAST score	310
E value	2.0e-28
Match length	149
% identity	46
NCBI Description	(AC007266) putative G9a protein [Arabidopsis thaliana]

Seq. No.	277603
Contig ID	78082_2.R1011
5'-most EST	LIB3069-033-Q1-K1-G8
Method	BLASTX
NCBI GI	g2655008
BLAST score	353
E value	2.0e-33
Match length	119
% identity	64
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	277604
Contig ID	78100_1.R1011
5'-most EST	uC-zmflmo17359f02a1

Seq. No.	277605
Contig ID	78109_1.R1011
5'-most EST	LIB3067-033-Q1-K1-B12
Method	BLASTX
NCBI GI	g4337175
BLAST score	341
E value	5.0e-32
Match length	114
% identity	52
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	277606
Contig ID	78124_1.R1011
5'-most EST	xjt700094275.h1
Method	BLASTX
NCBI GI	g4314358
BLAST score	500
E value	1.0e-50
Match length	158
% identity	65
NCBI Description	(AC006340) putative kinesin heavy chain protein [Arabidopsis thaliana]

Seq. No.	277607
Contig ID	78128_1.R1011
5'-most EST	LIB36-018-Q1-E1-F1

Seq. No.	277608
Contig ID	78130_1.R1011
5'-most EST	gct701177151.h1

Seq. No.	277609
Contig ID	78130_2.R1011
5'-most EST	hbs701180766.h1
Seq. No.	277610
Contig ID	78135_1.R1011
5'-most EST	uC-zmflmo17322e05b1
Seq. No.	277611
Contig ID	78137_1.R1011
5'-most EST	LIB3067-033-Q1-K1-E4
Seq. No.	277612
Contig ID	78143_1.R1011
5'-most EST	uC-zmroB73015d05b1
Seq. No.	277613
Contig ID	78143_2.R1011
5'-most EST	uC-zmflmo17421d12a1
Seq. No.	277614
Contig ID	78160_1.R1011
5'-most EST	LIB3067-033-Q1-K1-H11
Seq. No.	277615
Contig ID	78160_2.R1011
5'-most EST	tfd700571426.h1
Method	BLASTX
NCBI GI	g3250697
BLAST score	510
E value	1.0e-51
Match length	119
% identity	82
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]
Seq. No.	277616
Contig ID	78163_1.R1011
5'-most EST	LIB3067-033-Q1-K1-H4
Seq. No.	277617
Contig ID	78169_1.R1011
5'-most EST	LIB3067-034-Q1-K1-A1
Method	BLASTN
NCBI GI	g940880
BLAST score	366
E value	0.0e+00
Match length	543
% identity	94
NCBI Description	Z.mays zag2 gene
Seq. No.	277618
Contig ID	78180_1.R1011
5'-most EST	LIB3067-034-Q1-K1-B12
Method	BLASTX
NCBI GI	g729135
BLAST score	364
E value	2.0e-34

Match length	160
% identity	45
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No.	277619
Contig ID	78182_1.R1011
5'-most EST	LIB3067-034-Q1-K1-B3

Seq. No.	277620
Contig ID	78186_1.R1011
5'-most EST	yyf700351051.h1
Method	BLASTX
NCBI GI	g3876465
BLAST score	337
E value	3.0e-31
Match length	87
% identity	72
NCBI Description	(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E (SW:P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene;

Seq. No.	277621
Contig ID	78186_2.R1011
5'-most EST	tzu700205471.h1
Method	BLASTX
NCBI GI	g3876465
BLAST score	299
E value	3.0e-27
Match length	75
% identity	76
NCBI Description	(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E (SW:P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene;

Seq. No.	277622
Contig ID	78188_1.R1011
5'-most EST	tzu700203464.h1
Method	BLASTX
NCBI GI	g3688193
BLAST score	420
E value	9.0e-41
Match length	188
% identity	47
NCBI Description	(AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]

Seq. No.	277623
Contig ID	78189_1.R1011
5'-most EST	vmj700053753.r1
Method	BLASTX
NCBI GI	g2760606
BLAST score	725

E value	1.0e-76
Match length	154
% identity	87
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	277624
Contig ID	78193_1.R1011
5'-most EST	gwl700617069.h1

Seq. No.	277625
Contig ID	78195_1.R1011
5'-most EST	fdz701159503.h1
Method	BLASTX
NCBI GI	g2950395
BLAST score	194
E value	5.0e-31
Match length	85
% identity	81
NCBI Description	(AJ224847) oxidoreductase [Zea mays]

Seq. No.	277626
Contig ID	78206_1.R1011
5'-most EST	LIB3067-034-Q1-K1-D8
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	277627
Contig ID	78221_1.R1011
5'-most EST	uC-zmflmo17300c09b1

Seq. No.	277628
Contig ID	78231_1.R1011
5'-most EST	LIB3067-034-Q1-K1-G8

Seq. No.	277629
Contig ID	78234_1.R1011
5'-most EST	LIB3067-034-Q1-K1-H11
Method	BLASTX
NCBI GI	g2760830
BLAST score	355
E value	2.0e-33
Match length	232
% identity	42
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 277630

Contig ID	78250_1.R1011
5'-most EST	fC-zmf170034302Of4
Method	BLASTX
NCBI GI	g3947448
BLAST score	335
E value	8.0e-34
Match length	168
% identity	46
NCBI Description	(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi

Seq. No.	277631
Contig ID	78251_1.R1011
5'-most EST	LIB3067-035-Q1-K1-B11

Seq. No.	277632
Contig ID	78251_2.R1011
5'-most EST	ntr700075656.h1

Seq. No.	277633
Contig ID	78257_1.R1011
5'-most EST	LIB3067-035-Q1-K1-B8
Method	BLASTX
NCBI GI	g4539401
BLAST score	208
E value	2.0e-16
Match length	88
% identity	47
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	277634
Contig ID	78258_1.R1011
5'-most EST	uC-zmflmo17127b10b1
Method	BLASTX
NCBI GI	g4558567
BLAST score	202
E value	4.0e-15
Match length	123
% identity	36
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277635
Contig ID	78260_1.R1011
5'-most EST	xyt700346916.h1
Method	BLASTX
NCBI GI	g1931639
BLAST score	240
E value	5.0e-20
Match length	84
% identity	52

NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No. 277636
Contig ID 78286_1.R1011
5'-most EST uC-zmromo17088e08a1

Seq. No. 277637
Contig ID 78318_1.R1011
5'-most EST uC-zmflmo17103e10a1

Seq. No. 277638
Contig ID 78321_1.R1011
5'-most EST kem700611784.h1
Method BLASTX
NCBI GI g2252860
BLAST score 202
E value 3.0e-15
Match length 241
% identity 32
NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No. 277639
Contig ID 78322_1.R1011
5'-most EST LIB3067-036-Q1-K1-A9
Method BLASTX
NCBI GI g2864625
BLAST score 450
E value 2.0e-44
Match length 159
% identity 56
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 277640
Contig ID 78331_1.R1011
5'-most EST LIB3067-036-Q1-K1-C11

Seq. No. 277641
Contig ID 78332_1.R1011
5'-most EST LIB3067-036-Q1-K1-C12

Seq. No. 277642
Contig ID 78341_1.R1011
5'-most EST LIB3067-036-Q1-K1-D10
Method BLASTX
NCBI GI g1707043
BLAST score 145
E value 8.0e-09
Match length 73
% identity 42
NCBI Description (U80446) coded for by C. elegans cDNA yk172e6.3; coded for by C. elegans cDNA yk158f7.3; coded for by C. elegans cDNA yk158f7.5; coded for by C. elegans cDNA yk172e6.5 [Caenorhabditis elegans]

Seq. No. 277643
Contig ID 78355_1.R1011
5'-most EST uC-zmflmo17367g01a1

Seq. No.	277644
Contig ID	78365_1.R1011
5'-most EST	LIB3067-036-Q1-K1-G11

Seq. No.	277645
Contig ID	78377_1.R1011
5'-most EST	uC-zmflb73048d01b1

Seq. No.	277646
Contig ID	78386_1.R1011
5'-most EST	nbm700477042.h1
Method	BLASTX
NCBI GI	g4567250
BLAST score	223
E value	1.0e-17
Match length	140
% identity	36
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277647
Contig ID	78403_1.R1011
5'-most EST	LIB3067-037-Q1-K1-C3

Seq. No.	277648
Contig ID	78410_1.R1011
5'-most EST	LIB3067-037-Q1-K1-D11

Seq. No.	277649
Contig ID	78424_1.R1011
5'-most EST	LIB3067-037-Q1-K1-E9

Seq. No.	277650
Contig ID	78427_1.R1011
5'-most EST	uC-zmflb73306c05a1
Method	BLASTX
NCBI GI	g4454051
BLAST score	718
E value	6.0e-76
Match length	224
% identity	58
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	277651
Contig ID	78444_1.R1011
5'-most EST	LIB3067-037-Q1-K1-G7
Method	BLASTX
NCBI GI	g3033388
BLAST score	206
E value	4.0e-16
Match length	50
% identity	62
NCBI Description	(AC004238) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277652
Contig ID	78446_1.R1011

5'-most EST	wyr700242987.h1
Method	BLASTX
NCBI GI	g2239260
BLAST score	642
E value	3.0e-67
Match length	124
% identity	100
NCBI Description	(Y13734) cinnamoyl CoA reductase [Zea mays]

Seq. No.	277653
Contig ID	78451_1.R1011
5'-most EST	uC-zmroteosinte068c01b1
Method	BLASTX
NCBI GI	g2760317
BLAST score	519
E value	1.0e-52
Match length	121
% identity	83
NCBI Description	(AC002130) F1N21.1 [Arabidopsis thaliana]

Seq. No.	277654
Contig ID	78452_1.R1011
5'-most EST	LIB3067-037-Q1-K1-H4
Method	BLASTX
NCBI GI	g1168470
BLAST score	561
E value	1.0e-57
Match length	128
% identity	79
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	277655
Contig ID	78454_1.R1011
5'-most EST	uwc700155548.h1

Seq. No.	277656
Contig ID	78456_1.R1011
5'-most EST	uC-zmrob73022d12a1
Method	BLASTX
NCBI GI	g2654226
BLAST score	488
E value	8.0e-49
Match length	157
% identity	59
NCBI Description	(AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis thaliana]

Seq. No.	277657
Contig ID	78461_1.R1011
5'-most EST	pmx700083984.h1

Seq. No.	277658
Contig ID	78461_2.R1011

5'-most EST	LIB3067-039-Q1-K1-F8
Seq. No.	277659
Contig ID	78475_1.R1011
5'-most EST	tzu700202544.h1
Method	BLASTX
NCBI GI	g2130141
BLAST score	827
E value	5.0e-95
Match length	255
% identity	63
NCBI Description	mudrA protein - maize transposon MuDR >gi_540581 (M76978) mudrA [Zea mays] >gi_595816 (U14597) mudrA gene product [Zea mays]
Seq. No.	277660
Contig ID	78480_1.R1011
5'-most EST	LIB3067-038-Q1-K1-C2
Seq. No.	277661
Contig ID	78495_1.R1011
5'-most EST	uC-zmflb73022d03a1
Method	BLASTX
NCBI GI	g4467159
BLAST score	205
E value	6.0e-16
Match length	56
% identity	62
NCBI Description	(AL035540) hypothetical protein [Arabidopsis thaliana]
Seq. No.	277662
Contig ID	78514_1.R1011
5'-most EST	LIB3067-038-Q1-K1-G10
Seq. No.	277663
Contig ID	78520_1.R1011
5'-most EST	gct701167685.h1
Method	BLASTX
NCBI GI	g2244989
BLAST score	462
E value	5.0e-46
Match length	132
% identity	69
NCBI Description	(Z97340) strong similarity to naringenin 3-dioxygenase [Arabidopsis thaliana]
Seq. No.	277664
Contig ID	78522_1.R1011
5'-most EST	uC-zmflmo17024c01a1
Seq. No.	277665
Contig ID	78528_1.R1011
5'-most EST	LIB3067-038-Q1-K1-H5
Seq. No.	277666
Contig ID	78529_1.R1011
5'-most EST	LIB3137-002-Q1-K1-C4

09564705 - 040600

Seq. No.	277667
Contig ID	78530_1.R1011
5'-most EST	LIB3067-038-Q1-K1-H7
Method	BLASTX
NCBI GI	g4567271
BLAST score	247
E value	7.0e-21
Match length	86
% identity	62
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	277668
Contig ID	78550_1.R1011
5'-most EST	uwc700155876.h1

Seq. No.	277669
Contig ID	78552_1.R1011
5'-most EST	wty700170347.h1

Seq. No.	277670
Contig ID	78575_1.R1011
5'-most EST	vux700158048.h1
Method	BLASTX
NCBI GI	g4539345
BLAST score	401
E value	5.0e-39
Match length	128
% identity	63
NCBI Description	(AL035539) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277671
Contig ID	78578_1.R1011
5'-most EST	LIB3067-039-Q1-K1-F3

Seq. No.	277672
Contig ID	78580_2.R1011
5'-most EST	uwc700151202.h1
Method	BLASTX
NCBI GI	g99899
BLAST score	686
E value	3.0e-74
Match length	173
% identity	84
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) largest chain (isoform C) - soybean (fragment) >gi_18736_emb_CAA36736_ (X52495) DNA-directed RNA polymerase [Glycine max]

Seq. No.	277673
Contig ID	78613_1.R1011
5'-most EST	uC-zmflmo17134g02b1

Seq. No.	277674
Contig ID	78625_1.R1011
5'-most EST	pmx700086536.h1

Seq. No.	277675

Contig ID 78633_1.R1011
5'-most EST uC-zmflmo17278c01b1

Seq. No. 277676
Contig ID 78633_2.R1011
5'-most EST uC-zmflb731205e10a1

Seq. No. 277677
Contig ID 78641_1.R1011
5'-most EST LIB3067-040-Q1-K1-D5

Seq. No. 277678
Contig ID 78664_1.R1011
5'-most EST LIB3067-040-Q1-K1-F7

Seq. No. 277679
Contig ID 78683_1.R1011
5'-most EST xsy700211205.h1
Method BLASTX
NCBI GI g4587595
BLAST score 467
E value 2.0e-46
Match length 233
% identity 40
NCBI Description (AC006951) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No. 277680
Contig ID 78684_1.R1011
5'-most EST LIB3067-040-Q1-K1-H3

Seq. No. 277681
Contig ID 78687_1.R1011
5'-most EST uC-zmflmo17126h08b1
Method BLASTX
NCBI GI g3785995
BLAST score 527
E value 4.0e-53
Match length 154
% identity 74
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 277682
Contig ID 78688_1.R1011
5'-most EST wyr700240647.h1
Method BLASTX
NCBI GI g857395
BLAST score 288
E value 1.0e-25
Match length 87
% identity 64
NCBI Description (D50869) mitotic cyclin a2-type [Glycine max]

Seq. No. 277683
Contig ID 78715_1.R1011
5'-most EST uC-zmflmo17309g06b1
Method BLASTX

NCBI GI g2129636
BLAST score 319
E value 4.0e-29
Match length 172
% identity 41
NCBI Description lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No. 277684
Contig ID 78715_2.R1011
5'-most EST uC-zmflmo17309h12b1
Method BLASTX
NCBI GI g4314378
BLAST score 385
E value 7.0e-37
Match length 187
% identity 37
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 277685
Contig ID 78715_3.R1011
5'-most EST uC-zmflb73292g09b1

Seq. No. 277686
Contig ID 78716_1.R1011
5'-most EST pmx700086652.h1
Method BLASTX
NCBI GI g1854378
BLAST score 1061
E value 1.0e-162
Match length 341
% identity 84
NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No. 277687
Contig ID 78721_1.R1011
5'-most EST LIB3067-042-Q1-K1-E5

Seq. No. 277688
Contig ID 78721_2.R1011
5'-most EST uC-zmflb73031f11a1

Seq. No. 277689
Contig ID 78724_1.R1011
5'-most EST uC-zmflb73201c10b1
Method BLASTX
NCBI GI g2062167
BLAST score 398
E value 2.0e-38
Match length 122
% identity 59
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 277690
Contig ID 78730_1.R1011

5'-most EST	fdz701165304.h1
Seq. No.	277691
Contig ID	78733_1.R1011
5'-most EST	uC-zmflmo17317h07a1
Seq. No.	277692
Contig ID	78733_2.R1011
5'-most EST	uwc700154577.h1
Seq. No.	277693
Contig ID	78746_1.R1011
5'-most EST	LIB3067-042-Q1-K1-H6
Seq. No.	277694
Contig ID	78759_1.R1011
5'-most EST	uC-zmrob73061e04a1
Method	BLASTX
NCBI GI	g4101574
BLAST score	253
E value	2.0e-21
Match length	186
% identity	32
NCBI Description	(AF004876) 54TMp [Homo sapiens]
Seq. No.	277695
Contig ID	78762_1.R1011
5'-most EST	LIB3067-043-Q1-K1-B12
Seq. No.	277696
Contig ID	78766_1.R1011
5'-most EST	LIB3067-043-Q1-K1-B6
Method	BLASTX
NCBI GI	g3540182
BLAST score	222
E value	9.0e-33
Match length	162
% identity	54
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.	277697
Contig ID	78772_1.R1011
5'-most EST	LIB3067-043-Q1-K1-C2
Method	BLASTX
NCBI GI	g2462756
BLAST score	189
E value	2.0e-14
Match length	112
% identity	40
NCBI Description	(AC002292) putative receptor kinase [Arabidopsis thaliana]
Seq. No.	277698
Contig ID	78775_1.R1011
5'-most EST	uC-zmrob73006b01a1
Method	BLASTX
NCBI GI	g3360291
BLAST score	380

E value	1.0e-36
Match length	87
% identity	85
NCBI Description	(AF023165) leucine-rich repeat transmembrane protein kinase 2 [Zea mays]

Seq. No.	277699
Contig ID	78792_1.R1011
5'-most EST	LIB3069-051-Q1-K1-D4

Seq. No.	277700
Contig ID	78793_1.R1011
5'-most EST	uC-zmflb73194f07b2

Seq. No.	277701
Contig ID	78793_2.R1011
5'-most EST	uC-zmflb73285a10b1

Seq. No.	277702
Contig ID	78797_1.R1011
5'-most EST	uC-zmflb73079f04b2
Method	BLASTX
NCBI GI	g3169178
BLAST score	272
E value	9.0e-24
Match length	132
% identity	42
NCBI Description	(AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277703
Contig ID	78797_2.R1011
5'-most EST	LIB3067-043-Q1-K1-F1
Method	BLASTX
NCBI GI	g4468984
BLAST score	380
E value	3.0e-36
Match length	269
% identity	36
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	277704
Contig ID	78807_1.R1011
5'-most EST	pwr700450254.h1

Seq. No.	277705
Contig ID	78810_1.R1011
5'-most EST	uC-zmroteosinte120c08b2
Method	BLASTX
NCBI GI	g3540189
BLAST score	155
E value	6.0e-10
Match length	94
% identity	37
NCBI Description	(AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	277706
Contig ID	78811_1.R1011

5'-most EST	pmx700090275.h1
Method	BLASTX
NCBI GI	g4218120
BLAST score	447
E value	2.0e-56
Match length	161
% identity	64
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	277707
Contig ID	78812_1.R1011
5'-most EST	tzu700206852.h1
Method	BLASTX
NCBI GI	g1935909
BLAST score	874
E value	2.0e-94
Match length	177
% identity	93
NCBI Description	(U77345) lethal leaf-spot 1 [Zea mays]

Seq. No.	277708
Contig ID	78819_1.R1011
5'-most EST	uC-zmroteosinte034e09b1
Method	BLASTX
NCBI GI	g100535
BLAST score	289
E value	1.0e-25
Match length	79
% identity	68
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	277709
Contig ID	78819_2.R1011
5'-most EST	uC-zmflmo17221e05b1
Method	BLASTX
NCBI GI	g100535
BLAST score	281
E value	1.0e-24
Match length	77
% identity	69
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	277710
Contig ID	78827_1.R1011
5'-most EST	tfd700570868.h1
Method	BLASTX
NCBI GI	g2809237
BLAST score	483
E value	2.0e-48
Match length	206
% identity	51
NCBI Description	(AC002560) F21B7.6 [Arabidopsis thaliana]

Seq. No.	277711
Contig ID	78832_1.R1011
5'-most EST	LIB3067-044-Q1-K1-A9

Seq. No.	277712
Contig ID	78841_1.R1011
5'-most EST	uC-zmflmo17352g05a1

Seq. No.	277713
Contig ID	78890_1.R1011
5'-most EST	LIB3067-044-Q1-K1-G7

Seq. No.	277714
Contig ID	78904_1.R1011
5'-most EST	uC-zmflmo17171a03b1

Seq. No.	277715
Contig ID	78904_2.R1011
5'-most EST	dyk700102735.h1

Seq. No.	277716
Contig ID	78916_1.R1011
5'-most EST	uC-zmflmo17086e02a1
Method	BLASTX
NCBI GI	g4309738
BLAST score	570
E value	2.0e-58
Match length	192
% identity	60
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	277717
Contig ID	78916_2.R1011
5'-most EST	uC-zmflmo17309g11b1
Method	BLASTX
NCBI GI	g2829918
BLAST score	609
E value	5.0e-63
Match length	245
% identity	48
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	277718
Contig ID	78924_1.R1011
5'-most EST	nbm700470178.h1
Method	BLASTX
NCBI GI	g2342730
BLAST score	166
E value	2.0e-11
Match length	92
% identity	48
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277719
Contig ID	78932_1.R1011

5'-most EST	LIB3067-045-Q1-K1-C8
Seq. No.	277720
Contig ID	78935_1.R1011
5'-most EST	zla700380263.h1
Method	BLASTX
NCBI GI	g4220474
BLAST score	519
E value	2.0e-52
Match length	258
% identity	49
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]
Seq. No.	277721
Contig ID	78948_1.R1011
5'-most EST	ntr700075973.h1
Method	BLASTX
NCBI GI	g1561579
BLAST score	506
E value	5.0e-51
Match length	160
% identity	59
NCBI Description	(Y08253) spermine synthase 2 [Datura stramonium]
Seq. No.	277722
Contig ID	78949_1.R1011
5'-most EST	uC-zmflmo17393a03a1
Method	BLASTX
NCBI GI	g987693
BLAST score	185
E value	9.0e-14
Match length	39
% identity	92
NCBI Description	(D16685) lactate dehydrogenase [Oryza sativa]
Seq. No.	277723
Contig ID	78950_1.R1011
5'-most EST	LIB3067-045-Q1-K1-E3
Seq. No.	277724
Contig ID	78967_1.R1011
5'-most EST	rvt700548427.h1
Method	BLASTX
NCBI GI	g2352492
BLAST score	481
E value	2.0e-48
Match length	140
% identity	66
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]
Seq. No.	277725
Contig ID	78975_1.R1011
5'-most EST	LIB3067-045-Q1-K1-G6

Seq. No.	277726
Contig ID	78978_1.R1011
5'-most EST	LIB3067-045-Q1-K1-G9
Method	BLASTN
NCBI GI	g902585
BLAST score	42
E value	5.0e-14
Match length	66
% identity	91
NCBI Description	Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No.	277727
Contig ID	78981_1.R1011
5'-most EST	ntr700072966.h1
Method	BLASTX
NCBI GI	g2760323
BLAST score	603
E value	2.0e-62
Match length	151
% identity	68
NCBI Description	(AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No.	277728
Contig ID	78987_1.R1011
5'-most EST	uC-zmflb73012g01b1
Method	BLASTX
NCBI GI	g2462834
BLAST score	206
E value	5.0e-16
Match length	144
% identity	31
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277729
Contig ID	79002_1.R1011
5'-most EST	pmx700084118.h1

Seq. No.	277730
Contig ID	79007_1.R1011
5'-most EST	LIB3067-046-Q1-K1-C10

Seq. No.	277731
Contig ID	79009_1.R1011
5'-most EST	uC-zmflmo17420c04a1

Seq. No.	277732
Contig ID	79017_1.R1011
5'-most EST	tzu700207043.h1
Method	BLASTX
NCBI GI	g3702321
BLAST score	748
E value	2.0e-79
Match length	185
% identity	74
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No.	277733
Contig ID	79017_2.R1011
5'-most EST	LIB3069-054-Q1-K1-B11
Method	BLASTX
NCBI GI	g2494896
BLAST score	460
E value	4.0e-46
Match length	92
% identity	88
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi_2129749_pir__S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis thaliana >gi_1036803 (U36765) TGF-beta receptor interacting protein 1 homolog [Arabidopsis thaliana]

Seq. No.	277734
Contig ID	79019_1.R1011
5'-most EST	LIB3067-046-Q1-K1-D4

Seq. No.	277735
Contig ID	79031_1.R1011
5'-most EST	LIB3067-046-Q1-K1-E8

Seq. No.	277736
Contig ID	79032_1.R1011
5'-most EST	LIB3068-017-Q1-K1-G3
Method	BLASTX
NCBI GI	g3399767
BLAST score	182
E value	3.0e-13
Match length	87
% identity	44
NCBI Description	(U76298) uclacyanin I [Arabidopsis thaliana] >gi_3831466 (AC005700) uclacyanin I [Arabidopsis thaliana]

Seq. No.	277737
Contig ID	79035_1.R1011
5'-most EST	uC-zmroteosinte006c10b1
Method	BLASTX
NCBI GI	g4531434
BLAST score	349
E value	1.0e-32
Match length	177
% identity	41
NCBI Description	(AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	277738
Contig ID	79046_1.R1011
5'-most EST	uC-zmroteosinte066f11b1

Seq. No.	277739
Contig ID	79051_1.R1011
5'-most EST	LIB3067-046-Q1-K1-G8

Seq. No.	277740
Contig ID	79052_1.R1011

5'-most EST	LIB3067-046-Q1-K1-G9
Seq. No.	277741
Contig ID	79054_1.R1011
5'-most EST	tfd700574629.h1
Method	BLASTX
NCBI GI	g2245679
BLAST score	195
E value	1.0e-14
Match length	128
% identity	35
NCBI Description	(AF006655) V-ATPase C subunit [Drosophila melanogaster]
Seq. No.	277742
Contig ID	79061_1.R1011
5'-most EST	cyk700048978.f1
Seq. No.	277743
Contig ID	79075_1.R1011
5'-most EST	LIB3067-047-Q1-K1-A8
Method	BLASTN
NCBI GI	g1777706
BLAST score	220
E value	1.0e-120
Match length	224
% identity	100
NCBI Description	Zea mays 18S ribosomal RNA gene, partial sequence
Seq. No.	277744
Contig ID	79075_2.R1011
5'-most EST	uC-zmflmo17210d11a1
Method	BLASTN
NCBI GI	g1777706
BLAST score	169
E value	4.0e-90
Match length	169
% identity	100
NCBI Description	Zea mays 18S ribosomal RNA gene, partial sequence
Seq. No.	277745
Contig ID	79084_1.R1011
5'-most EST	xsy700213881.h1
Seq. No.	277746
Contig ID	79090_1.R1011
5'-most EST	LIB3067-047-Q1-K1-C12
Method	BLASTX
NCBI GI	g1149595
BLAST score	255
E value	6.0e-22
Match length	111
% identity	46
NCBI Description	(Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase [Brassica napus]
Seq. No.	277747
Contig ID	79099_1.R1011

5'-most EST	LIB3067-047-Q1-K1-D10
Method	BLASTX
NCBI GI	g4557491
BLAST score	460
E value	1.0e-45
Match length	207
% identity	43
NCBI Description	cleavage stimulation factor subunit 1 >gi_461848_sp_Q05048_CST1_HUMAN CLEAVAGE STIMULATION FACTOR, 50 KD SUBUNIT (CSTF 50 KD SUBUNIT) (CF-1 50 KD SUBUNIT) >gi_345801_pir__A45142 cleavage stimulation factor 50K chain - human >gi_180599 (L02547) cleavage stimulation factor [Homo sapiens]

Seq. No.	277748
Contig ID	79104_1.R1011
5'-most EST	zuv700355918.h1
Method	BLASTX
NCBI GI	g1695882
BLAST score	642
E value	8.0e-67
Match length	254
% identity	55
NCBI Description	(U63743) mitotic centromere-associated kinesin [Homo sapiens]

Seq. No.	277749
Contig ID	79139_1.R1011
5'-most EST	LIB3067-047-Q1-K1-H1
Method	BLASTX
NCBI GI	g2462834
BLAST score	157
E value	3.0e-10
Match length	98
% identity	36
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277750
Contig ID	79141_1.R1011
5'-most EST	tzu700201160.h1

Seq. No.	277751
Contig ID	79144_1.R1011
5'-most EST	pmx700088476.h1
Method	BLASTX
NCBI GI	g2738996
BLAST score	378
E value	4.0e-36
Match length	164
% identity	49
NCBI Description	(AF022457) CYP97B2p [Glycine max]

Seq. No.	277752
Contig ID	79144_2.R1011
5'-most EST	uC-zmflMo17005h12b1

Seq. No.	277753

Contig ID	79144_3.R1011
5'-most EST	fwa70̄0101827.h1
Method	BLASTX
NCBI GI	g2738996
BLAST score	183
E value	3.0e-13
Match length	90
% identity	46
NCBI Description	(AF022457) CYP97B2p [Glycine max]

Seq. No.	277754
Contig ID	79161_1.R1011
5'-most EST	uC-zmflmo17047d08a1

Seq. No.	277755
Contig ID	79162_1.R1011
5'-most EST	LIB3067-048-Q1-K1-B10
Method	BLASTX
NCBI GI	g4468980
BLAST score	867
E value	2.0e-93
Match length	198
% identity	79
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	277756
Contig ID	79170_1.R1011
5'-most EST	LIB3067-048-Q1-K1-B8

Seq. No.	277757
Contig ID	79173_1.R1011
5'-most EST	uC-zmflMo17092a12b1

Seq. No.	277758
Contig ID	79177_1.R1011
5'-most EST	cat70̄020611.r1
Method	BLASTX
NCBI GI	g2801448
BLAST score	210
E value	1.0e-16
Match length	39
% identity	92
NCBI Description	(AF028341) ubiquitin-conjugating enzyme 18 [Arabidopsis thaliana]

Seq. No.	277759
Contig ID	79191_1.R1011
5'-most EST	LIB3136-010-Q1-K1-H6
Method	BLASTX
NCBI GI	g3540180
BLAST score	359
E value	6.0e-41
Match length	221
% identity	48
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 277760

Contig ID	79195_1.R1011
5'-most EST	LIB3067-048-Q1-K1-E9
Seq. No.	277761
Contig ID	79209_1.R1011
5'-most EST	LIB3068-041-Q1-K1-H4
Seq. No.	277762
Contig ID	79215_1.R1011
5'-most EST	LIB3067-048-Q1-K1-H11
Seq. No.	277763
Contig ID	79230_1.R1011
5'-most EST	uC-zmflb73230d01b2
Method	BLASTX
NCBI GI	g4375829
BLAST score	599
E value	4.0e-62
Match length	182
% identity	66
NCBI Description	(AJ011977) RNA-directed RNA polymerase [Arabidopsis thaliana]
Seq. No.	277764
Contig ID	79231_1.R1011
5'-most EST	wty700166434.h1
Seq. No.	277765
Contig ID	79232_1.R1011
5'-most EST	uC-zmflmo17267f02a1
Method	BLASTX
NCBI GI	g3786324
BLAST score	158
E value	2.0e-10
Match length	62
% identity	48
NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]
Seq. No.	277766
Contig ID	79238_1.R1011
5'-most EST	LIB3067-049-Q1-K1-B4
Method	BLASTX
NCBI GI	g3877894
BLAST score	153
E value	6.0e-10
Match length	75
% identity	47
NCBI Description	(Z75954) Similarity to klebsiella oxytoca E-1 enzyme (TREMBL ID G401712) [Caenorhabditis elegans]
Seq. No.	277767
Contig ID	79243_1.R1011
5'-most EST	yyf700352251.h1
Seq. No.	277768
Contig ID	79252_1.R1011

5'-most EST	uC-zmflb73086f12b2
Seq. No.	277769
Contig ID	79256_1.R1011
5'-most EST	LIB3067-049-Q1-K1-D12
Seq. No.	277770
Contig ID	79256_2.R1011
5'-most EST	uC-zmflmo17248f09b1
Method	BLASTX
NCBI GI	g4544403
BLAST score	188
E value	9.0e-14
Match length	78
% identity	42
NCBI Description	(AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]
Seq. No.	277771
Contig ID	79259_1.R1011
5'-most EST	tzu700205089.h1
Method	BLASTX
NCBI GI	g2335097
BLAST score	1060
E value	1.0e-116
Match length	274
% identity	75
NCBI Description	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	277772
Contig ID	79260_1.R1011
5'-most EST	fwa700098618.h1
Method	BLASTX
NCBI GI	g1848214
BLAST score	293
E value	3.0e-26
Match length	74
% identity	74
NCBI Description	(Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]
Seq. No.	277773
Contig ID	79260_2.R1011
5'-most EST	ceu700429688.h1
Method	BLASTX
NCBI GI	g1848214
BLAST score	240
E value	1.0e-20
Match length	64
% identity	70
NCBI Description	(Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]
Seq. No.	277774
Contig ID	79262_1.R1011
5'-most EST	LIB3067-049-Q1-K1-D8

Method	BLASTX
NCBI GI	g3643249
BLAST score	282
E value	5.0e-25
Match length	111
% identity	51
NCBI Description	(AF090143) thaumatin-like protein precursor Mdtl1 [Malus domestica]

Seq. No.	277775
Contig ID	79291_1.R1011
5'-most EST	yyf700351493.h1

Seq. No.	277776
Contig ID	79298_1.R1011
5'-most EST	LIB3067-049-Q1-K1-H12

Seq. No.	277777
Contig ID	79310_1.R1011
5'-most EST	LIB3067-050-Q1-K1-A3
Method	BLASTX
NCBI GI	g1351662
BLAST score	280
E value	1.0e-24
Match length	180
% identity	37
NCBI Description	HYPOTHETICAL 74.4 KD PROTEIN C30D11.09 IN CHROMOSOME I >gi_2130408_pir__S62567 hypothetical protein SPAC30D11.09 - fission yeast (Schizosaccharomyces pombe) >gi_1065896_emb_CAA91895_ (Z67961) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	277778
Contig ID	79315_1.R1011
5'-most EST	LIB3137-013-Q1-K1-F4
Method	BLASTX
NCBI GI	g4490300
BLAST score	972
E value	1.0e-105
Match length	275
% identity	61
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	277779
Contig ID	79318_1.R1011
5'-most EST	LIB3067-050-Q1-K1-B2

Seq. No.	277780
Contig ID	79339_1.R1011
5'-most EST	LIB3068-006-Q1-K1-G11

Seq. No.	277781
Contig ID	79342_1.R1011
5'-most EST	yyf700351951.h1
Method	BLASTX
NCBI GI	g2979557
BLAST score	609

E value	2.0e-63
Match length	166
% identity	67
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana] >gi_3386625 (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277782
Contig ID	79349_1.R1011
5'-most EST	uC-zmroteosinte109c03b3
Method	BLASTX
NCBI GI	g3176690
BLAST score	830
E value	1.0e-101
Match length	225
% identity	86
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	277783
Contig ID	79349_2.R1011
5'-most EST	uC-zmflmo17134g09b1
Method	BLASTX
NCBI GI	g3176690
BLAST score	430
E value	1.0e-42
Match length	105
% identity	75
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	277784
Contig ID	79366_1.R1011
5'-most EST	LIB3067-050-Q1-K1-G7
Method	BLASTX
NCBI GI	g4432864
BLAST score	547
E value	8.0e-56
Match length	146
% identity	72
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277785
Contig ID	79368_1.R1011
5'-most EST	LIB3067-050-Q1-K1-G9
Method	BLASTX
NCBI GI	g3800951
BLAST score	293
E value	3.0e-26
Match length	166
% identity	45
NCBI Description	(AF100657) No definition line found [Caenorhabditis elegans]

Seq. No.	277786

Contig ID	79370_1.R1011
5'-most EST	tzu700204395.h1
Seq. No.	277787
Contig ID	79370_2.R1011
5'-most EST	LIB3067-050-Q1-K1-H10
Seq. No.	277788
Contig ID	79372_1.R1011
5'-most EST	LIB3067-050-Q1-K1-H12
Method	BLASTX
NCBI GI	g4586576
BLAST score	316
E value	3.0e-29
Match length	82
% identity	71
NCBI Description	(AB024992) multidrug resistance protein [Cicer arietinum]
Seq. No.	277789
Contig ID	79390_1.R1011
5'-most EST	tfd700575991.h1
Seq. No.	277790
Contig ID	79393_1.R1011
5'-most EST	wty700163009.h1
Method	BLASTX
NCBI GI	g3834307
BLAST score	259
E value	3.0e-22
Match length	63
% identity	73
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]
Seq. No.	277791
Contig ID	79393_2.R1011
5'-most EST	clt700042140.f1
Method	BLASTX
NCBI GI	g3834307
BLAST score	746
E value	4.0e-79
Match length	186
% identity	73
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]
Seq. No.	277792
Contig ID	79434_1.R1011
5'-most EST	ntr700073277.h1
Seq. No.	277793
Contig ID	79440_1.R1011
5'-most EST	LIB3067-051-Q1-K1-G7

Method	BLASTX
NCBI GI	g2492612
BLAST score	420
E value	2.0e-41
Match length	106
% identity	75
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi_1076734_pir__S52712 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) - rice >gi_755773_emb_CAA59749_ (X85747) 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) [Oryza sativa]

Seq. No.	277794
Contig ID	79440_2.R1011
5'-most EST	xsy700214293.h1
Method	BLASTX
NCBI GI	g2492612
BLAST score	241
E value	3.0e-20
Match length	60
% identity	75
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi_1076734_pir__S52712 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) - rice >gi_755773_emb_CAA59749_ (X85747) 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) [Oryza sativa]

Seq. No.	277795
Contig ID	79443_1.R1011
5'-most EST	LIB3067-051-Q1-K1-H1
Method	BLASTX
NCBI GI	g1931655
BLAST score	256
E value	7.0e-22
Match length	110
% identity	50
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	277796
Contig ID	79449_1.R1011
5'-most EST	uC-zmrob73055e05b1

Seq. No.	277797
Contig ID	79457_1.R1011
5'-most EST	LIB3067-052-Q1-K1-A4
Method	BLASTX
NCBI GI	g542070
BLAST score	187
E value	1.0e-13
Match length	63
% identity	56
NCBI Description	cytochrome P450 77A1 - eggplant

Seq. No.	277798
Contig ID	79469_1.R1011

5'-most EST	uC-zmflb73216c07b2
Method	BLASTX
NCBI GI	g4538943
BLAST score	385
E value	5.0e-37
Match length	89
% identity	79
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	277799
Contig ID	79473_1.R1011
5'-most EST	uC-zmflm017233a02b1
Method	BLASTX
NCBI GI	g3915070
BLAST score	561
E value	2.0e-57
Match length	128
% identity	86
NCBI Description	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) >gi_1841704_emb_CAB06653_ (Z85984) histidyl tRNA Synthetase [Oryza sativa]

Seq. No.	277800
Contig ID	79475_1.R1011
5'-most EST	LIB3067-052-Q1-K1-C11

Seq. No.	277801
Contig ID	79482_1.R1011
5'-most EST	LIB3137-062-Q1-K1-A8

Seq. No.	277802
Contig ID	79493_1.R1011
5'-most EST	LIB3067-052-Q1-K1-D9
Method	BLASTX
NCBI GI	g3914370
BLAST score	386
E value	4.0e-48
Match length	146
% identity	62
NCBI Description	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) >gi_419754_pir__S31083 glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) precursor - Arabidopsis thaliana >gi_217845_dbj_BAA00575_ (D00672) glycerol-3-phosphate acyltransferase [Arabidopsis thaliana] >gi_217847_dbj_BAA00576_ (D00673) glycerol-3-phosphate acyltransferase precursor [Arabidopsis thaliana]

Seq. No.	277803
Contig ID	79500_1.R1011
5'-most EST	uC-zmroteosinte063h03b1
Method	BLASTX
NCBI GI	g141435
BLAST score	259
E value	4.0e-22
Match length	118
% identity	42

NCBI Description	DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_98360_pir__E37854 folate biosynthesis protein 1 (sul 3' region) - Bacillus subtilis >gi_143411 (M34053) ORF1 [Bacillus subtilis] >gi_467467_dbj_BAA05313_ (D26185) unknown [Bacillus subtilis] >gi_2632345_emb_CAB11854_ (Z99104) dihydroneopterin aldolase [Bacillus subtilis]

Seq. No.	277804
Contig ID	79504_1.R1011
5'-most EST	LIB84-026-Q1-E1-H9

Seq. No.	277805
Contig ID	79506_1.R1011
5'-most EST	xyt700346895.h1

Seq. No.	277806
Contig ID	79506_2.R1011
5'-most EST	LIB84-003-Q1-E1-F3

Seq. No.	277807
Contig ID	79509_1.R1011
5'-most EST	uC-zmflmo17322g09b1
Method	BLASTX
NCBI GI	g1619952
BLAST score	162
E value	2.0e-10
Match length	185
% identity	30
NCBI Description	(U72149) putative RNA helicase [Saccharomyces cerevisiae]

Seq. No.	277808
Contig ID	79520_1.R1011
5'-most EST	uC-zmflm017093c06b1

Seq. No.	277809
Contig ID	79520_2.R1011
5'-most EST	pmx700091162.h1

Seq. No.	277810
Contig ID	79553_1.R1011
5'-most EST	uC-zmroteosinte021e06b1
Method	BLASTX
NCBI GI	g435942
BLAST score	1024
E value	1.0e-111
Match length	312
% identity	64
NCBI Description	(U04295) DNA-binding factor of bZIP class [Oryza sativa]

Seq. No.	277811
Contig ID	79592_1.R1011
5'-most EST	uC-zmrob73079f01b1
Method	BLASTX
NCBI GI	g3036810
BLAST score	337
E value	2.0e-31
Match length	98

% identity	64
NCBI Description	(AL022373) putative Myc-type transcription factor [Arabidopsis thaliana]

Seq. No.	277812
Contig ID	79596_1.R1011
5'-most EST	LIB3118-003-Q1-K1-B2
Method	BLASTX
NCBI GI	g4240305
BLAST score	181
E value	6.0e-13
Match length	162
% identity	35
NCBI Description	(AB020715) KIAA0908 protein [Homo sapiens]

Seq. No.	277813
Contig ID	79600_1.R1011
5'-most EST	LIB3067-053-Q1-K1-G8

Seq. No.	277814
Contig ID	79607_1.R1011
5'-most EST	uC-zmroteosinte033a03b1
Method	BLASTX
NCBI GI	g4191785
BLAST score	206
E value	7.0e-16
Match length	85
% identity	47
NCBI Description	(AC005917) putative hydrolase [Arabidopsis thaliana]

Seq. No.	277815
Contig ID	79609_1.R1011
5'-most EST	LIB3067-053-Q1-K1-H7
Method	BLASTX
NCBI GI	g1491776
BLAST score	572
E value	7.0e-59
Match length	181
% identity	60
NCBI Description	(M37636) cationic peroxidase [Arachis hypogaea]

Seq. No.	277816
Contig ID	79610_1.R1011
5'-most EST	LIB3067-053-Q1-K1-H9

Seq. No.	277817
Contig ID	79627_1.R1011
5'-most EST	LIB83-008-Q1-E1-C6
Method	BLASTN
NCBI GI	g563633
BLAST score	90
E value	9.0e-43
Match length	102
% identity	97
NCBI Description	Z.mays (MU141B) mRNA for U14 small nucleolar RNA

Seq. No.	277818

Contig ID	79639_1.R1011
5'-most EST	LIB3067-054-Q1-K1-D11

Seq. No.	277819
Contig ID	79640_1.R1011
5'-most EST	uC-zmflmo17079b06b1

Seq. No.	277820
Contig ID	79651_1.R1011
5'-most EST	ceu700432173.h1
Method	BLASTX
NCBI GI	g119723
BLAST score	282
E value	6.0e-25
Match length	87
% identity	61
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsis thaliana >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase [Arabidopsis thaliana]

Seq. No.	277821
Contig ID	79655_1.R1011
5'-most EST	uC-zmflb73192b11b1
Method	BLASTX
NCBI GI	g4432814
BLAST score	173
E value	5.0e-12
Match length	134
% identity	31
NCBI Description	(AC006593) unknown protein [Arabidopsis thaliana]

Seq. No.	277822
Contig ID	79670_1.R1011
5'-most EST	LIB3067-054-Q1-K1-G7

Seq. No.	277823
Contig ID	79671_1.R1011
5'-most EST	LIB3067-054-Q1-K1-G8

Seq. No.	277824
Contig ID	79673_1.R1011
5'-most EST	uC-zmflmo17179d12a1

Seq. No.	277825
Contig ID	79704_1.R1011
5'-most EST	uC-zmflb73359f09a2
Method	BLASTX
NCBI GI	g3047080
BLAST score	323
E value	8.0e-30
Match length	108
% identity	61
NCBI Description	(AF058914) contains similarity to Arabidopsis thaliana DNA-damage-repair/tolerance resistance protein DRT111

(SW:P42698) [Arabidopsis thaliana]

Seq. No.	277826
Contig ID	79704_2.R1011
5'-most EST	ceu700425091.h1
Method	BLASTX
NCBI GI	g3047080
BLAST score	186
E value	3.0e-28
Match length	88
% identity	70
NCBI Description	(AF058914) contains similarity to Arabidopsis thaliana DNA-damage-repair/tolerance resistance protein DRT111 (SW:P42698) [Arabidopsis thaliana]

Seq. No.	277827
Contig ID	79723_1.R1011
5'-most EST	uC-zmflmo17035f11b1

Seq. No.	277828
Contig ID	79724_1.R1011
5'-most EST	LIB3067-055-Q1-K1-D6
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	8.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	277829
Contig ID	79735_1.R1011
5'-most EST	wty700167208.h1

Seq. No.	277830
Contig ID	79748_1.R1011
5'-most EST	fdz701161380.h1
Method	BLASTX
NCBI GI	g4530126
BLAST score	349
E value	5.0e-33
Match length	130
% identity	57
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	277831
Contig ID	79758_1.R1011
5'-most EST	uC-zmflmo17179h09a1

Seq. No.	277832
Contig ID	79762_1.R1011
5'-most EST	LIB3067-056-Q1-K1-A9
Method	BLASTX
NCBI GI	g3249084
BLAST score	395
E value	6.0e-38

Match length	190
% identity	14
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	277833
Contig ID	79770_1.R1011
5'-most EST	LIB3067-056-Q1-K1-B6
Method	BLASTX
NCBI GI	g4580990
BLAST score	368
E value	5.0e-35
Match length	204
% identity	35
NCBI Description	(AF120335) putative transposase [Arabidopsis thaliana]

Seq. No.	277834
Contig ID	79778_1.R1011
5'-most EST	pmx700084405.h1
Method	BLASTX
NCBI GI	g2213600
BLAST score	333
E value	1.0e-30
Match length	161
% identity	43
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	277835
Contig ID	79803_1.R1011
5'-most EST	ceu700426675.h1

Seq. No.	277836
Contig ID	79806_1.R1011
5'-most EST	uC-zmflb73067c03b1
Method	BLASTX
NCBI GI	g4249382
BLAST score	1215
E value	1.0e-134
Match length	300
% identity	75
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	277837
Contig ID	79824_1.R1011
5'-most EST	gwl700616408.h1

Seq. No.	277838
Contig ID	79825_1.R1011
5'-most EST	LIB3067-056-Q1-K1-G8
Method	BLASTX
NCBI GI	g4588012
BLAST score	192
E value	2.0e-14
Match length	173

% identity	34
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	277839
Contig ID	79831_1.R1011
5'-most EST	uC-zmflmo17123f12a1

Seq. No.	277840
Contig ID	79832_1.R1011
5'-most EST	ceu700433651.h1

Seq. No.	277841
Contig ID	79836_1.R1011
5'-most EST	LIB3067-057-Q1-K1-A1
Method	BLASTX
NCBI GI	g1001227
BLAST score	359
E value	2.0e-33
Match length	137
% identity	46
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	277842
Contig ID	79875_1.R1011
5'-most EST	uC-zmflmo17079d03b1
Method	BLASTX
NCBI GI	g3600032
BLAST score	147
E value	4.0e-09
Match length	43
% identity	63
NCBI Description	(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	277843
Contig ID	79878_1.R1011
5'-most EST	LIB3067-057-Q1-K1-E2
Method	BLASTX
NCBI GI	g2661179
BLAST score	372
E value	1.0e-35
Match length	155
% identity	50
NCBI Description	(U80984) AtZW10 [Arabidopsis thaliana]

Seq. No.	277844
Contig ID	79881_1.R1011
5'-most EST	tzu700203354.h1

Seq. No.	277845
Contig ID	79915_1.R1011
5'-most EST	LIB3067-058-Q1-K1-B10

Seq. No.	277846
Contig ID	79917_1.R1011

5'-most EST	LIB3067-058-Q1-K1-B12
Method	BLASTX
NCBI GI	g2618698
BLAST score	657
E value	1.0e-68
Match length	204
% identity	61
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	277847
Contig ID	79917_2.R1011
5'-most EST	uC-zmflmo17179g09a1
Method	BLASTX
NCBI GI	g2618698
BLAST score	233
E value	2.0e-19
Match length	63
% identity	63
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	277848
Contig ID	79925_1.R1011
5'-most EST	wyr700242034.h1
Method	BLASTX
NCBI GI	g2444178
BLAST score	514
E value	7.0e-52
Match length	150
% identity	65
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	277849
Contig ID	79929_1.R1011
5'-most EST	wyr700235628.h1

Seq. No.	277850
Contig ID	79937_1.R1011
5'-most EST	dyk700105257.h1
Method	BLASTX
NCBI GI	g3176714
BLAST score	203
E value	2.0e-23
Match length	215
% identity	40
NCBI Description	(AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana]

Seq. No.	277851
Contig ID	79938_1.R1011
5'-most EST	LIB3067-058-Q1-K1-D3

Seq. No.	277852
Contig ID	79943_1.R1011
5'-most EST	LIB3136-032-Q1-K1-F4

Seq. No.	277853
Contig ID	79946_1.R1011

5'-most EST	LIB3067-058-Q1-K1-E12
Method	BLASTX
NCBI GI	g3702632
BLAST score	171
E value	7.0e-12
Match length	107
% identity	45
NCBI Description	(AL031824) putative transcriptional regulator [Schizosaccharomyces pombe] >gi_3859080_emb_CAA21957_ (AL033406) putative alcohol dehydrogenase repressor protein [Schizosaccharomyces pombe]

Seq. No.	277854
Contig ID	79951_1.R1011
5'-most EST	uC-zmflmo17265a05b1

Seq. No.	277855
Contig ID	79952_1.R1011
5'-most EST	gct701175159.h1
Method	BLASTX
NCBI GI	g3935150
BLAST score	1023
E value	1.0e-111
Match length	313
% identity	63
NCBI Description	(AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No.	277856
Contig ID	79961_1.R1011
5'-most EST	uC-zmflmo17273f12b1
Method	BLASTX
NCBI GI	g2191130
BLAST score	184
E value	7.0e-17
Match length	154
% identity	38
NCBI Description	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]

Seq. No.	277857
Contig ID	79970_1.R1011
5'-most EST	uC-zmflb73102b11a1

Seq. No.	277858
Contig ID	79971_1.R1011
5'-most EST	bdu700382874.h1

Seq. No.	277859
Contig ID	79974_1.R1011
5'-most EST	LIB3067-058-Q1-K1-H12
Method	BLASTX
NCBI GI	g2618684
BLAST score	499
E value	3.0e-50
Match length	156
% identity	64
NCBI Description	(AC002510) putative UDP-N-acetylglucosamine--dolichyl-phosphate

N-acetylglucosaminephosphotransferase [Arabidopsis thaliana] >gi_3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana]

Seq. No.	277860
Contig ID	79980_1.R1011
5'-most EST	uC-zmflb73233g11a1

Seq. No.	277861
Contig ID	79983_1.R1011
5'-most EST	clt700043404.f1
Method	BLASTX
NCBI GI	g3482974
BLAST score	497
E value	6.0e-50
Match length	176
% identity	55
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	277862
Contig ID	79997_1.R1011
5'-most EST	kem700611015.h1
Method	BLASTX
NCBI GI	g1091678
BLAST score	195
E value	1.0e-14
Match length	124
% identity	31
NCBI Description	activator-like transposable element [Pennisetum glaucum]

Seq. No.	277863
Contig ID	79998_1.R1011
5'-most EST	ceu700424308.h1

Seq. No.	277864
Contig ID	79999_1.R1011
5'-most EST	xjt700095578.h1
Method	BLASTX
NCBI GI	g3341443
BLAST score	235
E value	2.0e-19
Match length	115
% identity	40
NCBI Description	(AJ223074) acid phosphatase [Glycine max]

Seq. No.	277865
Contig ID	80011_1.R1011
5'-most EST	LIB3067-059-Q1-K1-D12

Seq. No.	277866
Contig ID	80055_1.R1011
5'-most EST	cat700016040.r1

Seq. No. 277867

Contig ID	80058_1.R1011
5'-most EST	uC-zmflmo17013e02b1
Method	BLASTX
NCBI GI	g4200165
BLAST score	229
E value	8.0e-19
Match length	65
% identity	69
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	277868
Contig ID	80058_2.R1011
5'-most EST	uC-zmflmo17159e06b1
Method	BLASTX
NCBI GI	g4200165
BLAST score	196
E value	1.0e-14
Match length	56
% identity	70
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	277869
Contig ID	80071_1.R1011
5'-most EST	uC-zmflb73106b10a1

Seq. No.	277870
Contig ID	80077_1.R1011
5'-most EST	LIB3067-060-Q1-K1-C11

Seq. No.	277871
Contig ID	80080_1.R1011
5'-most EST	qmh700030319.f1
Method	BLASTX
NCBI GI	g4115377
BLAST score	610
E value	2.0e-63
Match length	172
% identity	66
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	277872
Contig ID	80090_1.R1011
5'-most EST	hbs701185945.h1

Seq. No.	277873
Contig ID	80092_1.R1011
5'-most EST	pmx700085892.h1
Method	BLASTX
NCBI GI	g3024021
BLAST score	675
E value	4.0e-71
Match length	143
% identity	87
NCBI Description	INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D) >gi_2225883_dbj_BAA20878_ (AB004825) eukaryotic initiation factor 5A4 [Solanum tuberosum]

Seq. No.	277874
Contig ID	80105_1.R1011
5'-most EST	LIB3067-060-Q1-K1-F3
Method	BLASTX
NCBI GI	g2244867
BLAST score	270
E value	1.0e-23
Match length	138
% identity	39
NCBI Description	(Z97337) hydroxynitrile lyase [Arabidopsis thaliana]

Seq. No.	277875
Contig ID	80115_1.R1011
5'-most EST	uC-zmflb73070c02b1
Method	BLASTX
NCBI GI	g2829910
BLAST score	205
E value	7.0e-16
Match length	70
% identity	51
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	277876
Contig ID	80135_1.R1011
5'-most EST	LIB3069-001-Q1-K1-A2

Seq. No.	277877
Contig ID	80168_1.R1011
5'-most EST	LIB3068-001-Q1-K1-D8
Method	BLASTN
NCBI GI	g162876
BLAST score	326
E value	0.0e+00
Match length	366
% identity	97
NCBI Description	Bovine 2',3'-cyclic nucleotide 3'-phosphodiesterase (CNP) mRNA, complete cds

Seq. No.	277878
Contig ID	80179_1.R1011
5'-most EST	LIB3068-001-Q1-K1-E9

Seq. No.	277879
Contig ID	80218_1.R1011
5'-most EST	LIB36-009-Q1-E1-A8

Seq. No.	277880
Contig ID	80233_1.R1011
5'-most EST	LIB3068-002-Q1-K1-F12
Method	BLASTX
NCBI GI	g4220491
BLAST score	276
E value	4.0e-24
Match length	153
% identity	39
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277881
Contig ID	80241_1.R1011
5'-most EST	LIB3068-002-Q1-K1-H10
Method	BLASTX
NCBI GI	g2316016
BLAST score	227
E value	5.0e-40
Match length	147
% identity	56
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	277882
Contig ID	80261_1.R1011
5'-most EST	fC-zmst700622762d4

Seq. No.	277883
Contig ID	80277_1.R1011
5'-most EST	LIB3068-003-Q1-K1-G6

Seq. No.	277884
Contig ID	80278_1.R1011
5'-most EST	tfd700574245.h1
Method	BLASTX
NCBI GI	g166949
BLAST score	575
E value	5.0e-59
Match length	221
% identity	51
NCBI Description	(M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea americana]

Seq. No.	277885
Contig ID	80281_1.R1011
5'-most EST	LIB3068-003-Q1-K1-H12
Method	BLASTX
NCBI GI	g2183249
BLAST score	521
E value	5.0e-53
Match length	131
% identity	76
NCBI Description	(AF002211) glutathione-S-transferase [Triticum aestivum] >gi_4185800 (AF109714) glutathione S-transferase [Triticum aestivum]

Seq. No.	277886
Contig ID	80282_1.R1011
5'-most EST	wyr700243577.h1
Method	BLASTX
NCBI GI	g1353193
BLAST score	595
E value	1.0e-112
Match length	254
% identity	85
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	277887
Contig ID	80302_1.R1011
5'-most EST	LIB3136-008-Q1-K1-D7
Method	BLASTX
NCBI GI	g4432839
BLAST score	334
E value	1.0e-59
Match length	259
% identity	53
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	277888
Contig ID	80311_1.R1011
5'-most EST	uer700578102.h1

Seq. No.	277889
Contig ID	80315_1.R1011
5'-most EST	uC-zmroteosinte083f05b1
Method	BLASTX
NCBI GI	g4063751
BLAST score	896
E value	8.0e-97
Match length	252
% identity	69
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	277890
Contig ID	80330_1.R1011
5'-most EST	LIB3068-005-Q1-K1-C4
Method	BLASTX
NCBI GI	g2829879
BLAST score	180
E value	6.0e-13
Match length	149
% identity	32
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	277891
Contig ID	80332_1.R1011
5'-most EST	wen700334064.h1
Method	BLASTX
NCBI GI	g4467359
BLAST score	659
E value	6.0e-76
Match length	148
% identity	95
NCBI Description	(AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No.	277892
Contig ID	80333_1.R1011
5'-most EST	uC-zmf1b73171d04b1
Method	BLASTX
NCBI GI	g422029

BLAST score	735
E value	1.0e-77
Match length	250
% identity	60
NCBI Description	transcription factor OBF3.2, ocs element-binding - maize >gi_297018_emb_CAA48904_ (X69152) ocs-element binding factor 3.2 [Zea mays]

Seq. No.	277893
Contig ID	80333_2.R1011
5'-most EST	uC-zmflb73196f04b1
Method	BLASTX
NCBI GI	g497896
BLAST score	226
E value	2.0e-18
Match length	68
% identity	71
NCBI Description	(D12921) transcription factor HBP-1b(c1) [Triticum aestivum]

Seq. No.	277894
Contig ID	80333_3.R1011
5'-most EST	uC-zmflb73026g07b1
Method	BLASTX
NCBI GI	g497896
BLAST score	233
E value	7.0e-21
Match length	129
% identity	51
NCBI Description	(D12921) transcription factor HBP-1b(c1) [Triticum aestivum]

Seq. No.	277895
Contig ID	80333_6.R1011
5'-most EST	uC-zmflmo17023a04b1
Method	BLASTX
NCBI GI	g497896
BLAST score	177
E value	8.0e-27
Match length	168
% identity	46
NCBI Description	(D12921) transcription factor HBP-1b(c1) [Triticum aestivum]

Seq. No.	277896
Contig ID	80389_1.R1011
5'-most EST	LIB3068-006-Q1-K1-G12
Method	BLASTX
NCBI GI	g1173146
BLAST score	795
E value	3.0e-85
Match length	158
% identity	99
NCBI Description	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN >gi_1363609_pir__S58583 DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - maize chloroplast >gi_902253_emb_CAA60317_ (X86563) RNA polymerase alpha

subunit [Zea mays]

Seq. No.	277897
Contig ID	80394_1.R1011
5'-most EST	fwa700101661.h1
Method	BLASTX
NCBI GI	g3786324
BLAST score	760
E value	8.0e-82
Match length	286
% identity	53
NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]

Seq. No.	277898
Contig ID	80394_2.R1011
5'-most EST	LIB3068-006-Q1-K1-H2

Seq. No.	277899
Contig ID	80400_1.R1011
5'-most EST	LIB3068-007-Q1-K1-A9

Seq. No.	277900
Contig ID	80404_1.R1011
5'-most EST	LIB3068-007-Q1-K1-C10

Seq. No.	277901
Contig ID	80408_1.R1011
5'-most EST	cyk700049389.f1
Method	BLASTX
NCBI GI	g2266666
BLAST score	490
E value	2.0e-49
Match length	111
% identity	83
NCBI Description	(Y14202) hypothetical protein [Hordeum vulgare]

Seq. No.	277902
Contig ID	80421_1.R1011
5'-most EST	uC-zmflmo17217a07b1
Method	BLASTN
NCBI GI	g294844
BLAST score	144
E value	3.0e-75
Match length	270
% identity	92
NCBI Description	Saccharum hybrid cultivar H65-7052 membrane protein mRNA, complete cds

Seq. No.	277903
Contig ID	80428_1.R1011
5'-most EST	LIB3068-007-Q1-K1-G3

Seq. No.	277904
Contig ID	80430_1.R1011
5'-most EST	LIB3136-006-Q1-K1-E6
Method	BLASTX

NCBI GI	g3005931
BLAST score	630
E value	6.0e-66
Match length	145
% identity	81
NCBI Description	(AJ005016) ABC transporter [Homo sapiens]

Seq. No.	277905
Contig ID	80437_1.R1011
5'-most EST	uC-zmflb73195a08b1
Method	BLASTX
NCBI GI	g2961178
BLAST score	874
E value	3.0e-94
Match length	203
% identity	83
NCBI Description	(AF050675) GTP-binding protein [Oryza sativa]

Seq. No.	277906
Contig ID	80450_1.R1011
5'-most EST	uer700577710.h1
Method	BLASTX
NCBI GI	g1086225
BLAST score	331
E value	8.0e-31
Match length	128
% identity	52
NCBI Description	RING-finger protein (C-terminal) - Lotus japonicus >gi_558545_emb_CAA85321_ (Z36750) protein containing C-terminal RING-finger [Lotus japonicus] >gi_1771195_emb_CAA70734_ (Y09539) RING-finger protein [Lotus japonicus]

Seq. No.	277907
Contig ID	80464_1.R1011
5'-most EST	nbm700465925.h1
Method	BLASTX
NCBI GI	g3201680
BLAST score	143
E value	6.0e-09
Match length	77
% identity	40
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	277908
Contig ID	80468_1.R1011
5'-most EST	LIB3068-008-Q1-K1-D5

Seq. No.	277909
Contig ID	80471_1.R1011
5'-most EST	uC-zmflb73129g10b1

Seq. No.	277910
Contig ID	80489_1.R1011
5'-most EST	gct701180257.h1
Method	BLASTX
NCBI GI	g1653216

BLAST score 185
E value 1.0e-13
Match length 85
% identity 51
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]

Seq. No. 277911
Contig ID 80494_1.R1011
5'-most EST fdz701158919.h2
Method BLASTX
NCBI GI g1402878
BLAST score 441
E value 1.0e-43
Match length 166
% identity 49
NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 277912
Contig ID 80504_1.R1011
5'-most EST uC-zmroteosinte049d10b1

Seq. No. 277913
Contig ID 80505_1.R1011
5'-most EST LIB3068-009-Q1-K1-C10

Seq. No. 277914
Contig ID 80509_1.R1011
5'-most EST LIB3068-009-Q1-K1-C7

Seq. No. 277915
Contig ID 80560_1.R1011
5'-most EST LIB3068-011-Q1-K1-G12
Method BLASTX
NCBI GI g1871194
BLAST score 165
E value 4.0e-11
Match length 99
% identity 44
NCBI Description (U90439) DNA binding protein isolog [Arabidopsis thaliana]
>gi_2335092 (AC002339) putative DNA binding protein
[Arabidopsis thaliana]

Seq. No. 277916
Contig ID 80573_1.R1011
5'-most EST uC-zmflb73011b06b1
Method BLASTX
NCBI GI g3080427
BLAST score 788
E value 6.0e-84
Match length 287
% identity 47
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 277917
Contig ID 80582_1.R1011
5'-most EST LIB3068-010-Q1-K1-G12
Method BLASTX

NCBI GI	g1762144
BLAST score	220
E value	5.0e-25
Match length	106
% identity	53
NCBI Description	(U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No.	277918
Contig ID	80582_2.R1011
5'-most EST	uC-zmflb73257d10b3
Method	BLASTX
NCBI GI	g1762144
BLAST score	227
E value	5.0e-24
Match length	105
% identity	52
NCBI Description	(U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No.	277919
Contig ID	80620_1.R1011
5'-most EST	LIB3068-011-Q1-K1-D12
Method	BLASTX
NCBI GI	g4567310
BLAST score	227
E value	1.0e-18
Match length	59
% identity	78
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	277920
Contig ID	80623_1.R1011
5'-most EST	LIB3068-011-Q1-K1-E10

Seq. No.	277921
Contig ID	80624_1.R1011
5'-most EST	uC-zmflmo17036e04b2

Seq. No.	277922
Contig ID	80624_2.R1011
5'-most EST	LIB83-002-Q1-E1-C5

Seq. No.	277923
Contig ID	80624_3.R1011
5'-most EST	uC-zmflb73298h09b1

Seq. No.	277924
Contig ID	80624_4.R1011
5'-most EST	wyr700236095.h1

Seq. No.	277925
Contig ID	80638_1.R1011
5'-most EST	hbs701185225.h1
Method	BLASTX
NCBI GI	g464707
BLAST score	154
E value	1.0e-09
Match length	42

% identity	69
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	277926
Contig ID	80675_1.R1011
5'-most EST	uC-zmroteosinte119h02b2

Seq. No.	277927
Contig ID	80698_1.R1011
5'-most EST	LIB3068-012-Q1-K1-H1
Method	BLASTN
NCBI GI	g12888
BLAST score	317
E value	1.0e-178
Match length	328
% identity	99
NCBI Description	Maize mitochondrial gene for cytochrome c oxidase subunit I (COX I)

Seq. No.	277928
Contig ID	80709_1.R1011
5'-most EST	uC-zmflmo17259f06b1

Seq. No.	277929
Contig ID	80717_1.R1011
5'-most EST	LIB3068-013-Q1-K1-B9

Seq. No.	277930
Contig ID	80744_1.R1011
5'-most EST	xyt700345322.h1
Method	BLASTX
NCBI GI	g3047065
BLAST score	172
E value	5.0e-12
Match length	75
% identity	41
NCBI Description	(AF058825) contains similarity to human OS-9 precurosor (GB:U41635) [Arabidopsis thaliana]

Seq. No.	277931
Contig ID	80750_1.R1011
5'-most EST	LIB3068-013-Q1-K1-F9
Method	BLASTX

NCBI GI	g2626753
BLAST score	326
E value	2.0e-30
Match length	99
% identity	70
NCBI Description	(AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No.	277932
Contig ID	80754_1.R1011
5'-most EST	LIB3068-049-Q1-K1-F2
Method	BLASTX
NCBI GI	g3093294
BLAST score	1127
E value	1.0e-124
Match length	319
% identity	70
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	277933
Contig ID	80756_1.R1011
5'-most EST	LIB3068-013-Q1-K1-G3

Seq. No.	277934
Contig ID	80762_1.R1011
5'-most EST	xjt700096743.h1

Seq. No.	277935
Contig ID	80767_1.R1011
5'-most EST	LIB3068-014-Q1-K1-A4

Seq. No.	277936
Contig ID	80779_1.R1011
5'-most EST	uC-zmflm017205d05b1
Method	BLASTX
NCBI GI	g3219273
BLAST score	642
E value	3.0e-71
Match length	188
% identity	72
NCBI Description	(AB015316) MAP kinase kinase 5 [Arabidopsis thaliana]

Seq. No.	277937
Contig ID	80789_1.R1011
5'-most EST	LIB3068-014-Q1-K1-D8

Seq. No.	277938
Contig ID	80795_1.R1011
5'-most EST	LIB3068-014-Q1-K1-E5

Seq. No.	277939
Contig ID	80798_1.R1011
5'-most EST	LIB3068-035-Q1-K1-H2
Method	BLASTX
NCBI GI	g4220474
BLAST score	581
E value	4.0e-60
Match length	154

% identity	75
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	277940
Contig ID	80809_1.R1011
5'-most EST	uC-zmflB73021c03b1
Method	BLASTX
NCBI GI	g4426964
BLAST score	285
E value	2.0e-25
Match length	91
% identity	59
NCBI Description	(AF126255) purple acid phosphatase precursor [Anchusa officinalis]

Seq. No.	277941
Contig ID	80809_2.R1011
5'-most EST	uC-zmflmo17060h10b1
Method	BLASTX
NCBI GI	g4160280
BLAST score	168
E value	1.0e-11
Match length	47
% identity	66
NCBI Description	(AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No.	277942
Contig ID	80821_1.R1011
5'-most EST	uC-zmflmo17242f04b1
Method	BLASTX
NCBI GI	g4580990
BLAST score	202
E value	2.0e-15
Match length	118
% identity	35
NCBI Description	(AF120335) putative transposase [Arabidopsis thaliana]

Seq. No.	277943
Contig ID	80824_1.R1011
5'-most EST	rvt700552868.h1

Seq. No.	277944
Contig ID	80824_2.R1011
5'-most EST	pmx700091569.h1

Seq. No.	277945
Contig ID	80824_6.R1011
5'-most EST	cat700017340.r1

Seq. No.	277946
Contig ID	80841_1.R1011
5'-most EST	cyk700049656.f1
Method	BLASTX
NCBI GI	g4220481
BLAST score	368
E value	6.0e-35

Match length	159
% identity	48
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	277947
Contig ID	80850_1.R1011
5'-most EST	uC-zmflb73003g07b1

Seq. No.	277948
Contig ID	80866_1.R1011
5'-most EST	uC-zmflb73155h10b2
Method	BLASTX
NCBI GI	g2224915
BLAST score	345
E value	2.0e-32
Match length	134
% identity	54
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	277949
Contig ID	80866_2.R1011
5'-most EST	uwc700151790.h1
Method	BLASTX
NCBI GI	g2224915
BLAST score	325
E value	4.0e-30
Match length	125
% identity	53
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	277950
Contig ID	80866_3.R1011
5'-most EST	LIB83-014-Q1-E1-H10
Method	BLASTN
NCBI GI	g4099918
BLAST score	45
E value	4.0e-16
Match length	77
% identity	90
NCBI Description	Triticum aestivum pollen allergen homolog mRNA, complete cds

Seq. No.	277951
Contig ID	80877_1.R1011
5'-most EST	vux700161418.h1
Method	BLASTX
NCBI GI	g3928091
BLAST score	211
E value	1.0e-16
Match length	55
% identity	69
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	277952
Contig ID	80877_2.R1011
5'-most EST	nbm700476180.h1

Seq. No.	277953
Contig ID	80878_1.R1011
5'-most EST	uC-zmflB73004g12b1
Seq. No.	277954
Contig ID	80883_1.R1011
5'-most EST	LIB3068-047-Q1-K1-B10
Seq. No.	277955
Contig ID	80888_1.R1011
5'-most EST	LIB3068-016-Q1-K1-A6
Seq. No.	277956
Contig ID	80894_1.R1011
5'-most EST	LIB3068-016-Q1-K1-B11
Method	BLASTX
NCBI GI	g2739008
BLAST score	153
E value	7.0e-10
Match length	84
% identity	39
NCBI Description	(AF022463) CYP78A3p [Glycine max]
Seq. No.	277957
Contig ID	80925_1.R1011
5'-most EST	ceu700423091.h1
Method	BLASTX
NCBI GI	g4101589
BLAST score	412
E value	3.0e-40
Match length	133
% identity	56
NCBI Description	(AF005050) aspartyl aminopeptidase [Homo sapiens]
Seq. No.	277958
Contig ID	80927_1.R1011
5'-most EST	xjt700092585.h1
Method	BLASTX
NCBI GI	g3928091
BLAST score	395
E value	9.0e-38
Match length	118
% identity	63
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]
Seq. No.	277959
Contig ID	80946_1.R1011
5'-most EST	LIB3068-016-Q1-K1-H10
Seq. No.	277960
Contig ID	81026_1.R1011
5'-most EST	uC-zmflmo17204c10b1
Seq. No.	277961
Contig ID	81026_2.R1011
5'-most EST	LIB3068-018-Q1-K1-E10

Seq. No.	277962
Contig ID	81036_1.R1011
5'-most EST	uC-zmflb73298d07a1
Method	BLASTX
NCBI GI	g4558556
BLAST score	396
E value	8.0e-38
Match length	342
% identity	34
NCBI Description	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	277963
Contig ID	81041_1.R1011
5'-most EST	LIB3068-018-Q1-K1-H11

Seq. No.	277964
Contig ID	81046_1.R1011
5'-most EST	uC-zmflb73116b11b2
Method	BLASTX
NCBI GI	g1002800
BLAST score	384
E value	5.0e-37
Match length	91
% identity	74
NCBI Description	(U33917) Cpm7 [Craterostigma plantagineum]

Seq. No.	277965
Contig ID	81046_2.R1011
5'-most EST	LIB3068-038-Q1-K1-F11
Method	BLASTX
NCBI GI	g1002796
BLAST score	147
E value	2.0e-09
Match length	34
% identity	71
NCBI Description	(U33915) Cpm10 [Craterostigma plantagineum]

Seq. No.	277966
Contig ID	81047_1.R1011
5'-most EST	nbm700466048.h1
Method	BLASTX
NCBI GI	g3047114
BLAST score	577
E value	4.0e-59
Match length	301
% identity	42
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	277967
Contig ID	81055_1.R1011
5'-most EST	uC-zmflmo17408a08a1

Seq. No.	277968
Contig ID	81065_1.R1011
5'-most EST	uC-zmflb73174f12a1
Method	BLASTX

NCBI GI g3779024
BLAST score 176
E value 1.0e-12
Match length 50
% identity 84
NCBI Description (AC005171) unknown protein [Arabidopsis thaliana]

Seq. No. 277969
Contig ID 81070_1.R1011
5'-most EST uC-zmflmo17175a07b1
Method BLASTX
NCBI GI g2754818
BLAST score 185
E value 1.0e-13
Match length 113
% identity 44
NCBI Description (AF024615) (E)-B-farnesene synthase [Mentha x piperita]

Seq. No. 277970
Contig ID 81070_2.R1011
5'-most EST uC-zmflmo17320b07b1

Seq. No. 277971
Contig ID 81083_1.R1011
5'-most EST LIB3068-019-Q1-K1-G10
Method BLASTX
NCBI GI g3024871
BLAST score 193
E value 2.0e-14
Match length 86
% identity 47
NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005
>gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No. 277972
Contig ID 81095_1.R1011
5'-most EST LIB3068-020-Q1-K1-A11
Method BLASTX
NCBI GI g2232254
BLAST score 470
E value 4.0e-47
Match length 108
% identity 81
NCBI Description (AF005237) old-yellow-enzyme homolog [Catharanthus roseus]

Seq. No. 277973
Contig ID 81119_1.R1011
5'-most EST rvl700455941.h1
Method BLASTX
NCBI GI g2811226
BLAST score 834
E value 1.0e-112
Match length 280
% identity 73
NCBI Description (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi_2811232
(AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq. No.	277974
Contig ID	81140_1.R1011
5'-most EST	LIB3068-020-Q1-K1-H9
Method	BLASTN
NCBI GI	g4191760
BLAST score	46
E value	1.0e-16
Match length	102
% identity	86
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	277975
Contig ID	81174_1.R1011
5'-most EST	LIB3068-021-Q1-K1-E12
Method	BLASTX
NCBI GI	g3335365
BLAST score	458
E value	2.0e-45
Match length	182
% identity	55
NCBI Description	(AC003028) high affinity calcium antiporter [Arabidopsis thaliana]

Seq. No.	277976
Contig ID	81180_1.R1011
5'-most EST	LIB3068-021-Q1-K1-F2

Seq. No.	277977
Contig ID	81190_1.R1011
5'-most EST	LIB3068-051-Q1-K1-C8

Seq. No.	277978
Contig ID	81205_1.R1011
5'-most EST	uC-zmflmo17242f05b1
Method	BLASTN
NCBI GI	g4126518
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Setaria italica LINE retrotransposon, endonuclease region of FMLN1

Seq. No.	277979
Contig ID	81219_1.R1011
5'-most EST	LIB3068-022-Q1-K1-D9
Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	8.0e-11
Match length	36
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 277980

Contig ID	81244_1.R1011
5'-most EST	LIB3068-022-Q1-K1-H6
Method	BLASTX
NCBI GI	g1402878
BLAST score	337
E value	1.0e-31
Match length	118
% identity	59
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	277981
Contig ID	81257_1.R1011
5'-most EST	uC-zmflmo17046e03b1

Seq. No.	277982
Contig ID	81257_2.R1011
5'-most EST	uC-zmflmo17202e06a1
Method	BLASTN
NCBI GI	g1935910
BLAST score	52
E value	3.0e-20
Match length	124
% identity	85
NCBI Description	Zea mays lethal leaf-spot 1 (lls1) gene, partial cds

Seq. No.	277983
Contig ID	81265_1.R1011
5'-most EST	ceu700431972.h1

Seq. No.	277984
Contig ID	81301_1.R1011
5'-most EST	LIB3068-024-Q1-K1-A2
Method	BLASTX
NCBI GI	g4185499
BLAST score	184
E value	1.0e-13
Match length	140
% identity	34
NCBI Description	(AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.	277985
Contig ID	81307_1.R1011
5'-most EST	nbm700469733.h1

Seq. No.	277986
Contig ID	81308_1.R1011
5'-most EST	LIB3068-024-Q1-K1-B8

Seq. No.	277987
Contig ID	81317_1.R1011
5'-most EST	LIB3068-024-Q1-K1-E10
Method	BLASTX
NCBI GI	g4651204
BLAST score	262

E value	1.0e-22
Match length	86
% identity	57
NCBI Description	(AB026262) ring finger protein [Cicer arietinum]

Seq. No.	277988
Contig ID	81341_1.R1011
5'-most EST	nbm700465007.h1
Method	BLASTX
NCBI GI	g2632254
BLAST score	285
E value	3.0e-25
Match length	59
% identity	95
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	277989
Contig ID	81364_1.R1011
5'-most EST	uC-zmflmo17320b07a1
Method	BLASTN
NCBI GI	g22176
BLAST score	38
E value	9.0e-12
Match length	86
% identity	86
NCBI Description	Z.mays P gene

Seq. No.	277990
Contig ID	81364_2.R1011
5'-most EST	uC-zmflb73191f07b1
Method	BLASTX
NCBI GI	g3287832
BLAST score	294
E value	9.0e-48
Match length	283
% identity	37
NCBI Description	(+)-DELTA-CADINENE SYNTHASE (D-CADINENE SYNTHASE) >gi_1843647 (U88318) (+)-delta-cadinene synthase [Gossypium hirsutum]

Seq. No.	277991
Contig ID	81364_3.R1011
5'-most EST	LIB3068-025-Q1-K1-E11
Method	BLASTX
NCBI GI	g4105135
BLAST score	259
E value	2.0e-22
Match length	124
% identity	42
NCBI Description	(AF043299) vetispiradiene synthase 4 [Solanum tuberosum]

Seq. No.	277992
Contig ID	81376_1.R1011
5'-most EST	uC-zmflb73177h05b1

Seq. No.	277993
Contig ID	81377_1.R1011

5'-most EST	LIB3068-025-Q1-K1-G2
Method	BLASTX
NCBI GI	g4544374
BLAST score	152
E value	7.0e-10
Match length	78
% identity	44
NCBI Description	(AC006920) unknown protein [Arabidopsis thaliana]

Seq. No.	277994
Contig ID	81398_1.R1011
5'-most EST	LIB3068-026-Q1-K1-B2
Method	BLASTX
NCBI GI	g2244865
BLAST score	195
E value	9.0e-15
Match length	130
% identity	43
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	277995
Contig ID	81412_1.R1011
5'-most EST	vux700159513.h1
Method	BLASTX
NCBI GI	g1168654
BLAST score	376
E value	8.0e-36
Match length	91
% identity	71
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) - garden asparagus >gi_452712_emb_CAA54525_ (X77319) beta-galactosidase [Asparagus officinalis]

Seq. No.	277996
Contig ID	81419_1.R1011
5'-most EST	ceu700433442.h1
Method	BLASTX
NCBI GI	g2832661
BLAST score	311
E value	3.0e-28
Match length	100
% identity	60
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No.	277997
Contig ID	81427_1.R1011
5'-most EST	LIB3068-026-Q1-K1-G1
Method	BLASTX
NCBI GI	g4574141
BLAST score	168
E value	6.0e-12
Match length	41
% identity	78
NCBI Description	(AF073698) cysteine synthase [Oryza sativa]

Seq. No.	277998
Contig ID	81453_1.R1011
5'-most EST	pmx700086310.h1

Seq. No.	277999
Contig ID	81457_1.R1011
5'-most EST	hvj700624610.h1

Seq. No.	278000
Contig ID	81467_1.R1011
5'-most EST	uC-zmroteosinte024f04b1

Seq. No.	278001
Contig ID	81467_2.R1011
5'-most EST	uC-zmflb73220g04b2

Seq. No.	278002
Contig ID	81472_1.R1011
5'-most EST	dyk700104406.h1
Method	BLASTX
NCBI GI	g4165025
BLAST score	243
E value	4.0e-20
Match length	113
% identity	42
NCBI Description	(AF043611) zinc-finger protein MCG4 [Homo sapiens]

Seq. No.	278003
Contig ID	81476_1.R1011
5'-most EST	uC-zmflb73094c05a1

Seq. No.	278004
Contig ID	81476_2.R1011
5'-most EST	LIB3068-027-Q1-K1-F7

Seq. No.	278005
Contig ID	81490_1.R1011
5'-most EST	rvt700549362.h1

Seq. No.	278006
Contig ID	81495_1.R1011
5'-most EST	LIB3068-028-Q1-K1-A7
Method	BLASTX
NCBI GI	g2290532
BLAST score	638
E value	9.0e-67
Match length	164
% identity	72
NCBI Description	(U94748) AN11 [Petunia x hybrida]

Seq. No.	278007
Contig ID	81503_1.R1011
5'-most EST	afb700380813.h1
Method	BLASTX
NCBI GI	g3024500
BLAST score	494
E value	5.0e-50

Match length 107
% identity 88
NCBI Description RAS-RELATED PROTEIN RAB11A >gi_1370142_emb_CAA98177_ (Z73949) RAB11A [Lotus japonicus]

Seq. No. 278008
Contig ID 81503_2.R1011
5'-most EST LIB3069-034-Q1-K1-G10
Method BLASTX
NCBI GI g3024500
BLAST score 293
E value 1.0e-26
Match length 65
% identity 92
NCBI Description RAS-RELATED PROTEIN RAB11A >gi_1370142_emb_CAA98177_ (Z73949) RAB11A [Lotus japonicus]

Seq. No. 278009
Contig ID 81516_1.R1011
5'-most EST LIB3068-028-Q1-K1-G10

Seq. No. 278010
Contig ID 81516_3.R1011
5'-most EST gct701173260.h2

Seq. No. 278011
Contig ID 81518_1.R1011
5'-most EST xsy700217393.h1

Seq. No. 278012
Contig ID 81563_1.R1011
5'-most EST uC-zmflmo17187c06b1

Seq. No. 278013
Contig ID 81576_1.R1011
5'-most EST LIB3068-030-Q1-K1-D10

Seq. No. 278014
Contig ID 81582_1.R1011
5'-most EST uC-zmflmo17305c04a1
Method BLASTX
NCBI GI g4531444
BLAST score 219
E value 1.0e-17
Match length 78
% identity 60
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 278015
Contig ID 81595_1.R1011
5'-most EST LIB3068-030-Q1-K1-G7

Seq. No. 278016
Contig ID 81599_1.R1011
5'-most EST nbm700471557.h1

Seq. No. 278017

Contig ID	81635_1.R1011
5'-most EST	vux700160411.h1
Method	BLASTX
NCBI GI	g1171771
BLAST score	404
E value	3.0e-39
Match length	129
% identity	61
NCBI Description	NITRILASE 4 >gi_508737 (U09961) nitrilase [Arabidopsis thaliana]

Seq. No.	278018
Contig ID	81638_1.R1011
5'-most EST	LIB3068-051-Q1-K1-H12

Seq. No.	278019
Contig ID	81679_1.R1011
5'-most EST	uC-zmflb73136g05b1
Method	BLASTX
NCBI GI	g1245372
BLAST score	155
E value	9.0e-10
Match length	177
% identity	29
NCBI Description	(U50383) NN8-4AG [Homo sapiens]

Seq. No.	278020
Contig ID	81685_1.R1011
5'-most EST	uC-zmflmo17109g06b1

Seq. No.	278021
Contig ID	81693_1.R1011
5'-most EST	LIB3068-033-Q1-K1-A2
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	278022
Contig ID	81705_1.R1011
5'-most EST	uC-zmflb73195e01b1
Method	BLASTX
NCBI GI	g2791900
BLAST score	896
E value	1.0e-96
Match length	257
% identity	66
NCBI Description	(AJ000057) PP7 [Arabidopsis thaliana]

Seq. No.	278023
Contig ID	81711_1.R1011
5'-most EST	LIB3068-033-Q1-K1-D5
Method	BLASTX
NCBI GI	g4262147

BLAST score	325
E value	1.0e-29
Match length	128
% identity	48
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	278024
Contig ID	81711_2.R1011
5'-most EST	LIB3136-011-Q1-K1-H4

Seq. No.	278025
Contig ID	81729_1.R1011
5'-most EST	LIB3068-033-Q1-K1-F9

Seq. No.	278026
Contig ID	81759_1.R1011
5'-most EST	wty700171327.h1
Method	BLASTX
NCBI GI	g4455206
BLAST score	170
E value	3.0e-12
Match length	66
% identity	47
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	278027
Contig ID	81760_1.R1011
5'-most EST	gct701173962.h1

Seq. No.	278028
Contig ID	81779_1.R1011
5'-most EST	LIB3068-037-Q1-K1-B3
Method	BLASTX
NCBI GI	g2642428
BLAST score	143
E value	8.0e-09
Match length	117
% identity	33
NCBI Description	(AC002391) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	278029
Contig ID	81790_1.R1011
5'-most EST	uC-zmflb73064h07a2

Seq. No.	278030
Contig ID	81797_1.R1011
5'-most EST	uC-zmflb73065f02b1

Seq. No.	278031
Contig ID	81797_2.R1011
5'-most EST	uC-zmflmo17293e11b1

Seq. No.	278032
Contig ID	81808_1.R1011

5'-most EST	LIB3068-035-Q1-K1-A8
Method	BLASTX
NCBI GI	g3549652
BLAST score	443
E value	6.0e-44
Match length	98
% identity	89
NCBI Description	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]

Seq. No.	278033
Contig ID	81817_1.R1011
5'-most EST	LIB3068-035-Q1-K1-C1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	278034
Contig ID	81831_1.R1011
5'-most EST	LIB3068-035-Q1-K1-D6
Method	BLASTX
NCBI GI	g4432832
BLAST score	268
E value	2.0e-23
Match length	145
% identity	44
NCBI Description	(AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No.	278035
Contig ID	81835_1.R1011
5'-most EST	LIB3068-035-Q1-K1-E3

Seq. No.	278036
Contig ID	81847_1.R1011
5'-most EST	uC-zmflb73245e05b2

Seq. No.	278037
Contig ID	81847_2.R1011
5'-most EST	LIB3068-035-Q1-K1-F8

Seq. No.	278038
Contig ID	81878_1.R1011
5'-most EST	uC-zmflb73063a04b1
Method	BLASTX
NCBI GI	g4559351
BLAST score	255
E value	5.0e-27
Match length	218
% identity	38
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278039
Contig ID	81880_1.R1011

5'-most EST	LIB3068-036-Q1-K1-C5
Method	BLASTX
NCBI GI	g2832677
BLAST score	238
E value	8.0e-27
Match length	123
% identity	54
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278040
Contig ID	81883_1.R1011
5'-most EST	ntr700072453.h1
Method	BLASTX
NCBI GI	g1076647
BLAST score	337
E value	2.0e-31
Match length	114
% identity	55
NCBI Description	alcohol dehydrogenase 2 - garden petunia >gi_829592 (U25536) alcohol dehydrogenase-2 [Petunia hybrida]

Seq. No.	278041
Contig ID	81886_2.R1011
5'-most EST	hbs701185442.h1

Seq. No.	278042
Contig ID	81889_1.R1011
5'-most EST	LIB3136-042-P1-K1-C6
Method	BLASTX
NCBI GI	g3695021
BLAST score	631
E value	1.0e-65
Match length	167
% identity	71
NCBI Description	(AF055849) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278043
Contig ID	81895_1.R1011
5'-most EST	cjh700195687.h1
Method	BLASTN
NCBI GI	g3452291
BLAST score	381
E value	0.0e+00
Match length	524
% identity	94
NCBI Description	Zea mays retrotransposon Huck-2 3' LTR, partial sequence

Seq. No.	278044
Contig ID	81896_1.R1011
5'-most EST	uC-zmflmo17242a02b1

Seq. No.	278045
Contig ID	81907_1.R1011
5'-most EST	uC-zmflb73030b03b1
Method	BLASTX
NCBI GI	g3047114
BLAST score	323

E value	2.0e-29
Match length	105
% identity	55
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	278046
Contig ID	81917_1.R1011
5'-most EST	fdz701159849.h1
Method	BLASTX
NCBI GI	g600855
BLAST score	497
E value	3.0e-50
Match length	178
% identity	56
NCBI Description	(U17887) bZIP protein [Arabidopsis thaliana]

Seq. No.	278047
Contig ID	81923_1.R1011
5'-most EST	cjh700193721.h1

Seq. No.	278048
Contig ID	81930_1.R1011
5'-most EST	uC-zmflmo17201a01b1

Seq. No.	278049
Contig ID	81941_1.R1011
5'-most EST	gct701176210.h1

Seq. No.	278050
Contig ID	81969_1.R1011
5'-most EST	LIB3068-038-Q1-K1-D10
Method	BLASTX
NCBI GI	g416564
BLAST score	276
E value	2.0e-24
Match length	88
% identity	66
NCBI Description	ABCISIC ACID-INDUCIBLE PROTEIN KINASE >gi_422013_pir__A46408 abscisic acid-inducible serine/threonine protein kinase homolog - wheat (fragment) >gi_170664 (M94726) protein kinase [Triticum aestivum]

Seq. No.	278051
Contig ID	81979_1.R1011
5'-most EST	uC-zmflb73326h07a1

Seq. No.	278052
Contig ID	81990_1.R1011
5'-most EST	LIB3068-038-Q1-K1-F4

Seq. No.	278053
Contig ID	81994_1.R1011
5'-most EST	LIB3068-038-Q1-K1-G1
Method	BLASTX
NCBI GI	g4371280
BLAST score	476
E value	2.0e-47

Match length 149
% identity 64
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 278054
Contig ID 81994_2.R1011
5'-most EST tfd700575025.h1

Seq. No. 278055
Contig ID 82016_1.R1011
5'-most EST pmx700091636.h1
Method BLASTX
NCBI GI g1663648
BLAST score 212
E value 5.0e-17
Match length 94
% identity 51
NCBI Description (U75321) chromaffin granule ATPase II homolog [Mus musculus]

Seq. No. 278056
Contig ID 82020_1.R1011
5'-most EST rvl700453736.h1
Method BLASTX
NCBI GI g3688187
BLAST score 239
E value 9.0e-20
Match length 187
% identity 36
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 278057
Contig ID 82026_1.R1011
5'-most EST fC-zmst700335017a5
Method BLASTX
NCBI GI g4539455
BLAST score 400
E value 8.0e-39
Match length 122
% identity 61
NCBI Description (AL049500) T5C23.70 [Arabidopsis thaliana]

Seq. No. 278058
Contig ID 82046_1.R1011
5'-most EST LIB3068-039-Q1-K1-E7

Seq. No. 278059
Contig ID 82053_1.R1011
5'-most EST xmt700264879.h1

Seq. No. 278060
Contig ID 82064_1.R1011
5'-most EST uC-zmflb73201h12b1

Seq. No. 278061
Contig ID 82082_1.R1011
5'-most EST uC-zmroteosinte035g04b2

Seq. No.	278062
Contig ID	82085_1.R1011
5'-most EST	uC-zmflb73011e10b1
Method	BLASTX
NCBI GI	g2104679
BLAST score	968
E value	0.0e+00
Match length	474
% identity	72
NCBI Description	(X97906) transcription factor [Vicia faba]

Seq. No.	278063
Contig ID	82089_1.R1011
5'-most EST	uC-zmflb73008d08a1

Seq. No.	278064
Contig ID	82091_1.R1011
5'-most EST	ceu700424038.h1

Seq. No.	278065
Contig ID	82121_1.R1011
5'-most EST	wty700167044.h1

Seq. No.	278066
Contig ID	82163_1.R1011
5'-most EST	wyr700242227.h1

Seq. No.	278067
Contig ID	82181_1.R1011
5'-most EST	LIB3068-043-Q1-K1-C1

Seq. No.	278068
Contig ID	82203_1.R1011
5'-most EST	uC-zmflm017025b10b1

Seq. No.	278069
Contig ID	82209_1.R1011
5'-most EST	LIB3068-043-Q1-K1-F7

Seq. No.	278070
Contig ID	82229_1.R1011
5'-most EST	uC-zmflmo17198h09b1

Seq. No.	278071
Contig ID	82241_1.R1011
5'-most EST	LIB3068-044-Q1-K1-D1
Method	BLASTN
NCBI GI	g1777706
BLAST score	61
E value	1.0e-25
Match length	179
% identity	80
NCBI Description	Zea mays 18S ribosomal RNA gene, partial sequence

Seq. No.	278072
Contig ID	82250_1.R1011

5'-most EST	wyr700239251.h1
Method	BLASTX
NCBI GI	g4006868
BLAST score	324
E value	1.0e-29
Match length	310
% identity	40
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	278073
Contig ID	82253_1.R1011
5'-most EST	ceu700432262.h1
Method	BLASTX
NCBI GI	g2501572
BLAST score	274
E value	4.0e-24
Match length	164
% identity	35
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No.	278074
Contig ID	82266_1.R1011
5'-most EST	uwc700154856.h1

Seq. No.	278075
Contig ID	82290_1.R1011
5'-most EST	uC-zmroteosinte093h11b2

Seq. No.	278076
Contig ID	82297_1.R1011
5'-most EST	uC-zmflmo17286g10b1
Method	BLASTX
NCBI GI	g168445
BLAST score	503
E value	5.0e-51
Match length	121
% identity	82
NCBI Description	(L00973) acidic class I chitinase [Zea mays]

Seq. No.	278077
Contig ID	82313_1.R1011
5'-most EST	LIB3068-046-Q1-K1-A1

Seq. No.	278078
Contig ID	82328_1.R1011
5'-most EST	uC-zmroteosinte004e12b1

Seq. No.	278079
Contig ID	82328_2.R1011
5'-most EST	tfd700571085.h1

Seq. No.	278080
Contig ID	82352_1.R1011
5'-most EST	uC-zmflb73039f10b1

Seq. No.	278081

Contig ID	82355_1.R1011
5'-most EST	uC-zmflmo17242g07b1
Seq. No.	278082
Contig ID	82358_1.R1011
5'-most EST	LIB3068-047-Q1-K1-A11
Method	BLASTX
NCBI GI	g4337175
BLAST score	284
E value	2.0e-25
Match length	110
% identity	50
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.	278083
Contig ID	82358_2.R1011
5'-most EST	wyr700238701.h1
Method	BLASTX
NCBI GI	g4337175
BLAST score	145
E value	2.0e-09
Match length	56
% identity	54
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.	278084
Contig ID	82387_1.R1011
5'-most EST	uC-zmflmo17153e09b1
Method	BLASTX
NCBI GI	g3297824
BLAST score	214
E value	5.0e-17
Match length	125
% identity	45
NCBI Description	(AL031032) bZIP transcription factor-like protein [Arabidopsis thaliana]
Seq. No.	278085
Contig ID	82391_1.R1011
5'-most EST	uC-zmroteosinte039d11b1
Seq. No.	278086
Contig ID	82409_1.R1011
5'-most EST	LIB3068-048-Q1-K1-A11
Method	BLASTX
NCBI GI	g2660670
BLAST score	400
E value	6.0e-39
Match length	138
% identity	54
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No.	278087
Contig ID	82426_1.R1011
5'-most EST	uC-zmrob73036g05b1
Method	BLASTX
NCBI GI	g4154352
BLAST score	313
E value	2.0e-28
Match length	171
% identity	43
NCBI Description	(AF110333) PrMC3 [Pinus radiata]

Seq. No.	278088
Contig ID	82432_1.R1011
5'-most EST	LIB3069-028-Q1-K1-B2

Seq. No.	278089
Contig ID	82442_1.R1011
5'-most EST	uC-zmflb73019h10b1
Method	BLASTX
NCBI GI	g4585991
BLAST score	1055
E value	1.0e-115
Match length	332
% identity	65
NCBI Description	(AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis thaliana]

Seq. No.	278090
Contig ID	82456_1.R1011
5'-most EST	LIB3068-049-Q1-K1-A1

Seq. No.	278091
Contig ID	82463_2.R1011
5'-most EST	nwy70443418.h1
Method	BLASTX
NCBI GI	g4263818
BLAST score	211
E value	3.0e-17
Match length	122
% identity	38
NCBI Description	(AC006067) unknown protein [Arabidopsis thaliana]

Seq. No.	278092
Contig ID	82474_1.R1011
5'-most EST	LIB3068-049-Q1-K1-C2
Method	BLASTX
NCBI GI	g1777312
BLAST score	266
E value	4.0e-23
Match length	84
% identity	63
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 278093

Contig ID	82477_1.R1011
5'-most EST	dyk700106939.h1
Method	BLASTX
NCBI GI	g2129516
BLAST score	445
E value	1.0e-69
Match length	321
% identity	48
NCBI Description	1-aminocyclopropane-1-carboxylate oxidase homolog (clone 2A6) - Arabidopsis thaliana >gi_599622_emb_CAA58151_ (X83096) 2A6 [Arabidopsis thaliana] >gi_2809261 (AC002560) F21B7.30 [Arabidopsis thaliana]

Seq. No.	278094
Contig ID	82495_1.R1011
5'-most EST	qmh700026311.f1
Method	BLASTX
NCBI GI	g4039152
BLAST score	170
E value	6.0e-12
Match length	36
% identity	78
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_ (AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	278095
Contig ID	82495_2.R1011
5'-most EST	ntr700075048.h1
Method	BLASTX
NCBI GI	g4039152
BLAST score	221
E value	6.0e-18
Match length	52
% identity	75
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_ (AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	278096
Contig ID	82495_3.R1011
5'-most EST	LIB3068-049-Q1-K1-F6
Method	BLASTX
NCBI GI	g4039152
BLAST score	218
E value	1.0e-17
Match length	52
% identity	73
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_ (AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	278097
Contig ID	82503_1.R1011
5'-most EST	vux700160159.h1

Seq. No. 278098

Contig ID	82505_1.R1011
5'-most EST	fdz701164183.h1
Seq. No.	278099
Contig ID	82517_1.R1011
5'-most EST	LIB3068-050-Q1-K1-A7
Seq. No.	278100
Contig ID	82540_1.R1011
5'-most EST	uC-zmflb73404e09a1
Seq. No.	278101
Contig ID	82540_2.R1011
5'-most EST	xsy700214950.h1
Seq. No.	278102
Contig ID	82565_1.R1011
5'-most EST	LIB3068-051-Q1-K1-A1
Method	BLASTX
NCBI GI	g1351359
BLAST score	200
E value	1.0e-15
Match length	42
% identity	79
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein - potato >gi_488712_emb_CAA55860_ (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]
Seq. No.	278103
Contig ID	82566_1.R1011
5'-most EST	uC-zmflmo17283b08b1
Seq. No.	278104
Contig ID	82569_1.R1011
5'-most EST	LIB3068-051-Q1-K1-A6
Method	BLASTX
NCBI GI	g3885334
BLAST score	733
E value	9.0e-78
Match length	221
% identity	62
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]
Seq. No.	278105
Contig ID	82573_1.R1011
5'-most EST	LIB3068-051-Q1-K1-B2
Method	BLASTX
NCBI GI	g4539660
BLAST score	526
E value	1.0e-53
Match length	152
% identity	67
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	278106
Contig ID	82579_1.R1011
5'-most EST	uC-zmflb73122c11b2
Method	BLASTX
NCBI GI	g3249105
BLAST score	740
E value	2.0e-78
Match length	274
% identity	57
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	278107
Contig ID	82582_1.R1011
5'-most EST	uC-zmflb73301b03b2

Seq. No.	278108
Contig ID	82597_1.R1011
5'-most EST	cat700016405.r1

Seq. No.	278109
Contig ID	82597_2.R1011
5'-most EST	ceu700428783.h1
Method	BLASTN
NCBI GI	g22430
BLAST score	71
E value	2.0e-31
Match length	111
% identity	91
NCBI Description	Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate dehydrogenase subunit A

Seq. No.	278110
Contig ID	82597_4.R1011
5'-most EST	uC-zmflb731215f04a1

Seq. No.	278111
Contig ID	82627_1.R1011
5'-most EST	LIB3068-059-Q1-K1-G7
Method	BLASTN
NCBI GI	g949979
BLAST score	296
E value	1.0e-166
Match length	361
% identity	95
NCBI Description	Z.mays Glossy2 locus DNA

Seq. No.	278112
Contig ID	82631_1.R1011
5'-most EST	nbm700468386.h1
Method	BLASTX
NCBI GI	g4097585
BLAST score	440
E value	2.0e-43
Match length	170
% identity	56
NCBI Description	(U64925) NTGP4 [Nicotiana tabacum]

Seq. No.	278113
Contig ID	82631_3.R1011
5'-most EST	mwy700438149.h1
Method	BLASTX
NCBI GI	g4097585
BLAST score	212
E value	5.0e-17
Match length	76
% identity	59
NCBI Description	(U64925) NTGP4 [Nicotiana tabacum]

Seq. No.	278114
Contig ID	82632_1.R1011
5'-most EST	LIB3068-052-Q1-K1-B8
Method	BLASTX
NCBI GI	g899608
BLAST score	1009
E value	1.0e-110
Match length	208
% identity	26
NCBI Description	(U29158) polyubiquitin [Zea mays]

Seq. No.	278115
Contig ID	82638_1.R1011
5'-most EST	LIB3068-052-Q1-K1-C3
Method	BLASTN
NCBI GI	g902200
BLAST score	216
E value	1.0e-118
Match length	400
% identity	97
NCBI Description	Z.mays complete chloroplast genome

Seq. No.	278116
Contig ID	82639_1.R1011
5'-most EST	tzu700201316.h1
Method	BLASTX
NCBI GI	g4455159
BLAST score	959
E value	1.0e-104
Match length	265
% identity	67
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	278117
Contig ID	82644_1.R1011
5'-most EST	LIB3068-052-Q1-K1-D10

Seq. No.	278118
Contig ID	82680_1.R1011
5'-most EST	LIB3068-053-Q1-K1-A4

Seq. No.	278119
Contig ID	82680_2.R1011
5'-most EST	tzu700202178.h1

Seq. No.	278120
Contig ID	82680_5.R1011
5'-most EST	LIB3137-004-Q1-K1-G3
Seq. No.	278121
Contig ID	82685_1.R1011
5'-most EST	LIB3068-053-Q1-K1-B2
Seq. No.	278122
Contig ID	82689_1.R1011
5'-most EST	fwa70O098075.h1
Seq. No.	278123
Contig ID	82693_1.R1011
5'-most EST	uC-zmflmo17289f06b1
Method	BLASTX
NCBI GI	g4544412
BLAST score	490
E value	5.0e-49
Match length	328
% identity	36
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.	278124
Contig ID	82717_1.R1011
5'-most EST	LIB3068-053-Q1-K1-F8
Seq. No.	278125
Contig ID	82720_1.R1011
5'-most EST	LIB3068-053-Q1-K1-G11
Method	BLASTX
NCBI GI	g2293112
BLAST score	183
E value	2.0e-13
Match length	141
% identity	34
NCBI Description	(Y10579) potassium channel [Vicia faba]
Seq. No.	278126
Contig ID	82730_1.R1011
5'-most EST	wen70O334796.h1
Method	BLASTX
NCBI GI	g2244754
BLAST score	185
E value	2.0e-13
Match length	185
% identity	36
NCBI Description	(Z97335) heat shock transcription factor homolog [Arabidopsis thaliana]
Seq. No.	278127
Contig ID	82731_1.R1011
5'-most EST	uwc70O150788.h1
Method	BLASTX
NCBI GI	g4586021
BLAST score	575
E value	3.0e-59

Match length 148
% identity 74
NCBI Description (AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No. 278128
Contig ID 82731_2.R1011
5'-most EST pmx700085405.h1
Method BLASTX
NCBI GI g3309243
BLAST score 504
E value 4.0e-51
Match length 124
% identity 78
NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No. 278129
Contig ID 82754_1.R1011
5'-most EST uC-zmrob73045b08a1

Seq. No. 278130
Contig ID 82766_1.R1011
5'-most EST xjt700092241.h1

Seq. No. 278131
Contig ID 82774_1.R1011
5'-most EST uC-zmflb73300c06b1
Method BLASTX
NCBI GI g4538941
BLAST score 671
E value 2.0e-70
Match length 245
% identity 58
NCBI Description (AL049483) NPR1 like protein [Arabidopsis thaliana]

Seq. No. 278132
Contig ID 82786_1.R1011
5'-most EST LIB3068-055-Q1-K1-B7

Seq. No. 278133
Contig ID 82803_1.R1011
5'-most EST LIB3068-055-Q1-K1-E7

Seq. No. 278134
Contig ID 82804_1.R1011
5'-most EST uC-zmflm017233f10b1
Method BLASTX
NCBI GI g4432864
BLAST score 612
E value 2.0e-63
Match length 242
% identity 48
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 278135
Contig ID 82807_1.R1011

5'-most EST	LIB3068-055-Q1-K1-F2
Method	BLASTX
NCBI GI	g4262241
BLAST score	168
E value	1.0e-11
Match length	112
% identity	42
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	278136
Contig ID	82822_1.R1011
5'-most EST	ceu700433425.h1
Method	BLASTX
NCBI GI	g2462911
BLAST score	189
E value	1.0e-18
Match length	76
% identity	71
NCBI Description	(Z83832) UDP-glucose:sterol glucosyltransferase [Avena sativa]

Seq. No.	278137
Contig ID	82840_1.R1011
5'-most EST	LIB3068-056-Q1-K1-E4

Seq. No.	278138
Contig ID	82857_1.R1011
5'-most EST	LIB3068-057-Q1-K1-A6

Seq. No.	278139
Contig ID	82868_1.R1011
5'-most EST	hbs701185969.h1
Method	BLASTX
NCBI GI	g4100646
BLAST score	234
E value	2.0e-19
Match length	62
% identity	71
NCBI Description	(AF001948) putative ubiquitin conjugating enzyme [Pinus resinosa]

Seq. No.	278140
Contig ID	82883_1.R1011
5'-most EST	uC-zmflb73194c10b2
Method	BLASTX
NCBI GI	g1655536
BLAST score	559
E value	2.0e-57
Match length	195
% identity	59
NCBI Description	(Y09095) chloride channel [Arabidopsis thaliana] >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel protein [Arabidopsis thaliana]

Seq. No.	278141
Contig ID	82891_1.R1011
5'-most EST	pmx700087648.h1

Method	BLASTX
NCBI GI	g3834303
BLAST score	531
E value	8.0e-54
Match length	257
% identity	46
NCBI Description	(AC005679) F9K20.3 [Arabidopsis thaliana]

Seq. No.	278142
Contig ID	82897_1.R1011
5'-most EST	LIB3068-057-Q1-K1-H11
Method	BLASTX
NCBI GI	g1491776
BLAST score	213
E value	5.0e-17
Match length	86
% identity	53
NCBI Description	(M37636) cationic peroxidase [Arachis hypogaea]

Seq. No.	278143
Contig ID	82901_1.R1011
5'-most EST	LIB84-030-Q1-E1-B3
Method	BLASTX
NCBI GI	g1871194
BLAST score	356
E value	1.0e-33
Match length	112
% identity	59
NCBI Description	(U90439) DNA binding protein isolog [Arabidopsis thaliana] >gi_2335092 (AC002339) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	278144
Contig ID	82901_2.R1011
5'-most EST	tfd700573106.h1
Method	BLASTX
NCBI GI	g1871194
BLAST score	186
E value	1.0e-26
Match length	107
% identity	58
NCBI Description	(U90439) DNA binding protein isolog [Arabidopsis thaliana] >gi_2335092 (AC002339) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	278145
Contig ID	82906_1.R1011
5'-most EST	uC-zmflmo17128b08b1

Seq. No.	278146
Contig ID	82906_2.R1011
5'-most EST	nwy700447896.h1

Seq. No.	278147
Contig ID	82910_1.R1011
5'-most EST	LIB3068-058-Q1-K1-B1

Seq. No.	278148
Contig ID	82927_1.R1011
5'-most EST	uC-zmflmo17102b04a1

Seq. No.	278149
Contig ID	82933_1.R1011
5'-most EST	uC-zmflMo17014c01b1
Method	BLASTX
NCBI GI	g1841464
BLAST score	369
E value	4.0e-35
Match length	98
% identity	39
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	278150
Contig ID	82945_1.R1011
5'-most EST	xmt700256837.h1

Seq. No.	278151
Contig ID	82953_1.R1011
5'-most EST	uC-zmflmo17180g06b1

Seq. No.	278152
Contig ID	82966_1.R1011
5'-most EST	LIB3136-040-P1-K1-G2

Seq. No.	278153
Contig ID	82973_1.R1011
5'-most EST	LIB3136-022-Q1-K1-E4
Method	BLASTX
NCBI GI	g2388571
BLAST score	584
E value	3.0e-60
Match length	213
% identity	55
NCBI Description	(AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb_X98321). [Arabidopsis thaliana] >gi_2738254 (U97684) peroxidase precursor [Arabidopsis thaliana]

Seq. No.	278154
Contig ID	82980_1.R1011
5'-most EST	LIB3068-059-Q1-K1-C12

Seq. No.	278155
Contig ID	82989_1.R1011
5'-most EST	uC-zmflmo17339e06b1
Method	BLASTX
NCBI GI	g1172972
BLAST score	676
E value	5.0e-71
Match length	136
% identity	96
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 >gi_1363589_pir__S58589 ribosomal protein L16 - maize chloroplast >gi_902259_emb_CAA60323_ (X86563) ribosomal protein L16 [Zea mays]

Seq. No.	278156
Contig ID	83000_1.R1011
5'-most EST	LIB3068-059-Q1-K1-F6
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	278157
Contig ID	83010_1.R1011
5'-most EST	LIB3068-059-Q1-K1-H10
Method	BLASTX
NCBI GI	g4415942
BLAST score	159
E value	1.0e-10
Match length	95
% identity	40
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278158
Contig ID	83013_1.R1011
5'-most EST	xsy700217594.h1
Method	BLASTX
NCBI GI	g4455159
BLAST score	574
E value	4.0e-59
Match length	158
% identity	71
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	278159
Contig ID	83022_1.R1011
5'-most EST	xsy700213676.h1

Seq. No.	278160
Contig ID	83038_1.R1011
5'-most EST	uC-zmflmo17308h11b1
Method	BLASTX
NCBI GI	g3128217
BLAST score	399
E value	1.0e-38
Match length	151
% identity	58
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana] >gi_3337374 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278161
Contig ID	83052_1.R1011
5'-most EST	LIB36-005-Q1-E1-D8
Method	BLASTX
NCBI GI	g1346867
BLAST score	161

E value	1.0e-10
Match length	34
% identity	100
NCBI Description	PHOTOSYSTEM II REACTION CENTRE M PROTEIN >gi_1363583_pir__S58540 photosystem II protein psbM - maize chloroplast >gi_902210_emb_CAA60274_ (X86563) PSII low MW protein [Zea mays]

Seq. No.	278162
Contig ID	83064_1.R1011
5'-most EST	cyk700050166.f1

Seq. No.	278163
Contig ID	83066_1.R1011
5'-most EST	uC-zmflb73060f07b1
Method	BLASTX
NCBI GI	g2213643
BLAST score	571
E value	1.0e-79
Match length	188
% identity	80
NCBI Description	(U57338) glossy1 homolog [Oryza sativa]

Seq. No.	278164
Contig ID	83068_1.R1011
5'-most EST	LIB3068-060-Q1-K1-G8
Method	BLASTX
NCBI GI	g3402705
BLAST score	275
E value	4.0e-24
Match length	66
% identity	70
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278165
Contig ID	83071_1.R1011
5'-most EST	LIB3068-060-Q1-K1-H10
Method	BLASTX
NCBI GI	g3402711
BLAST score	256
E value	8.0e-22
Match length	116
% identity	42
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	278166
Contig ID	83075_1.R1011
5'-most EST	LIB3068-060-Q1-K1-H8

Seq. No.	278167
Contig ID	83086_1.R1011
5'-most EST	uC-zmflb73196b05b1

Seq. No.	278168
Contig ID	83092_1.R1011
5'-most EST	xjt700092462.h1

Seq. No. 278169
Contig ID 83127_1.R1011
5'-most EST uwc700149803.h1

Seq. No. 278170
Contig ID 83131_1.R1011
5'-most EST LIB3068-062-Q1-K1-B7

Seq. No. 278171
Contig ID 83133_1.R1011
5'-most EST uC-zmflm017214b08b1
Method BLASTX
NCBI GI g4056460
BLAST score 260
E value 6.0e-22
Match length 165
% identity 40
NCBI Description (AC005990) Contains similarity to gb_L26505 Met30p from Saccharomyces cerevisiae. ESTs gb_F14133, gb_T46217, gb_AA404758 and gb_Z37647 come from this gene. [Arabidopsis thaliana]

Seq. No. 278172
Contig ID 83146_1.R1011
5'-most EST gct701176323.h1
Method BLASTX
NCBI GI g4538979
BLAST score 332
E value 8.0e-31
Match length 128
% identity 46
NCBI Description (AL049487) putative protein [Arabidopsis thaliana]

Seq. No. 278173
Contig ID 83146_2.R1011
5'-most EST uC-zmflb73207e05b1

Seq. No. 278174
Contig ID 83152_1.R1011
5'-most EST LIB3068-062-Q1-K1-E10

Seq. No. 278175
Contig ID 83156_1.R1011
5'-most EST LIB3068-062-Q1-K1-E7

Seq. No. 278176
Contig ID 83176_1.R1011
5'-most EST LIB3069-001-Q1-K1-A12
Method BLASTX
NCBI GI g3193284
BLAST score 426
E value 8.0e-42
Match length 157
% identity 54
NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	278177
Contig ID	83180_1.R1011
5'-most EST	uC-zmflb73344a03a2

Seq. No.	278178
Contig ID	83180_2.R1011
5'-most EST	LIB3136-005-Q1-K1-H12

Seq. No.	278179
Contig ID	83180_3.R1011
5'-most EST	uC-zmflb73256e10b1

Seq. No.	278180
Contig ID	83181_1.R1011
5'-most EST	LIB3069-001-Q1-K1-A8

Seq. No.	278181
Contig ID	83190_1.R1011
5'-most EST	dyk700103293.h1

Seq. No.	278182
Contig ID	83193_1.R1011
5'-most EST	ntr700076345.h1
Method	BLASTX
NCBI GI	g2880043
BLAST score	398
E value	3.0e-38
Match length	252
% identity	36
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	278183
Contig ID	83195_1.R1011
5'-most EST	ceu700423940.h1
Method	BLASTX
NCBI GI	g2842744
BLAST score	298
E value	5.0e-27
Match length	70
% identity	74
NCBI Description	ENHANCER OF RUDIMENTARY HOMOLOG >gi_1595812 (U67398) enhancer of rudimentary homolog ATER [Arabidopsis thaliana]

Seq. No.	278184
Contig ID	83206_1.R1011
5'-most EST	LIB3069-001-Q1-K1-D4

Seq. No.	278185
Contig ID	83214_1.R1011
5'-most EST	uC-zmflb73144d06b1
Method	BLASTX
NCBI GI	g2565011
BLAST score	258
E value	4.0e-22
Match length	179
% identity	32

NCBI Description	(AC002983) putative MuDR-A-like transposon protein [Arabidopsis thaliana]
Seq. No.	278186
Contig ID	83221_1.R1011
5'-most EST	uC-zmflb73262h01a2
Seq. No.	278187
Contig ID	83221_2.R1011
5'-most EST	uC-zmflb73410h12a1
Seq. No.	278188
Contig ID	83227_1.R1011
5'-most EST	LIB3069-001-Q1-K1-F3
Method	BLASTX
NCBI GI	g3273196
BLAST score	231
E value	4.0e-19
Match length	103
% identity	47
NCBI Description	(AB010915) responce regulator1 [Arabidopsis thaliana] >gi_3323583 (AF057282) two-component response regulator homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_ (AB008487) response regulator 4 [Arabidopsis thaliana]
Seq. No.	278189
Contig ID	83231_1.R1011
5'-most EST	uC-zmflB73047b12b1
Method	BLASTX
NCBI GI	g1076414
BLAST score	480
E value	2.0e-48
Match length	134
% identity	69
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.	278190
Contig ID	83232_1.R1011
5'-most EST	uC-zmflmo17404c11a1
Seq. No.	278191
Contig ID	83234_1.R1011
5'-most EST	LIB3069-001-Q1-K1-G1
Seq. No.	278192
Contig ID	83238_1.R1011
5'-most EST	LIB3069-001-Q1-K1-G2
Method	BLASTX
NCBI GI	g2982455
BLAST score	165
E value	2.0e-11
Match length	38
% identity	74
NCBI Description	(AL022223) putative uracil phosphoribosyl transferase [Arabidopsis thaliana]

Docket No. PI0004

Seq. No.	278193
Contig ID	83241_1.R1011
5'-most EST	LIB3069-001-Q1-K1-G5

Seq. No.	278194
Contig ID	83246_1.R1011
5'-most EST	LIB3069-001-Q1-K1-H1
Method	BLASTX
NCBI GI	g3075391
BLAST score	164
E value	4.0e-11
Match length	74
% identity	53
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	278195
Contig ID	83250_1.R1011
5'-most EST	rvt700551237.h1
Method	BLASTX
NCBI GI	g2673906
BLAST score	495
E value	7.0e-50
Match length	116
% identity	76
NCBI Description	(AC002561) putative DNA polymerase delta small subunit [Arabidopsis thaliana]

Seq. No.	278196
Contig ID	83252_1.R1011
5'-most EST	fwa700101928.h1
Method	BLASTX
NCBI GI	g2098713
BLAST score	691
E value	7.0e-73
Match length	194
% identity	67
NCBI Description	(U82977) pectinesterase [Citrus sinensis]

Seq. No.	278197
Contig ID	83267_1.R1011
5'-most EST	uC-zmflmo17127c11a1

Seq. No.	278198
Contig ID	83273_1.R1011
5'-most EST	LIB3069-002-Q1-K1-B8
Method	BLASTX
NCBI GI	g4335754
BLAST score	1041
E value	1.0e-113
Match length	270
% identity	68
NCBI Description	(AC006284) putative acid phophatase (contains metallo-phosphoesterase motif, prosite: QDOC50185) [Arabidopsis thaliana]

Seq. No. 278199

Contig ID	83277_1.R1011
5'-most EST	cat700019847.r1

Seq. No.	278200
Contig ID	83280_1.R1011
5'-most EST	uC-zmroteosinte011e07b1
Method	BLASTX
NCBI GI	g4325370
BLAST score	507
E value	9.0e-82
Match length	198
% identity	73
NCBI Description	(AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana]

Seq. No.	278201
Contig ID	83291_1.R1011
5'-most EST	LIB3069-002-Q1-K1-D3

Seq. No.	278202
Contig ID	83307_1.R1011
5'-most EST	uC-zmflmo17342a11b1
Method	BLASTX
NCBI GI	g2829887
BLAST score	934
E value	1.0e-101
Match length	369
% identity	54
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	278203
Contig ID	83308_1.R1011
5'-most EST	LIB3069-002-Q1-K1-E9

Seq. No.	278204
Contig ID	83309_1.R1011
5'-most EST	fdz701164319.h1

Seq. No.	278205
Contig ID	83313_1.R1011
5'-most EST	pwr700450868.h1
Method	BLASTX
NCBI GI	g4586107
BLAST score	347
E value	1.0e-32
Match length	131
% identity	15
NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	278206
Contig ID	83319_1.R1011
5'-most EST	LIB3069-002-Q1-K1-G10
Method	BLASTX
NCBI GI	g3522939
BLAST score	265
E value	1.0e-28

Match length	78
% identity	82
NCBI Description	(AC004411) putative squamosa-promoter binding protein [Arabidopsis thaliana]

Seq. No.	278207
Contig ID	83334_1.R1011
5'-most EST	LIB3069-025-Q1-K1-G6
Method	BLASTX
NCBI GI	g4235644
BLAST score	468
E value	1.0e-46
Match length	211
% identity	45
NCBI Description	(AF119040) polyprotein [Lycopersicon esculentum]

Seq. No.	278208
Contig ID	83338_1.R1011
5'-most EST	LIB3069-002-Q1-K1-H9
Method	BLASTX
NCBI GI	g4539335
BLAST score	330
E value	2.0e-30
Match length	91
% identity	58
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	278209
Contig ID	83339_1.R1011
5'-most EST	uC-zmflb73173g03b1
Method	BLASTX
NCBI GI	g584867
BLAST score	302
E value	5.0e-27
Match length	93
% identity	56
NCBI Description	CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5) >gi_481959_pir__S40266 gene CYP77A2 protein - eggplant >gi_542071_pir__S41598 cytochrome P450 77A2 - eggplant >gi_438241_emb_CAA50646_ (X71655) CYP77A2 [Solanum melongena]

Seq. No.	278210
Contig ID	83347_1.R1011
5'-most EST	LIB3069-003-Q1-K1-B1

Seq. No.	278211
Contig ID	83378_1.R1011
5'-most EST	uC-zmroB73017c09b1
Method	BLASTX
NCBI GI	g1619602
BLAST score	373
E value	1.0e-35
Match length	98
% identity	67
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	278212
Contig ID	83388_1.R1011
5'-most EST	wty700173028.h1
Method	BLASTX
NCBI GI	g3327240
BLAST score	358
E value	9.0e-34
Match length	98
% identity	74
NCBI Description	(AB016071) homeobox gene [Oryza sativa]

Seq. No.	278213
Contig ID	83388_2.R1011
5'-most EST	uC-zmflmo17132g02a1
Method	BLASTN
NCBI GI	g1008878
BLAST score	235
E value	1.0e-129
Match length	349
% identity	93
NCBI Description	Zea mays RS1 mRNA, complete cds

Seq. No.	278214
Contig ID	83389_1.R1011
5'-most EST	LIB3069-003-Q1-K1-F10
Method	BLASTX
NCBI GI	g2388963
BLAST score	174
E value	4.0e-12
Match length	127
% identity	31
NCBI Description	(Z98979) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	278215
Contig ID	83394_1.R1011
5'-most EST	uC-zmflMo17084b02b1
Method	BLASTX
NCBI GI	g4583431
BLAST score	443
E value	8.0e-44
Match length	82
% identity	100
NCBI Description	(AF126489) rough sheath2 protein [Zea mays]

Seq. No.	278216
Contig ID	83406_1.R1011
5'-most EST	LIB3069-003-Q1-K1-G9
Method	BLASTX
NCBI GI	g3056602
BLAST score	367
E value	5.0e-35
Match length	121
% identity	55
NCBI Description	(AC004255) T1F9.23 [Arabidopsis thaliana]

Seq. No.	278217
Contig ID	83408_1.R1011

5'-most EST	LIB3069-003-Q1-K1-H10
Seq. No.	278218
Contig ID	83427_1.R1011
5'-most EST	uC-zmflb73129f07b1
Method	BLASTX
NCBI GI	g2286123
BLAST score	159
E value	2.0e-10
Match length	69
% identity	43
NCBI Description	(U95607) testis specific DNAj-homolog [Mus musculus]
Seq. No.	278219
Contig ID	83430_1.R1011
5'-most EST	LIB3069-004-Q1-K1-B7
Seq. No.	278220
Contig ID	83432_1.R1011
5'-most EST	LIB3069-004-Q1-K1-B9
Seq. No.	278221
Contig ID	83447_1.R1011
5'-most EST	gwl700613389.h1
Seq. No.	278222
Contig ID	83451_1.R1011
5'-most EST	cyk700051741.f1
Method	BLASTX
NCBI GI	g1354849
BLAST score	379
E value	2.0e-36
Match length	148
% identity	51
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]
Seq. No.	278223
Contig ID	83456_1.R1011
5'-most EST	uC-zmflmo17164g02b1
Method	BLASTX
NCBI GI	g4126960
BLAST score	152
E value	7.0e-10
Match length	77
% identity	40
NCBI Description	(AB017482) retinal oxidase/aldehyde oxidase [Mus musculus]
Seq. No.	278224
Contig ID	83463_1.R1011
5'-most EST	LIB3069-004-Q1-K1-E8
Method	BLASTX
NCBI GI	g2760328
BLAST score	417
E value	8.0e-41
Match length	117
% identity	63
NCBI Description	(AC002130) F1N21.13 [Arabidopsis thaliana]

Seq. No.	278225
Contig ID	83466_1.R1011
5'-most EST	nbm700474892.h1
Seq. No.	278226
Contig ID	83467_1.R1011
5'-most EST	uC-zmflb73186e05a1
Seq. No.	278227
Contig ID	83486_1.R1011
5'-most EST	LIB3069-004-Q1-K1-H10
Method	BLASTX
NCBI GI	g3152606
BLAST score	257
E value	4.0e-22
Match length	56
% identity	80
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]
Seq. No.	278228
Contig ID	83488_1.R1011
5'-most EST	nbm700471369.h1
Seq. No.	278229
Contig ID	83499_1.R1011
5'-most EST	LIB3136-027-P1-K1-F5
Method	BLASTX
NCBI GI	g3643604
BLAST score	197
E value	4.0e-15
Match length	80
% identity	49
NCBI Description	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	278230
Contig ID	83510_1.R1011
5'-most EST	LIB3069-005-Q1-K1-B3
Seq. No.	278231
Contig ID	83510_2.R1011
5'-most EST	pmx700091840.h1
Seq. No.	278232
Contig ID	83511_1.R1011
5'-most EST	LIB3069-005-Q1-K1-B4
Seq. No.	278233
Contig ID	83513_1.R1011
5'-most EST	LIB3069-005-Q1-K1-B6
Method	BLASTX
NCBI GI	g1168263
BLAST score	324
E value	5.0e-30
Match length	149

% identity	21
NCBI Description	ATP-BINDING CASSETTE TRANSPORTER 2 >gi_1082239_pir__B54774 ATP binding cassette transporter ABC2 - human (fragment) >gi_495259_emb_CAA53531_ (X75927) abc2 [Mus musculus]

Seq. No.	278234
Contig ID	83523_1.R1011
5'-most EST	vux700158166.h1
Method	BLASTN
NCBI GI	g22123
BLAST score	60
E value	5.0e-25
Match length	64
% identity	49
NCBI Description	Maize alcohol dehydrogenase 1 gene (Adh1-1S)

Seq. No.	278235
Contig ID	83534_1.R1011
5'-most EST	xsy700208831.h1
Method	BLASTX
NCBI GI	g2392895
BLAST score	272
E value	3.0e-33
Match length	147
% identity	50
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	278236
Contig ID	83544_1.R1011
5'-most EST	uC-zmroteosinte058c06b2
Method	BLASTX
NCBI GI	g2104689
BLAST score	210
E value	8.0e-29
Match length	246
% identity	34
NCBI Description	(U92793) alpha glucosidase II, alpha subunit [Mus musculus]

Seq. No.	278237
Contig ID	83571_1.R1011
5'-most EST	ymt700224449.h1
Method	BLASTX
NCBI GI	g1871184
BLAST score	253
E value	1.0e-21
Match length	128
% identity	41
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	278238
Contig ID	83572_1.R1011
5'-most EST	LIB3069-005-Q1-K1-H3
Method	BLASTX
NCBI GI	g4191791
BLAST score	326
E value	3.0e-30

Match length	74
% identity	77
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	278239
Contig ID	83581_1.R1011
5'-most EST	LIB3069-006-Q1-K1-A11

Seq. No.	278240
Contig ID	83585_1.R1011
5'-most EST	LIB3069-006-Q1-K1-A4

Seq. No.	278241
Contig ID	83587_1.R1011
5'-most EST	uC-zmflmo17199b09b1
Method	BLASTX
NCBI GI	g4371285
BLAST score	334
E value	7.0e-31
Match length	134
% identity	53
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278242
Contig ID	83587_2.R1011
5'-most EST	uC-zmroteosinte093e11b2
Method	BLASTX
NCBI GI	g4371285
BLAST score	564
E value	1.0e-57
Match length	172
% identity	62
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278243
Contig ID	83587_3.R1011
5'-most EST	LIB3069-006-Q1-K1-A7
Method	BLASTX
NCBI GI	g4371285
BLAST score	517
E value	1.0e-52
Match length	174
% identity	58
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278244
Contig ID	83596_1.R1011
5'-most EST	uC-zmroB73017f10b1

Seq. No.	278245
Contig ID	83606_1.R1011
5'-most EST	LIB3069-006-Q1-K1-C5

Seq. No.	278246
Contig ID	83621_1.R1011
5'-most EST	uC-zmflmo17021g08b1

Method	BLASTX
NCBI GI	g3935183
BLAST score	542
E value	4.0e-55
Match length	264
% identity	44
NCBI Description	(AC004557) F17L21.26 [Arabidopsis thaliana]

Seq. No.	278247
Contig ID	83626_1.R1011
5'-most EST	ymt700224348.h1

Seq. No.	278248
Contig ID	83634_1.R1011
5'-most EST	LIB3069-006-Q1-K1-F5

Seq. No.	278249
Contig ID	83634_2.R1011
5'-most EST	tfd700575850.h1

Seq. No.	278250
Contig ID	83641_1.R1011
5'-most EST	LIB3069-006-Q1-K1-G2

Seq. No.	278251
Contig ID	83645_1.R1011
5'-most EST	uC-zmflb73365e05a1
Method	BLASTX
NCBI GI	g2583121
BLAST score	168
E value	2.0e-11
Match length	45
% identity	67
NCBI Description	(AC002387) putative phosphotransferase [Arabidopsis thaliana]

Seq. No.	278252
Contig ID	83649_1.R1011
5'-most EST	LIB3069-006-Q1-K1-H1

Seq. No.	278253
Contig ID	83650_1.R1011
5'-most EST	uC-zmflmo17102d04a1

Seq. No.	278254
Contig ID	83664_1.R1011
5'-most EST	LIB3069-008-Q1-K1-A3

Seq. No.	278255
Contig ID	83670_1.R1011
5'-most EST	vqh700053145.r1

Seq. No.	278256
Contig ID	83674_1.R1011
5'-most EST	LIB3069-008-Q1-K1-B3
Method	BLASTX
NCBI GI	g1169735

BLAST score	614
E value	7.0e-64
Match length	196
% identity	63
NCBI Description	FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN) >gi_2135120_pir__S45340 FKBP-rapamycin-associated protein (FRAP) - human >gi_508482 (L34075) FKBP-rapamycin associated protein [Homo sapiens]

Seq. No.	278257
Contig ID	83676_1.R1011
5'-most EST	LIB3069-008-Q1-K1-B5

Seq. No.	278258
Contig ID	83691_1.R1011
5'-most EST	uC-zmflmo17075a07b2

Seq. No.	278259
Contig ID	83711_1.R1011
5'-most EST	uC-zmflb73349b04a2
Method	BLASTX
NCBI GI	g2632252
BLAST score	900
E value	4.0e-97
Match length	270
% identity	64
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	278260
Contig ID	83711_2.R1011
5'-most EST	uC-zmroB73013h05b1
Method	BLASTX
NCBI GI	g2632254
BLAST score	313
E value	6.0e-29
Match length	85
% identity	65
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	278261
Contig ID	83716_1.R1011
5'-most EST	uC-zmflmo170112c06b1

Seq. No.	278262
Contig ID	83736_1.R1011
5'-most EST	wty700170869.h1
Method	BLASTX
NCBI GI	g2947063
BLAST score	671
E value	3.0e-70
Match length	306
% identity	46
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	278263
Contig ID	83750_1.R1011

5'-most EST	uC-zmflb73117c08b2
Seq. No.	278264
Contig ID	83768_1.R1011
5'-most EST	LIB3069-009-Q1-K1-D6
Method	BLASTX
NCBI GI	g4160294
BLAST score	520
E value	1.0e-52
Match length	160
% identity	59
NCBI Description	(Y18644) methyltransferase-like protein 1 [Mus musculus]
Seq. No.	278265
Contig ID	83771_1.R1011
5'-most EST	LIB3069-009-Q1-K1-E1
Seq. No.	278266
Contig ID	83778_1.R1011
5'-most EST	LIB3069-009-Q1-K1-E7
Seq. No.	278267
Contig ID	83795_2.R1011
5'-most EST	ceu700422576.h1
Seq. No.	278268
Contig ID	83798_1.R1011
5'-most EST	uC-zmflb73075f10a1
Method	BLASTX
NCBI GI	g3924594
BLAST score	150
E value	1.0e-09
Match length	61
% identity	56
NCBI Description	(AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi_4262139_gb_AAD14439_ (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]
Seq. No.	278269
Contig ID	83809_1.R1011
5'-most EST	uC-zmflmo17295c03b1
Seq. No.	278270
Contig ID	83811_1.R1011
5'-most EST	LIB3069-009-Q1-K1-H9
Seq. No.	278271
Contig ID	83812_1.R1011
5'-most EST	LIB3069-010-Q1-K1-A1
Method	BLASTX
NCBI GI	g2231149
BLAST score	980
E value	1.0e-106
Match length	255
% identity	80
NCBI Description	(L81152) integral membrane protein [Oryza sativa]

Seq. No.	278272
Contig ID	83836_1.R1011
5'-most EST	uC-zmflmo17086c12a1
Seq. No.	278273
Contig ID	83866_1.R1011
5'-most EST	LIB3069-010-Q1-K1-G12
Seq. No.	278274
Contig ID	83889_1.R1011
5'-most EST	hbs701185342.h1
Seq. No.	278275
Contig ID	83918_1.R1011
5'-most EST	LIB3069-019-Q1-K1-C5
Seq. No.	278276
Contig ID	83925_1.R1011
5'-most EST	LIB3069-011-Q1-K1-D6
Seq. No.	278277
Contig ID	83933_1.R1011
5'-most EST	xmt700262705.h1
Method	BLASTX
NCBI GI	g2829911
BLAST score	244
E value	7.0e-43
Match length	147
% identity	65
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.	278278
Contig ID	83933_2.R1011
5'-most EST	uC-zmflb73404a02a1
Method	BLASTX
NCBI GI	g2829911
BLAST score	244
E value	1.0e-20
Match length	65
% identity	71
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.	278279
Contig ID	83969_1.R1011
5'-most EST	xdb700339388.h1
Method	BLASTX
NCBI GI	g3600049
BLAST score	304
E value	1.0e-27
Match length	78
% identity	73
NCBI Description	(AF080120) similar to initiation factor IF2-beta (Pfam: GTP_EFTU.hmm, score: 226.67) [Arabidopsis thaliana]
Seq. No.	278280
Contig ID	83980_1.R1011
5'-most EST	LIB3069-044-Q1-K1-D12

Seq. No.	278281
Contig ID	83989_1.R1011
5'-most EST	uC-zmflb73271a08a1

Seq. No.	278282
Contig ID	83993_1.R1011
5'-most EST	LIB3136-018-Q1-K1-D3
Method	BLASTX
NCBI GI	g1363749
BLAST score	171
E value	1.0e-11
Match length	135
% identity	33
NCBI Description	probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae) >gi_632679 (U20162) Cdc73p [Saccharomyces cerevisiae]

Seq. No.	278283
Contig ID	83994_1.R1011
5'-most EST	LIB3069-012-Q1-K1-C12
Method	BLASTX
NCBI GI	g1899060
BLAST score	191
E value	2.0e-14
Match length	84
% identity	43
NCBI Description	(U79669) endosperm C-24 sterol methyltransferase [Zea mays]

Seq. No.	278284
Contig ID	84009_1.R1011
5'-most EST	LIB3069-012-Q1-K1-D8

Seq. No.	278285
Contig ID	84023_1.R1011
5'-most EST	uC-zmroteosinte116a09b2

Seq. No.	278286
Contig ID	84025_1.R1011
5'-most EST	uC-zmflMo17064e10b1
Method	BLASTX
NCBI GI	g2651303
BLAST score	1547
E value	1.0e-173
Match length	500
% identity	63
NCBI Description	(AC002336) putative potassium transporter [Arabidopsis thaliana]

Seq. No.	278287
Contig ID	84034_1.R1011
5'-most EST	uC-zmroteosinte036e12b1
Method	BLASTX
NCBI GI	g2462745
BLAST score	439
E value	5.0e-75
Match length	224

% identity 57
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 278288
Contig ID 84041_1.R1011
5'-most EST uC-zmroteosinte004e03b1

Seq. No. 278289
Contig ID 84053_1.R1011
5'-most EST LIB3069-014-Q1-K1-A12

Seq. No. 278290
Contig ID 84061_1.R1011
5'-most EST LIB3069-014-Q1-K1-A9

Seq. No. 278291
Contig ID 84064_1.R1011
5'-most EST LIB3069-014-Q1-K1-B11

Seq. No. 278292
Contig ID 84065_1.R1011
5'-most EST LIB3069-014-Q1-K1-B12

Seq. No. 278293
Contig ID 84074_1.R1011
5'-most EST LIB3069-013-Q1-K1-C11

Seq. No. 278294
Contig ID 84075_1.R1011
5'-most EST LIB3069-014-Q1-K1-C12

Seq. No. 278295
Contig ID 84082_1.R1011
5'-most EST LIB3069-014-Q1-K1-C9

Seq. No. 278296
Contig ID 84083_1.R1011
5'-most EST LIB3069-013-Q1-K1-D1

Seq. No. 278297
Contig ID 84085_1.R1011
5'-most EST LIB3069-014-Q1-K1-D12

Seq. No. 278298
Contig ID 84102_1.R1011
5'-most EST LIB3069-013-Q1-K1-E7

Seq. No. 278299
Contig ID 84104_1.R1011
5'-most EST LIB3069-014-Q1-K1-E9

Seq. No. 278300
Contig ID 84106_1.R1011
5'-most EST LIB3069-014-Q1-K1-F11

Seq. No. 278301
Contig ID 84107_1.R1011

5'-most EST	LIB3069-014-Q1-K1-F12
Seq. No.	278302
Contig ID	84118_1.R1011
5'-most EST	LIB3069-014-Q1-K1-G11
Seq. No.	278303
Contig ID	84129_2.R1011
5'-most EST	LIB3069-013-Q1-K1-H10
Method	BLASTX
NCBI GI	g66009
BLAST score	156
E value	2.0e-10
Match length	83
% identity	45
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH (AA 1-337) [Zea mays]
Seq. No.	278304
Contig ID	84130_1.R1011
5'-most EST	LIB3069-014-Q1-K1-H10
Seq. No.	278305
Contig ID	84138_1.R1011
5'-most EST	LIB3069-014-Q1-K1-H9
Seq. No.	278306
Contig ID	84184_1.R1011
5'-most EST	LIB3069-015-Q1-K1-B3
Seq. No.	278307
Contig ID	84185_1.R1011
5'-most EST	mwy700440003.h1
Method	BLASTX
NCBI GI	g1708191
BLAST score	291
E value	2.0e-26
Match length	110
% identity	55
NCBI Description	HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]
Seq. No.	278308
Contig ID	84190_1.R1011
5'-most EST	LIB3069-015-Q1-K1-C1
Seq. No.	278309
Contig ID	84209_1.R1011
5'-most EST	uC-zmflb73167c05a1
Method	BLASTX
NCBI GI	g399026
BLAST score	554
E value	1.0e-56
Match length	213
% identity	50
NCBI Description	ALLIIN LYASE PRECURSOR (ALLIINASE) (CYSTEINE SULPHOXIDE

LYASE) >gi_419807_pir__S29300 alliin lyase (EC 4.4.1.4) precursor - shallot (fragment) >gi_15946_emb_CAA78266_ (Z12620) precursor alliinase [Allium ascalonicum]

Seq. No.	278310
Contig ID	84210_1.R1011
5'-most EST	xsy700213688.h1
Method	BLASTX
NCBI GI	g2501494
BLAST score	397
E value	2.0e-38
Match length	206
% identity	45
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 5) >gi_542015_pir__S41951 UTP-glucose glucosyltransferase - cassava >gi_453249_emb_CAA54612_ (X77462) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No.	278311
Contig ID	84217_1.R1011
5'-most EST	vmj700053727.r1
Method	BLASTX
NCBI GI	g3806098
BLAST score	714
E value	3.0e-75
Match length	276
% identity	54
NCBI Description	(AF079100) arginine-tRNA-protein transferase 1; Ate1p [Arabidopsis thaliana]

Seq. No.	278312
Contig ID	84249_1.R1011
5'-most EST	ymt700218807.h1
Method	BLASTX
NCBI GI	g2129559
BLAST score	1534
E value	1.0e-171
Match length	521
% identity	56
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	278313
Contig ID	84249_3.R1011
5'-most EST	fC-zmle700429868f2
Method	BLASTX
NCBI GI	g2190558
BLAST score	297
E value	1.0e-28
Match length	122
% identity	52
NCBI Description	(AC001229) F5I14.14 [Arabidopsis thaliana]

Seq. No.	278314
Contig ID	84260_1.R1011
5'-most EST	LIB3069-016-Q1-K1-B1
Seq. No.	278315
Contig ID	84266_1.R1011
5'-most EST	LIB3069-016-Q1-K1-B4
Seq. No.	278316
Contig ID	84285_1.R1011
5'-most EST	ceu700423145.h1
Seq. No.	278317
Contig ID	84307_1.R1011
5'-most EST	uC-zmroteosinte004e11b1
Method	BLASTX
NCBI GI	g2213594
BLAST score	1058
E value	1.0e-115
Match length	300
% identity	66
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.	278318
Contig ID	84319_1.R1011
5'-most EST	LIB3069-016-Q1-K1-G12
Seq. No.	278319
Contig ID	84365_1.R1011
5'-most EST	uC-zmflmo17059a07b1
Method	BLASTX
NCBI GI	g2245378
BLAST score	939
E value	1.0e-101
Match length	294
% identity	63
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]
Seq. No.	278320
Contig ID	84365_2.R1011
5'-most EST	hvj700623176.h1
Method	BLASTX
NCBI GI	g2245378
BLAST score	506
E value	3.0e-51
Match length	162
% identity	60
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]
Seq. No.	278321
Contig ID	84368_1.R1011
5'-most EST	LIB3069-017-Q1-K1-C8
Seq. No.	278322
Contig ID	84382_1.R1011
5'-most EST	xmt700267479.h1

Seq. No.	278323
Contig ID	84396_1.R1011
5'-most EST	qmh700029770.f1
Method	BLASTX
NCBI GI	g3894159
BLAST score	384
E value	7.0e-37
Match length	178
% identity	45
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278324
Contig ID	84398_1.R1011
5'-most EST	uwc700153572.h1

Seq. No.	278325
Contig ID	84398_2.R1011
5'-most EST	dyk700102090.h1

Seq. No.	278326
Contig ID	84406_1.R1011
5'-most EST	LIB3069-017-Q1-K1-G3
Method	BLASTX
NCBI GI	g2623307
BLAST score	208
E value	2.0e-16
Match length	136
% identity	40
NCBI Description	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]

Seq. No.	278327
Contig ID	84409_1.R1011
5'-most EST	gct701180357.h1
Method	BLASTX
NCBI GI	g1117821
BLAST score	242
E value	4.0e-20
Match length	86
% identity	53
NCBI Description	(U31454) MNG10 [Manduca sexta]

Seq. No.	278328
Contig ID	84421_1.R1011
5'-most EST	rvt700549896.h1
Method	BLASTX
NCBI GI	g1946360
BLAST score	423
E value	2.0e-41
Match length	146
% identity	55
NCBI Description	(U93215) elicitor response element binding protein WRKY3 isolog [Arabidopsis thaliana]

Seq. No.	278329
Contig ID	84427_1.R1011

5'-most EST	uC-zmflb73300a02b1
Seq. No.	278330
Contig ID	84427_2.R1011
5'-most EST	gct701168885.h1
Seq. No.	278331
Contig ID	84429_1.R1011
5'-most EST	pwr700452428.h1
Seq. No.	278332
Contig ID	84442_1.R1011
5'-most EST	LIB3069-018-Q1-K1-C6
Method	BLASTX
NCBI GI	g4587517
BLAST score	453
E value	3.0e-45
Match length	117
% identity	71
NCBI Description	(AC007060) T5I8.6 [Arabidopsis thaliana]
Seq. No.	278333
Contig ID	84453_1.R1011
5'-most EST	uC-zmflb73274c12b1
Seq. No.	278334
Contig ID	84456_1.R1011
5'-most EST	pmx700090174.h1
Seq. No.	278335
Contig ID	84465_1.R1011
5'-most EST	uC-zmflB73108h05b2
Seq. No.	278336
Contig ID	84465_2.R1011
5'-most EST	cyk700050130.f1
Seq. No.	278337
Contig ID	84465_3.R1011
5'-most EST	uC-zmflmo17301h04b1
Seq. No.	278338
Contig ID	84476_1.R1011
5'-most EST	hbs701182896.h1
Method	BLASTX
NCBI GI	g3395435
BLAST score	262
E value	2.0e-22
Match length	200
% identity	39
NCBI Description	(AC004683) myosin heavy chain-like protein [Arabidopsis thaliana]
Seq. No.	278339
Contig ID	84491_1.R1011
5'-most EST	LIB3069-019-Q1-K1-A9

Seq. No.	278340
Contig ID	84505_1.R1011
5'-most EST	uC-zmflb73213a02b1
Method	BLASTX
NCBI GI	g4559356
BLAST score	194
E value	1.0e-14
Match length	131
% identity	29
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278341
Contig ID	84505_4.R1011
5'-most EST	uC-zmflb73290b11b1

Seq. No.	278342
Contig ID	84535_1.R1011
5'-most EST	LIB3069-019-Q1-K1-F10

Seq. No.	278343
Contig ID	84570_1.R1011
5'-most EST	uC-zmflb73257e03b3
Method	BLASTX
NCBI GI	g4056615
BLAST score	855
E value	1.0e-107
Match length	260
% identity	77
NCBI Description	(AF067401) Scl1 protein [Oryza sativa]

Seq. No.	278344
Contig ID	84593_1.R1011
5'-most EST	LIB3069-020-Q1-K1-C3
Method	BLASTX
NCBI GI	g4587988
BLAST score	203
E value	2.0e-15
Match length	261
% identity	28
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278345
Contig ID	84608_1.R1011
5'-most EST	LIB3069-020-Q1-K1-D8

Seq. No.	278346
Contig ID	84622_1.R1011
5'-most EST	LIB3069-020-Q1-K1-F1
Method	BLASTX
NCBI GI	g2443887
BLAST score	416
E value	7.0e-41
Match length	143
% identity	59
NCBI Description	(AC002294) Similar to transcription factor gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No.	278347
Contig ID	84625_2.R1011
5'-most EST	uC-zmflb73127g01b2

Seq. No.	278348
Contig ID	84627_1.R1011
5'-most EST	LIB3069-020-Q1-K1-F5
Method	BLASTX
NCBI GI	g3892057
BLAST score	364
E value	1.0e-34
Match length	169
% identity	46
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278349
Contig ID	84635_1.R1011
5'-most EST	LIB3069-020-Q1-K1-G12
Method	BLASTX
NCBI GI	g4469025
BLAST score	180
E value	6.0e-13
Match length	55
% identity	56
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	278350
Contig ID	84643_1.R1011
5'-most EST	xsy700211560.h1
Method	BLASTX
NCBI GI	g3033400
BLAST score	415
E value	1.0e-40
Match length	120
% identity	62
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	278351
Contig ID	84643_2.R1011
5'-most EST	uC-zmflmo17125g07a1
Method	BLASTX
NCBI GI	g2494111
BLAST score	148
E value	2.0e-09
Match length	48
% identity	54
NCBI Description	(AC002376) Contains similarity to Glycine protein kinase 6 (gb_M67449). [Arabidopsis thaliana]

Seq. No.	278352
Contig ID	84648_1.R1011
5'-most EST	LIB3069-020-Q1-K1-H5

Seq. No.	278353
Contig ID	84652_1.R1011
5'-most EST	uC-zmflB73009h06b1

Seq. No.	278354
Contig ID	84667_1.R1011
5'-most EST	gct701177533.h1
Method	BLASTX
NCBI GI	g3256035
BLAST score	791
E value	2.0e-84
Match length	224
% identity	74
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No.	278355
Contig ID	84674_1.R1011
5'-most EST	uC-zmflmo17285d06b1

Seq. No.	278356
Contig ID	84677_1.R1011
5'-most EST	uC-zmflb73015f12b1
Method	BLASTX
NCBI GI	g1771160
BLAST score	282
E value	5.0e-25
Match length	133
% identity	43
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	278357
Contig ID	84683_1.R1011
5'-most EST	cyk700049244.f1
Method	BLASTX
NCBI GI	g3047085
BLAST score	1000
E value	1.0e-109
Match length	323
% identity	60
NCBI Description	(AF058914) No definition line found [Arabidopsis thaliana]

Seq. No.	278358
Contig ID	84686_1.R1011
5'-most EST	uC-zmflb73073c10b3
Method	BLASTX
NCBI GI	g2444180
BLAST score	874
E value	4.0e-94
Match length	284
% identity	61
NCBI Description	(U94785) unconventional myosin [Helianthus annuus]

Seq. No.	278359
Contig ID	84693_1.R1011
5'-most EST	uC-zmflb73048g09b1
Method	BLASTX
NCBI GI	g1477468

BLAST score	361
E value	5.0e-34
Match length	178
% identity	48
NCBI Description	(U35244) vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]

Seq. No.	278360
Contig ID	84698_1.R1011
5'-most EST	LIB3069-021-Q1-K1-E3
Method	BLASTX
NCBI GI	g3413700
BLAST score	547
E value	4.0e-56
Match length	154
% identity	69
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	278361
Contig ID	84701_1.R1011
5'-most EST	LIB3069-021-Q1-K1-E6

Seq. No.	278362
Contig ID	84708_1.R1011
5'-most EST	uC-zmflb73184b06a1
Method	BLASTX
NCBI GI	g516118
BLAST score	1469
E value	1.0e-163
Match length	612
% identity	51
NCBI Description	(L08469) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	278363
Contig ID	84708_5.R1011
5'-most EST	wty700162886.h1

Seq. No.	278364
Contig ID	84719_1.R1011
5'-most EST	xmt700261908.h1
Method	BLASTX
NCBI GI	g3510253
BLAST score	419
E value	7.0e-41
Match length	125
% identity	65
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278365
Contig ID	84720_1.R1011
5'-most EST	LIB3069-021-Q1-K1-G2

Seq. No.	278366
Contig ID	84740_1.R1011
5'-most EST	ymt700223477.h1
Method	BLASTX
NCBI GI	g2828293

BLAST score	279
E value	2.0e-24
Match length	212
% identity	36
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	278367
Contig ID	84742_1.R1011
5'-most EST	LIB3069-022-Q1-K1-A12

Seq. No.	278368
Contig ID	84743_1.R1011
5'-most EST	LIB3069-022-Q1-K1-A2

Seq. No.	278369
Contig ID	84767_1.R1011
5'-most EST	ceu70l0426003.h1

Seq. No.	278370
Contig ID	84770_1.R1011
5'-most EST	LIB3069-022-Q1-K1-C8
Method	BLASTX
NCBI GI	g2244971
BLAST score	414
E value	1.0e-40
Match length	115
% identity	70
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278371
Contig ID	84798_1.R1011
5'-most EST	gct701174070.h1
Method	BLASTX
NCBI GI	g3057120
BLAST score	275
E value	2.0e-24
Match length	104
% identity	54
NCBI Description	(AF023159) starch synthase DULL1 [Zea mays]

Seq. No.	278372
Contig ID	84800_1.R1011
5'-most EST	LIB3069-022-Q1-K1-F2

Seq. No.	278373
Contig ID	84801_1.R1011
5'-most EST	nbm700466946.h1
Method	BLASTX
NCBI GI	g2865623
BLAST score	385
E value	6.0e-37
Match length	120
% identity	65
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	278374
Contig ID	84803_1.R1011
5'-most EST	uC-zmroteosinte091e06b2
Method	BLASTX
NCBI GI	g4455035
BLAST score	273
E value	7.0e-24
Match length	128
% identity	41
NCBI Description	(AF116238) pseudouridine synthase 1 [Homo sapiens]

Seq. No.	278375
Contig ID	84804_1.R1011
5'-most EST	LIB3069-022-Q1-K1-F6

Seq. No.	278376
Contig ID	84809_1.R1011
5'-most EST	LIB3069-025-Q1-K1-F10
Method	BLASTX
NCBI GI	g4417287
BLAST score	326
E value	3.0e-30
Match length	131
% identity	47
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	278377
Contig ID	84812_1.R1011
5'-most EST	LIB3069-022-Q1-K1-G3
Method	BLASTX
NCBI GI	g3063693
BLAST score	608
E value	3.0e-63
Match length	151
% identity	71
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	278378
Contig ID	84815_1.R1011
5'-most EST	LIB3069-022-Q1-K1-G6

Seq. No.	278379
Contig ID	84834_1.R1011
5'-most EST	LIB3069-023-Q1-K1-A5

Seq. No.	278380
Contig ID	84857_1.R1011
5'-most EST	uC-zmflmo170114a02b1
Method	BLASTX
NCBI GI	g2914703
BLAST score	535
E value	2.0e-54
Match length	159
% identity	67
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	278381

Contig ID	84868_1.R1011
5'-most EST	LIB3069-023-Q1-K1-E7
Method	BLASTX
NCBI GI	g4138265
BLAST score	322
E value	2.0e-29
Match length	159
% identity	38
NCBI Description	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]

Seq. No.	278382
Contig ID	84869_1.R1011
5'-most EST	uC-zmflb73131e11a1

Seq. No.	278383
Contig ID	84873_1.R1011
5'-most EST	LIB3069-023-Q1-K1-F6

Seq. No.	278384
Contig ID	84876_1.R1011
5'-most EST	xsy700213826.h1
Method	BLASTX
NCBI GI	g4539386
BLAST score	302
E value	2.0e-27
Match length	90
% identity	61
NCBI Description	(AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No.	278385
Contig ID	84877_1.R1011
5'-most EST	LIB3069-023-Q1-K1-G11

Seq. No.	278386
Contig ID	84878_1.R1011
5'-most EST	LIB3069-036-Q1-K1-E6
Method	BLASTX
NCBI GI	g4454043
BLAST score	395
E value	3.0e-40
Match length	128
% identity	69
NCBI Description	(AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	278387
Contig ID	84891_1.R1011
5'-most EST	LIB3069-023-Q1-K1-H7

Seq. No.	278388
Contig ID	84899_1.R1011
5'-most EST	LIB3069-024-Q1-K1-A6

Seq. No.	278389
Contig ID	84921_1.R1011
5'-most EST	LIB3069-024-Q1-K1-C5
Method	BLASTX

NCBI GI	g3935137
BLAST score	200
E value	2.0e-15
Match length	84
% identity	50
NCBI Description	(AC005106) T25N20.1 [Arabidopsis thaliana]

Seq. No.	278390
Contig ID	84932_1.R1011
5'-most EST	yyf700350414.h1

Seq. No.	278391
Contig ID	84963_1.R1011
5'-most EST	uC-zmflb73053f04b2

Seq. No.	278392
Contig ID	84981_1.R1011
5'-most EST	LIB3069-025-Q1-K1-A10
Method	BLASTX
NCBI GI	g2688830
BLAST score	150
E value	1.0e-09
Match length	133
% identity	31
NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	278393
Contig ID	84990_1.R1011
5'-most EST	uC-zmrob73055e04b1

Seq. No.	278394
Contig ID	85007_1.R1011
5'-most EST	LIB3069-025-Q1-K1-C8

Seq. No.	278395
Contig ID	85011_1.R1011
5'-most EST	LIB3069-025-Q1-K1-D12

Seq. No.	278396
Contig ID	85017_1.R1011
5'-most EST	uC-zmflb73235e03b2
Method	BLASTX
NCBI GI	g1084461
BLAST score	161
E value	7.0e-11
Match length	58
% identity	55
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	278397
Contig ID	85033_1.R1011
5'-most EST	ymt700221260.h1

Seq. No.	278398
Contig ID	85042_1.R1011
5'-most EST	wty700172436.h1

Seq. No.	278399
Contig ID	85059_1.R1011
5'-most EST	fdz701160722.h1

Seq. No.	278400
Contig ID	85094_1.R1011
5'-most EST	xmt700263765.h1

Seq. No.	278401
Contig ID	85107_1.R1011
5'-most EST	LIB3069-026-Q1-K1-E12
Method	BLASTX
NCBI GI	g3319342
BLAST score	253
E value	2.0e-21
Match length	130
% identity	38
NCBI Description	(AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

Seq. No.	278402
Contig ID	85125_1.R1011
5'-most EST	uC-zmflb73284b06b1
Method	BLASTX
NCBI GI	g2760839
BLAST score	585
E value	2.0e-60
Match length	193
% identity	58
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	278403
Contig ID	85141_1.R1011
5'-most EST	LIB3069-027-Q1-K1-G3

Seq. No.	278404
Contig ID	85167_1.R1011
5'-most EST	uC-zmflmo17132b07b1
Method	BLASTX
NCBI GI	g3287695
BLAST score	1102
E value	1.0e-120
Match length	415
% identity	55
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	278405
Contig ID	85167_2.R1011
5'-most EST	gct701175478.h1
Method	BLASTX
NCBI GI	g3287695
BLAST score	425
E value	7.0e-42
Match length	148

% identity	54
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	278406
Contig ID	85216_1.R1011
5'-most EST	LIB3069-027-Q1-K1-H10

Seq. No.	278407
Contig ID	85225_1.R1011
5'-most EST	uC-zmflmo17321b04b1
Method	BLASTX
NCBI GI	g3152595
BLAST score	467
E value	2.0e-46
Match length	246
% identity	51
NCBI Description	(AC002986) Similar to D. melanogaster sno gene gb_U95760. EST gb_N97148 and gb_Z26221 come from this gene. [Arabidopsis thaliana]

Seq. No.	278408
Contig ID	85226_1.R1011
5'-most EST	LIB3069-028-Q1-K1-A10

Seq. No.	278409
Contig ID	85261_1.R1011
5'-most EST	uC-zmflb73126h02b1

Seq. No.	278410
Contig ID	85264_1.R1011
5'-most EST	LIB3069-028-Q1-K1-D6

Seq. No.	278411
Contig ID	85273_1.R1011
5'-most EST	LIB3069-028-Q1-K1-E5
Method	BLASTX
NCBI GI	g4544473
BLAST score	296
E value	1.0e-26
Match length	202
% identity	39
NCBI Description	(AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	278412
Contig ID	85280_1.R1011
5'-most EST	uC-zmflmo17199b06b1
Method	BLASTX
NCBI GI	g1655536
BLAST score	238
E value	1.0e-19
Match length	78
% identity	60
NCBI Description	(Y09095) chloride channel [Arabidopsis thaliana] >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel protein [Arabidopsis thaliana]

Seq. No.	278413
Contig ID	85291_1.R1011
5'-most EST	uC-zmflmo17075g09b2

Seq. No.	278414
Contig ID	85294_1.R1011
5'-most EST	gw1700617054.h1
Method	BLASTX
NCBI GI	g2258469
BLAST score	599
E value	9.0e-62
Match length	139
% identity	88
NCBI Description	(AF009179) replication protein A1 [Oryza sativa]

Seq. No.	278415
Contig ID	85294_2.R1011
5'-most EST	LIB3069-028-Q1-K1-G7
Method	BLASTX
NCBI GI	g2258469
BLAST score	1251
E value	1.0e-138
Match length	281
% identity	83
NCBI Description	(AF009179) replication protein A1 [Oryza sativa]

Seq. No.	278416
Contig ID	85337_1.R1011
5'-most EST	LIB3069-029-Q1-K1-C6
Method	BLASTX
NCBI GI	g1931649
BLAST score	422
E value	5.0e-60
Match length	223
% identity	53
NCBI Description	(U95973) DNA helicase isolog [Arabidopsis thaliana]

Seq. No.	278417
Contig ID	85351_1.R1011
5'-most EST	uC-zmflmo17220g08b1
Method	BLASTX
NCBI GI	g1369981
BLAST score	179
E value	1.0e-12
Match length	88
% identity	41
NCBI Description	(X95609) mec-8 [Caenorhabditis elegans] >gi_3874374_emb_CAB02754_ (Z81037) similar to mecanosensory gene mec-8; cDNA EST EMBL:T00424 comes from this gene; cDNA EST yk494a10.3 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST yk505h10.3 comes from this gene; cDNA EST yk2... >gi_3877217_emb_CAB03111_ (Z81084) similar to mecanosensory gene mec-8; cDNA EST EMBL:T00424 comes from this gene; cDNA EST yk494a10.3 comes from this gene; cDNA EST yk333a11.3 comes from this gene; cDNA EST yk505h10.3 comes from this gene; cDNA EST yk2

Seq. No.	278418
Contig ID	85351_2.R1011
5'-most EST	tfd70O575116.h1

Seq. No.	278419
Contig ID	85354_1.R1011
5'-most EST	LIB3069-029-Q1-K1-E10
Method	BLASTX
NCBI GI	g2342725
BLAST score	402
E value	4.0e-39
Match length	100
% identity	75
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278420
Contig ID	85364_1.R1011
5'-most EST	LIB3069-029-Q1-K1-F11
Method	BLASTX
NCBI GI	g1001135
BLAST score	366
E value	1.0e-40
Match length	164
% identity	55
NCBI Description	(D64001) acetolactate synthase [Synechocystis sp.]

Seq. No.	278421
Contig ID	85369_1.R1011
5'-most EST	LIB3069-029-Q1-K1-F6

Seq. No.	278422
Contig ID	85370_1.R1011
5'-most EST	uC-zmflmo17327d12a1

Seq. No.	278423
Contig ID	85372_1.R1011
5'-most EST	LIB3069-031-Q1-K1-D2
Method	BLASTX
NCBI GI	g3702324
BLAST score	178
E value	1.0e-12
Match length	144
% identity	31
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278424
Contig ID	85391_1.R1011
5'-most EST	LIB3069-029-Q1-K1-H9
Method	BLASTX
NCBI GI	g2809259
BLAST score	179
E value	1.0e-21
Match length	80
% identity	66
NCBI Description	(AC002560) F21B7.28 [Arabidopsis thaliana]

Seq. No.	278425
Contig ID	85401_1.R1011
5'-most EST	uC-zmflb73011h09b1
Method	BLASTX
NCBI GI	g3142291
BLAST score	296
E value	1.0e-26
Match length	150
% identity	44
NCBI Description	(AC002411) Contains similarity to adenylate cyclase gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes from this gene. [Arabidopsis thaliana]

Seq. No.	278426
Contig ID	85401_3.R1011
5'-most EST	wyr700240214.h1
Method	BLASTX
NCBI GI	g3142291
BLAST score	545
E value	1.0e-55
Match length	200
% identity	53
NCBI Description	(AC002411) Contains similarity to adenylate cyclase gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes from this gene. [Arabidopsis thaliana]

Seq. No.	278427
Contig ID	85406_1.R1011
5'-most EST	xdb700338381.h1
Method	BLASTX
NCBI GI	g4539455
BLAST score	282
E value	4.0e-25
Match length	99
% identity	58
NCBI Description	(AL049500) T5C23.70 [Arabidopsis thaliana]

Seq. No.	278428
Contig ID	85431_1.R1011
5'-most EST	uC-zmflmo17262a08a1

Seq. No.	278429
Contig ID	85436_1.R1011
5'-most EST	wyr700243230.h1
Method	BLASTX
NCBI GI	g3334230
BLAST score	520
E value	8.0e-53
Match length	203
% identity	52
NCBI Description	D-HYDANTOINASE (DIHYDROPYRIMIDINASE) (DHPASE) >gi_2828803 (U84197) D-hydantoinase [Pseudomonas putida]

Seq. No.	278430
Contig ID	85452_1.R1011
5'-most EST	nbm700471782.h1
Method	BLASTX

NCBI GI	g1946360
BLAST score	262
E value	1.0e-22
Match length	148
% identity	43
NCBI Description	(U93215) elicitor response element binding protein WRKY3 isolog [Arabidopsis thaliana]

Seq. No.	278431
Contig ID	85458_1.R1011
5'-most EST	LIB3069-030-Q1-K1-H12
Method	BLASTX
NCBI GI	g4102839
BLAST score	276
E value	2.0e-24
Match length	68
% identity	75
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	278432
Contig ID	85460_1.R1011
5'-most EST	LIB3069-030-Q1-K1-H4

Seq. No.	278433
Contig ID	85478_1.R1011
5'-most EST	ymt700220985.h1
Method	BLASTX
NCBI GI	g4544431
BLAST score	605
E value	1.0e-62
Match length	192
% identity	64
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278434
Contig ID	85481_1.R1011
5'-most EST	ymt700224156.h1

Seq. No.	278435
Contig ID	85500_1.R1011
5'-most EST	LIB3069-046-Q1-K1-C12

Seq. No.	278436
Contig ID	85507_1.R1011
5'-most EST	LIB3069-031-Q1-K1-E10
Method	BLASTX
NCBI GI	g3152576
BLAST score	150
E value	9.0e-10
Match length	96
% identity	39
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	278437
Contig ID	85509_1.R1011
5'-most EST	uC-zmflmo17050d05b2

Seq. No.	278438
Contig ID	85509_2.R1011
5'-most EST	uC-zmflmo17344a12a1
Seq. No.	278439
Contig ID	85518_1.R1011
5'-most EST	LIB3069-031-Q1-K1-F11
Seq. No.	278440
Contig ID	85522_1.R1011
5'-most EST	LIB3069-031-Q1-K1-F4
Seq. No.	278441
Contig ID	85530_1.R1011
5'-most EST	ymt700220201.h1
Method	BLASTX
NCBI GI	g1168470
BLAST score	987
E value	1.0e-107
Match length	328
% identity	60
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]
Seq. No.	278442
Contig ID	85542_1.R1011
5'-most EST	uC-zmflmo17156b10b1
Seq. No.	278443
Contig ID	85561_1.R1011
5'-most EST	LIB3069-032-Q1-K1-B12
Seq. No.	278444
Contig ID	85581_1.R1011
5'-most EST	uC-zmflb73140b02b1
Method	BLASTX
NCBI GI	g2339978
BLAST score	639
E value	9.0e-67
Match length	202
% identity	62
NCBI Description	(Y11336) RGA1 protein [Arabidopsis thaliana]
Seq. No.	278445
Contig ID	85591_1.R1011
5'-most EST	LIB3069-032-Q1-K1-E3
Seq. No.	278446
Contig ID	85592_1.R1011
5'-most EST	uC-zmroteosinte058c09b2
Method	BLASTX
NCBI GI	g4115371
BLAST score	197

E value	1.0e-14
Match length	185
% identity	37
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	278447
Contig ID	85593_1.R1011
5'-most EST	wen700335564.h1
Method	BLASTX
NCBI GI	g2262143
BLAST score	273
E value	6.0e-24
Match length	103
% identity	48
NCBI Description	(AC002330) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	278448
Contig ID	85597_1.R1011
5'-most EST	LIB3069-032-Q1-K1-E4

Seq. No.	278449
Contig ID	85600_1.R1011
5'-most EST	dyk700105418.h1
Method	BLASTX
NCBI GI	g2979558
BLAST score	622
E value	2.0e-64
Match length	304
% identity	44
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278450
Contig ID	85615_1.R1011
5'-most EST	LIB3069-032-Q1-K1-G12

Seq. No.	278451
Contig ID	85616_1.R1011
5'-most EST	xsy700208451.h1
Method	BLASTX
NCBI GI	g3157926
BLAST score	295
E value	3.0e-26
Match length	264
% identity	34
NCBI Description	(AC002131) Strong similarity to extensin-like protein gb_Z34465 from Zea mays. [Arabidopsis thaliana]

Seq. No.	278452
Contig ID	85627_1.R1011
5'-most EST	pwr700452876.h1
Method	BLASTN
NCBI GI	g4321977
BLAST score	40
E value	1.0e-12
Match length	56
% identity	93

NCBI Description	Zea mays beta-amylase (Amy2) gene, complete cds
Seq. No.	278453
Contig ID	85634_1.R1011
5'-most EST	LIB3069-034-Q1-K1-A10
Seq. No.	278454
Contig ID	85635_1.R1011
5'-most EST	hvj70619223.h1
Method	BLASTX
NCBI GI	g2829904
BLAST score	514
E value	5.0e-52
Match length	174
% identity	58
NCBI Description	(AC002311) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	278455
Contig ID	85636_1.R1011
5'-most EST	uC-zmflmo17018b02a1
Seq. No.	278456
Contig ID	85665_1.R1011
5'-most EST	uC-zmflmo17269c12b1
Seq. No.	278457
Contig ID	85720_1.R1011
5'-most EST	LIB3069-034-Q1-K1-A3
Method	BLASTX
NCBI GI	g3335060
BLAST score	319
E value	2.0e-29
Match length	170
% identity	40
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
Seq. No.	278458
Contig ID	85723_1.R1011
5'-most EST	LIB3069-034-Q1-K1-A6
Seq. No.	278459
Contig ID	85728_1.R1011
5'-most EST	LIB3069-034-Q1-K1-D2
Seq. No.	278460
Contig ID	85732_1.R1011
5'-most EST	LIB3069-034-Q1-K1-B3
Method	BLASTX
NCBI GI	g2982452
BLAST score	314
E value	7.0e-29
Match length	110
% identity	58
NCBI Description	(AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	278461
Contig ID	85744_1.R1011
5'-most EST	uC-zmflmo17212f05a1

Seq. No.	278462
Contig ID	85746_1.R1011
5'-most EST	LIB3069-034-Q1-K1-C9
Method	BLASTX
NCBI GI	g2239083
BLAST score	376
E value	1.0e-35
Match length	215
% identity	43
NCBI Description	(Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	278463
Contig ID	85748_1.R1011
5'-most EST	LIB3069-034-Q1-K1-D10
Method	BLASTN
NCBI GI	g507770
BLAST score	34
E value	4.0e-09
Match length	74
% identity	86
NCBI Description	Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete cds

Seq. No.	278464
Contig ID	85749_1.R1011
5'-most EST	LIB3069-034-Q1-K1-D11
Method	BLASTX
NCBI GI	g1729980
BLAST score	329
E value	1.0e-30
Match length	82
% identity	72
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175 thaumatin-like protein - Arabidopsis thaliana >gi_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >gi_1094863_prf__2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	278465
Contig ID	85755_1.R1011
5'-most EST	LIB3069-034-Q1-K1-D8
Method	BLASTX
NCBI GI	g4336610
BLAST score	827
E value	9.0e-89
Match length	164
% identity	99
NCBI Description	(AF099112) sigma factor; Sig3 [Zea mays]

Seq. No.	278466
Contig ID	85764_1.R1011
5'-most EST	LIB3137-021-Q1-K1-G4

Seq. No.	278467
Contig ID	85770_1.R1011
5'-most EST	uC-zmroteosinte029h07b1
Method	BLASTX
NCBI GI	g3025329
BLAST score	263
E value	1.0e-22
Match length	140
% identity	44
NCBI Description	HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V >gi_3877534_emb_CAB01212_ (Z77663) Similarity to S.pombe hypothetical proteinSPAC4G9.01 (TR:E223656) [Caenorhabditis elegans]

Seq. No.	278468
Contig ID	85783_1.R1011
5'-most EST	xsy700213744.h1

Seq. No.	278469
Contig ID	85788_1.R1011
5'-most EST	LIB3069-034-Q1-K1-H12
Method	BLASTX
NCBI GI	g1079274
BLAST score	153
E value	1.0e-09
Match length	178
% identity	30
NCBI Description	tropomyosin alpha chain - axolotl >gi_520748 (L35107) tropomyosin [Ambystoma mexicanum]

Seq. No.	278470
Contig ID	85799_1.R1011
5'-most EST	LIB3069-035-Q1-K1-A3
Method	BLASTX
NCBI GI	g3096912
BLAST score	156
E value	2.0e-10
Match length	82
% identity	43
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	278471
Contig ID	85804_1.R1011
5'-most EST	ntr700072673.h1

Seq. No.	278472
Contig ID	85811_1.R1011
5'-most EST	uC-zmroteosinte080a06b1
Method	BLASTX
NCBI GI	g3024505
BLAST score	495
E value	7.0e-50
Match length	134

% identity	72
NCBI Description	RAS-RELATED PROTEIN RAB11D >gi_623580 (L29270) putative [Nicotiana tabacum]

Seq. No.	278473
Contig ID	85824_1.R1011
5'-most EST	LIB3069-035-Q1-K1-C4

Seq. No.	278474
Contig ID	85833_1.R1011
5'-most EST	LIB3069-035-Q1-K1-D2

Seq. No.	278475
Contig ID	85842_1.R1011
5'-most EST	uC-zmflMo17010f10b1
Method	BLASTX
NCBI GI	g122771
BLAST score	455
E value	4.0e-45
Match length	186
% identity	52
NCBI Description	TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR HBP1) >gi_100808_pir__S15346 transcription factor HBP-1a - wheat >gi_100838_pir__A41349 histone-specific transcription factor HBP1 - wheat >gi_21633_emb_CAA40101_ (X56781) HBP-1a [Triticum aestivum] >gi_170749 (M28704) DNA-binding protein [Triticum aestivum] >gi_1199790_dbj_BAA07289_ (D38111) transcription factor HBP-1a(17) [Triticum aestivum]

Seq. No.	278476
Contig ID	85847_1.R1011
5'-most EST	hbs701183939.h1
Method	BLASTX
NCBI GI	g3702324
BLAST score	201
E value	4.0e-15
Match length	186
% identity	30
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278477
Contig ID	85855_1.R1011
5'-most EST	LIB3069-035-Q1-K1-F4
Method	BLASTX
NCBI GI	g2347189
BLAST score	355
E value	1.0e-33
Match length	83
% identity	82
NCBI Description	(AC002338) hypothetical protein [Arabidopsis thaliana] >gi_3150399 (AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278478
Contig ID	85859_1.R1011
5'-most EST	fwa700097506.h1

Method	BLASTX
NCBI GI	g4507657
BLAST score	759
E value	3.0e-80
Match length	549
% identity	36
NCBI Description	tripeptidyl peptidase II >gi_136107_sp_P29144_TPP2_HUMAN TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL AMINOPEPTIDASE) >gi_1082875_pir__S54376 tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi_339880 (M73047) tripeptidyl peptidase II [Homo sapiens]

Seq. No.	278479
Contig ID	85866_1.R1011
5'-most EST	rvl700458645.h1
Method	BLASTX
NCBI GI	g1522681
BLAST score	272
E value	7.0e-24
Match length	157
% identity	40
NCBI Description	(U49240) symplekin [Homo sapiens] >gi_2143262_emb_CAA71861_ (Y10931) symplekin [Homo sapiens]

Seq. No.	278480
Contig ID	85888_1.R1011
5'-most EST	LIB3069-036-Q1-K1-B1
Method	BLASTX
NCBI GI	g3169012
BLAST score	436
E value	6.0e-43
Match length	96
% identity	88
NCBI Description	(AJ002610) putative calmodulin binding transporter protein [Hordeum vulgare]

Seq. No.	278481
Contig ID	85902_1.R1011
5'-most EST	ypc700802181.h1
Method	BLASTX
NCBI GI	g1699023
BLAST score	152
E value	1.0e-09
Match length	68
% identity	47
NCBI Description	(U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi_1699051 (U78867) putative aspartate-arginine-rich mRNA binding protein [Arabidopsis thaliana]

Seq. No.	278482
Contig ID	85914_1.R1011
5'-most EST	xmt700260940.h1

Seq. No.	278483
Contig ID	85915_1.R1011
5'-most EST	LIB3069-036-Q1-K1-D6

Seq. No.	278484
Contig ID	85920_1.R1011
5'-most EST	wty700169450.h1

Seq. No.	278485
Contig ID	85928_1.R1011
5'-most EST	cat700021764.r1

Seq. No.	278486
Contig ID	85933_1.R1011
5'-most EST	uC-zmroteosinte006b07b1

Seq. No.	278487
Contig ID	85933_2.R1011
5'-most EST	wev700405002.h1

Seq. No.	278488
Contig ID	85967_1.R1011
5'-most EST	LIB3069-037-Q1-K1-A4
Method	BLASTX
NCBI GI	g2809251
BLAST score	602
E value	1.0e-62
Match length	145
% identity	72
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No.	278489
Contig ID	85969_1.R1011
5'-most EST	LIB3069-037-Q1-K1-A6

Seq. No.	278490
Contig ID	85971_1.R1011
5'-most EST	LIB3069-037-Q1-K1-A8

Seq. No.	278491
Contig ID	85992_1.R1011
5'-most EST	wty700166477.h1
Method	BLASTX
NCBI GI	g4539305
BLAST score	169
E value	1.0e-11
Match length	61
% identity	52
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	278492
Contig ID	85994_1.R1011
5'-most EST	LIB3070-004-Q1-N1-H2

Seq. No.	278493
Contig ID	85995_1.R1011
5'-most EST	LIB3069-037-Q1-K1-D1
Method	BLASTX
NCBI GI	g2739386
BLAST score	320

E value	5.0e-33
Match length	108
% identity	71
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	278494
Contig ID	85997_1.R1011
5'-most EST	hbs701185832.h2

Seq. No.	278495
Contig ID	86013_1.R1011
5'-most EST	LIB3069-037-Q1-K1-E6
Method	BLASTX
NCBI GI	g3043612
BLAST score	147
E value	6.0e-09
Match length	88
% identity	41
NCBI Description	(AB011116) KIAA0544 protein [Homo sapiens]

Seq. No.	278496
Contig ID	86028_1.R1011
5'-most EST	LIB3069-037-Q1-K1-G11

Seq. No.	278497
Contig ID	86040_1.R1011
5'-most EST	LIB3069-037-Q1-K1-H2
Method	BLASTX
NCBI GI	g4234852
BLAST score	433
E value	1.0e-48
Match length	254
% identity	45
NCBI Description	(AF082133) gag-pol polyprotein [Zea mays]

Seq. No.	278498
Contig ID	86051_1.R1011
5'-most EST	uC-zmflb73301g04b2
Method	BLASTX
NCBI GI	g4587584
BLAST score	565
E value	6.0e-58
Match length	204
% identity	52
NCBI Description	(AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	278499
Contig ID	86057_2.R1011
5'-most EST	LIB3136-027-P1-K1-D2

Seq. No.	278500
Contig ID	86074_1.R1011
5'-most EST	LIB3137-057-Q1-K1-E1

Seq. No.	278501
Contig ID	86089_1.R1011
5'-most EST	LIB3069-038-Q1-K1-E11

Seq. No.	278502
Contig ID	86095_1.R1011
5'-most EST	LIB3069-038-Q1-K1-E7

Seq. No.	278503
Contig ID	86096_1.R1011
5'-most EST	LIB3069-038-Q1-K1-E8

Seq. No.	278504
Contig ID	86104_1.R1011
5'-most EST	LIB3069-038-Q1-K1-F7
Method	BLASTX
NCBI GI	g2429290
BLAST score	298
E value	6.0e-27
Match length	106
% identity	58
NCBI Description	(AF014469) peroxidase [Oryza sativa]

Seq. No.	278505
Contig ID	86116_1.R1011
5'-most EST	LIB3069-038-Q1-K1-H11

Seq. No.	278506
Contig ID	86120_1.R1011
5'-most EST	LIB3069-038-Q1-K1-H8

Seq. No.	278507
Contig ID	86126_1.R1011
5'-most EST	mwy700438135.h1

Seq. No.	278508
Contig ID	86130_1.R1011
5'-most EST	uC-zmflb73204c06b1
Method	BLASTX
NCBI GI	g4249386
BLAST score	382
E value	2.0e-36
Match length	303
% identity	30
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	278509
Contig ID	86131_1.R1011
5'-most EST	uC-zmrob73033c11a1
Method	BLASTX
NCBI GI	g1491615
BLAST score	173
E value	2.0e-12
Match length	69
% identity	48
NCBI Description	(X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	278510
Contig ID	86152_1.R1011
5'-most EST	nbm700466991.h1
Method	BLASTX
NCBI GI	g4539400
BLAST score	495
E value	1.0e-49
Match length	187
% identity	52
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	278511
Contig ID	86160_1.R1011
5'-most EST	xmt700264675.h1

Seq. No.	278512
Contig ID	86161_1.R1011
5'-most EST	xjt700092418.h1
Method	BLASTX
NCBI GI	g1353193
BLAST score	323
E value	6.0e-30
Match length	113
% identity	63
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	278513
Contig ID	86183_1.R1011
5'-most EST	uC-zmflmo17266c11b1
Method	BLASTX
NCBI GI	g1666096
BLAST score	217
E value	2.0e-31
Match length	140
% identity	57
NCBI Description	(Y09113) dioxygenase [Marah macrocarpus]

Seq. No.	278514
Contig ID	86201_1.R1011
5'-most EST	uC-zmroteosinte077d05b1
Method	BLASTX
NCBI GI	g3582344
BLAST score	239
E value	4.0e-20
Match length	69
% identity	62
NCBI Description	(AC005496) putative cell division protein [Arabidopsis thaliana]

Seq. No.	278515
Contig ID	86229_1.R1011
5'-most EST	uC-zmflb73061h08b1
Method	BLASTX
NCBI GI	g4467149
BLAST score	460

E value 5.0e-46
Match length 87
% identity 93
NCBI Description (AL035540) putative transcription factor (MYB4) [Arabidopsis thaliana]

Seq. No. 278516
Contig ID 86230_1.R1011
5'-most EST xsy700213006.h1

Seq. No. 278517
Contig ID 86244_1.R1011
5'-most EST vux700161568.h1

Seq. No. 278518
Contig ID 86247_1.R1011
5'-most EST uC-zmflMo17086d09b1

Seq. No. 278519
Contig ID 86249_1.R1011
5'-most EST uC-zmflb73106a02a1

Seq. No. 278520
Contig ID 86254_1.R1011
5'-most EST LIB3069-040-Q1-K1-F10
Method BLASTX
NCBI GI g1402890
BLAST score 480
E value 2.0e-48
Match length 133
% identity 62
NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 278521
Contig ID 86256_1.R1011
5'-most EST LIB3069-040-Q1-K1-F12

Seq. No. 278522
Contig ID 86257_1.R1011
5'-most EST LIB3069-043-Q1-K1-A4

Seq. No. 278523
Contig ID 86264_1.R1011
5'-most EST LIB3069-040-Q1-K1-F9
Method BLASTX
NCBI GI g3885880
BLAST score 689
E value 8.0e-73
Match length 156
% identity 82
NCBI Description (AF093628) protochlorophyllide reductase homolog [Oryza sativa]

Seq. No. 278524
Contig ID 86267_1.R1011
5'-most EST LIB3069-040-Q1-K1-G11

Seq. No.	278525
Contig ID	86278_1.R1011
5'-most EST	uC-zmroteosinte002d09b1
Method	BLASTX
NCBI GI	g1653395
BLAST score	936
E value	1.0e-101
Match length	315
% identity	58
NCBI Description	(D90913) PET112 [Synechocystis sp.]

Seq. No.	278526
Contig ID	86289_1.R1011
5'-most EST	cyk700048666.f1

Seq. No.	278527
Contig ID	86313_1.R1011
5'-most EST	uwc700150647.h1

Seq. No.	278528
Contig ID	86321_1.R1011
5'-most EST	uC-zmflmo17037c05b1

Seq. No.	278529
Contig ID	86359_2.R1011
5'-most EST	LIB3069-041-Q1-K1-G6

Seq. No.	278530
Contig ID	86368_1.R1011
5'-most EST	uC-zmroteosinte077e03b1
Method	BLASTX
NCBI GI	g2829886
BLAST score	427
E value	5.0e-42
Match length	120
% identity	72
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	278531
Contig ID	86370_1.R1011
5'-most EST	LIB3069-042-Q1-K1-A5

Seq. No.	278532
Contig ID	86371_1.R1011
5'-most EST	ntr700073673.h1

Seq. No.	278533
Contig ID	86381_1.R1011
5'-most EST	LIB3069-042-Q1-K1-B1

Seq. No.	278534
Contig ID	86383_1.R1011
5'-most EST	wty700167195.h1
Method	BLASTX
NCBI GI	g4204287
BLAST score	257
E value	9.0e-45

Match length	98
% identity	80
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	278535
Contig ID	86383_2.R1011
5'-most EST	LIB3069-042-Q1-K1-B11

Seq. No.	278536
Contig ID	86393_1.R1011
5'-most EST	qmh700026223.f1

Seq. No.	278537
Contig ID	86402_1.R1011
5'-most EST	gwl700617022.h1

Seq. No.	278538
Contig ID	86427_1.R1011
5'-most EST	pmx700088794.h1
Method	BLASTX
NCBI GI	g2252863
BLAST score	308
E value	1.0e-36
Match length	145
% identity	57
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]

Seq. No.	278539
Contig ID	86429_1.R1011
5'-most EST	uC-zmf1B73042b10b1
Method	BLASTX
NCBI GI	g1531756
BLAST score	246
E value	2.0e-20
Match length	50
% identity	88
NCBI Description	(X82413) proline-rich-like protein [Asparagus officinalis]

Seq. No.	278540
Contig ID	86430_1.R1011
5'-most EST	LIB3069-042-Q1-K1-F5
Method	BLASTX
NCBI GI	g4539009
BLAST score	503
E value	1.0e-50
Match length	166
% identity	59
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	278541
Contig ID	86433_1.R1011
5'-most EST	uC-zmf1b73232e01b1
Method	BLASTX
NCBI GI	g419760
BLAST score	562

E value	1.0e-57
Match length	270
% identity	33
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	278542
Contig ID	86448_1.R1011
5'-most EST	cyk700051711.f1
Method	BLASTX
NCBI GI	g2760839
BLAST score	652
E value	5.0e-68
Match length	240
% identity	54
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	278543
Contig ID	86458_1.R1011
5'-most EST	LIB3069-043-Q1-K1-A10

Seq. No.	278544
Contig ID	86466_1.R1011
5'-most EST	LIB3136-024-Q1-K1-B3

Seq. No.	278545
Contig ID	86471_1.R1011
5'-most EST	xsy700214807.h1

Seq. No.	278546
Contig ID	86472_1.R1011
5'-most EST	LIB3069-043-Q1-K1-B2

Seq. No.	278547
Contig ID	86486_1.R1011
5'-most EST	tzu700204189.h1
Method	BLASTX
NCBI GI	g3329368
BLAST score	502
E value	9.0e-51
Match length	158
% identity	57
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	278548
Contig ID	86486_2.R1011
5'-most EST	uC-zmflmo17127f03b1
Method	BLASTX
NCBI GI	g3329368
BLAST score	275
E value	4.0e-24
Match length	78
% identity	67
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	278549

Contig ID	86488_1.R1011
5'-most EST	LIB3137-060-Q1-K1-G11
Method	BLASTX
NCBI GI	g2739046
BLAST score	299
E value	7.0e-27
Match length	133
% identity	46
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	278550
Contig ID	86496_1.R1011
5'-most EST	uC-zmf1Mo17092c10b1

Seq. No.	278551
Contig ID	86503_1.R1011
5'-most EST	LIB3069-043-Q1-K1-E3
Method	BLASTX
NCBI GI	g2191144
BLAST score	556
E value	5.0e-57
Match length	135
% identity	74
NCBI Description	(AF007269) A_IG002N01.24 gene product [Arabidopsis thaliana]

Seq. No.	278552
Contig ID	86505_1.R1011
5'-most EST	xmt700262823.h1

Seq. No.	278553
Contig ID	86509_1.R1011
5'-most EST	LIB3069-043-Q1-K1-F1
Method	BLASTX
NCBI GI	g4510348
BLAST score	601
E value	4.0e-62
Match length	199
% identity	57
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	278554
Contig ID	86509_2.R1011
5'-most EST	ceu700421678.h1
Method	BLASTX
NCBI GI	g4510348
BLAST score	213
E value	5.0e-17
Match length	75
% identity	59
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	278555
Contig ID	86510_1.R1011
5'-most EST	uC-zmf1mo17067e07b1
Method	BLASTX

NCBI GI	g1717871
BLAST score	458
E value	3.0e-84
Match length	306
% identity	53
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15) >gi_1078006_pir__S53974 hypothetical protein YMR304w - yeast (Saccharomyces cerevisiae) >gi_798946_emb_CAA89137_ (Z49212) unknown [Saccharomyces cerevisiae]

Seq. No.	278556
Contig ID	86512_1.R1011
5'-most EST	uC-zmflb73121f12b2

Seq. No.	278557
Contig ID	86513_1.R1011
5'-most EST	LIB3069-043-Q1-K1-F2

Seq. No.	278558
Contig ID	86517_1.R1011
5'-most EST	LIB3069-043-Q1-K1-F6

Seq. No.	278559
Contig ID	86523_1.R1011
5'-most EST	LIB3069-043-Q1-K1-G11

Seq. No.	278560
Contig ID	86525_1.R1011
5'-most EST	uC-zmflmo17201e01b1

Seq. No.	278561
Contig ID	86530_1.R1011
5'-most EST	uC-zmflB73106b10b1
Method	BLASTX
NCBI GI	g4580395
BLAST score	316
E value	4.0e-59
Match length	264
% identity	48
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	278562
Contig ID	86541_1.R1011
5'-most EST	tfd700572763.h1

Seq. No.	278563
Contig ID	86551_1.R1011
5'-most EST	uC-zmflmo17330a11b1
Method	BLASTX
NCBI GI	g2749982
BLAST score	557
E value	5.0e-57
Match length	242
% identity	48

NCBI Description (AF036705) Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. elegans cDNA yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans cDNA yk257d4.5;

Seq. No. 278564
Contig ID 86555_1.R1011
5'-most EST kyv700142560.h1

Seq. No. 278565
Contig ID 86564_1.R1011
5'-most EST LIB3069-044-Q1-K1-C12
Method BLASTX
NCBI GI g4417293
BLAST score 317
E value 3.0e-29
Match length 124
% identity 47
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 278566
Contig ID 86584_1.R1011
5'-most EST uC-zmflb73125h12b2

Seq. No. 278567
Contig ID 86597_1.R1011
5'-most EST LIB3069-044-Q1-K1-F7

Seq. No. 278568
Contig ID 86598_1.R1011
5'-most EST uC-zmflb73305e06b2
Method BLASTX
NCBI GI g4314358
BLAST score 835
E value 1.0e-89
Match length 280
% identity 57
NCBI Description (AC006340) putative kinesin heavy chain protein [Arabidopsis thaliana]

Seq. No. 278569
Contig ID 86609_1.R1011
5'-most EST hvj700619151.h1
Method BLASTX
NCBI GI g4544422
BLAST score 236
E value 9.0e-20
Match length 90
% identity 54
NCBI Description (AC006955) putative fimbrin [Arabidopsis thaliana]

Seq. No. 278570
Contig ID 86621_1.R1011
5'-most EST rvt700549648.h1

Seq. No. 278571

Contig ID	86629_1.R1011
5'-most EST	nbm700466247.h1
Method	BLASTX
NCBI GI	g4099605
BLAST score	390
E value	3.0e-37
Match length	172
% identity	49
NCBI Description	(U88836) translational activator GCN1 [Homo sapiens]

Seq. No.	278572
Contig ID	86630_1.R1011
5'-most EST	fwa700097961.h1
Method	BLASTX
NCBI GI	g4262154
BLAST score	212
E value	8.0e-17
Match length	116
% identity	47
NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No.	278573
Contig ID	86651_1.R1011
5'-most EST	uC-zmflmo17318h09a1

Seq. No.	278574
Contig ID	86663_1.R1011
5'-most EST	vux700160026.h1

Seq. No.	278575
Contig ID	86664_1.R1011
5'-most EST	hbs701182766.h1

Seq. No.	278576
Contig ID	86667_1.R1011
5'-most EST	uwc700152275.h1
Method	BLASTX
NCBI GI	g1065515
BLAST score	309
E value	5.0e-28
Match length	145
% identity	43
NCBI Description	(U40420) weak similarity to procollagen alpha chain 1(V) chain [Caenorhabditis elegans]

Seq. No.	278577
Contig ID	86669_1.R1011
5'-most EST	LIB3069-045-Q1-K1-D7

Seq. No.	278578
Contig ID	86670_1.R1011
5'-most EST	LIB3069-045-Q1-K1-D8
Method	BLASTX
NCBI GI	g3320462
BLAST score	223
E value	2.0e-29

Match length	144
% identity	48
NCBI Description	(AF062467) polygalacturonase precursor [Cucumis melo]

Seq. No.	278579
Contig ID	86671_1.R1011
5'-most EST	LIB3069-045-Q1-K1-D9

Seq. No.	278580
Contig ID	86671_2.R1011
5'-most EST	xmt700262391.h1

Seq. No.	278581
Contig ID	86674_1.R1011
5'-most EST	LIB3069-045-Q1-K1-E11

Seq. No.	278582
Contig ID	86701_1.R1011
5'-most EST	xsy700207426.h1
Method	BLASTX
NCBI GI	g3668086
BLAST score	702
E value	9.0e-74
Match length	262
% identity	57
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	278583
Contig ID	86702_1.R1011
5'-most EST	LIB3069-045-Q1-K1-G9

Seq. No.	278584
Contig ID	86703_1.R1011
5'-most EST	uC-zmf1B73008g06b1
Method	BLASTX
NCBI GI	g3080415
BLAST score	664
E value	1.0e-69
Match length	194
% identity	66
NCBI Description	(AL022604) cysteine proteinase-like protein [Arabidopsis thaliana]

Seq. No.	278585
Contig ID	86706_1.R1011
5'-most EST	LIB3069-045-Q1-K1-H12
Method	BLASTX
NCBI GI	g2281090
BLAST score	477
E value	7.0e-48
Match length	152
% identity	64
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278586
Contig ID	86724_1.R1011
5'-most EST	uC-zmf1b73196a03b1

Seq. No.	278587
Contig ID	86724_2.R1011
5'-most EST	uC-zmflb73283a02b2

Seq. No.	278588
Contig ID	86725_1.R1011
5'-most EST	uC-zmroteosinte068g03b1

Seq. No.	278589
Contig ID	86727_2.R1011
5'-most EST	fdz701160841.h1

Seq. No.	278590
Contig ID	86730_1.R1011
5'-most EST	uC-zmroteosinte096g07b2
Method	BLASTX
NCBI GI	g1438883
BLAST score	804
E value	1.0e-87
Match length	238
% identity	67
NCBI Description	(U43840) GmCK3p [Glycine max]

Seq. No.	278591
Contig ID	86746_1.R1011
5'-most EST	LIB3069-046-Q1-K1-E1

Seq. No.	278592
Contig ID	86752_1.R1011
5'-most EST	uC-zmroteosinte029e07b1
Method	BLASTX
NCBI GI	g4582430
BLAST score	561
E value	1.0e-57
Match length	201
% identity	55
NCBI Description	(AC007196) nonsense-mediated mRNA decay protein [Arabidopsis thaliana]

Seq. No.	278593
Contig ID	86759_1.R1011
5'-most EST	LIB3137-001-Q1-K1-A2

Seq. No.	278594
Contig ID	86763_1.R1011
5'-most EST	xmt700263473.h1
Method	BLASTX
NCBI GI	g4337174
BLAST score	315
E value	6.0e-29
Match length	80
% identity	74
NCBI Description	(AC006416) Similar to gi_1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb_U32764. [Arabidopsis thaliana]

Seq. No.	278595
Contig ID	86764_1.R1011
5'-most EST	ceu700432792.h1
Method	BLASTX
NCBI GI	g3152606
BLAST score	311
E value	2.0e-28
Match length	66
% identity	77
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No.	278596
Contig ID	86780_1.R1011
5'-most EST	LIB3069-047-Q1-K1-A9
Method	BLASTX
NCBI GI	g4558550
BLAST score	583
E value	2.0e-60
Match length	162
% identity	68
NCBI Description	(AC007138) putative protein transport factor [Arabidopsis thaliana]

Seq. No.	278597
Contig ID	86795_1.R1011
5'-most EST	uC-zmflb73126h02a1

Seq. No.	278598
Contig ID	86810_1.R1011
5'-most EST	uC-zmroteosinte009a08b1
Method	BLASTX
NCBI GI	g3123130
BLAST score	879
E value	7.0e-95
Match length	230
% identity	71
NCBI Description	HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN T32G6.2 IN CHROMOSOME II >gi_2618685 (AC002510) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >gi_3241948 (AC004625) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana]

Seq. No.	278599
Contig ID	86811_1.R1011
5'-most EST	hbs701184542.h1

Seq. No.	278600
Contig ID	86835_1.R1011
5'-most EST	LIB3069-047-Q1-K1-G7
Method	BLASTX
NCBI GI	g1087073
BLAST score	184
E value	1.0e-13
Match length	53
% identity	62
NCBI Description	(S79243) calmodulin-binding heat-shock protein, CaMBP

[Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa]
[Nicotiana tabacum]

Seq. No.	278601
Contig ID	86849_1.R1011
5'-most EST	uC-zmflmo17320f03b1

Seq. No.	278602
Contig ID	86852_1.R1011
5'-most EST	uC-zmflmo17029a10b1
Method	BLASTX
NCBI GI	g1871187
BLAST score	285
E value	3.0e-25
Match length	149
% identity	46
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	278603
Contig ID	86869_1.R1011
5'-most EST	xjt700096523.h1

Seq. No.	278604
Contig ID	86881_1.R1011
5'-most EST	LIB3069-048-Q1-K1-C8

Seq. No.	278605
Contig ID	86888_1.R1011
5'-most EST	uC-zmflb73069c03b1
Method	BLASTX
NCBI GI	g4587615
BLAST score	1264
E value	1.0e-139
Match length	324
% identity	70
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	278606
Contig ID	86904_1.R1011
5'-most EST	LIB3069-048-Q1-K1-F5
Method	BLASTX
NCBI GI	g2661179
BLAST score	244
E value	1.0e-20
Match length	62
% identity	76
NCBI Description	(U80984) AtZW10 [Arabidopsis thaliana]

Seq. No.	278607
Contig ID	86916_1.R1011
5'-most EST	LIB3069-048-Q1-K1-G5
Method	BLASTX
NCBI GI	g3953471
BLAST score	300
E value	7.0e-27
Match length	128

% identity	49
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	278608
Contig ID	86917_1.R1011
5'-most EST	LIB3136-045-Q1-K1-B3
Method	BLASTX
NCBI GI	g4580472
BLAST score	851
E value	3.0e-91
Match length	239
% identity	67
NCBI Description	(AC006081) DNA binding protein;similar to CDC27 and nuclear scaffold proteins [Arabidopsis thaliana]

Seq. No.	278609
Contig ID	86918_1.R1011
5'-most EST	LIB3069-048-Q1-K1-G7
Method	BLASTX
NCBI GI	g4006855
BLAST score	338
E value	2.0e-39
Match length	149
% identity	58
NCBI Description	(Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	278610
Contig ID	86919_1.R1011
5'-most EST	LIB3069-048-Q1-K1-G8
Method	BLASTX
NCBI GI	g3540184
BLAST score	263
E value	7.0e-23
Match length	140
% identity	40
NCBI Description	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No.	278611
Contig ID	86931_1.R1011
5'-most EST	dyk700106469.h1

Seq. No.	278612
Contig ID	86942_1.R1011
5'-most EST	mwy700443250.h2
Method	BLASTX
NCBI GI	g2190187
BLAST score	322
E value	1.0e-29
Match length	219
% identity	33
NCBI Description	(D64087) nuclear matrix constituent protein 1 (NMCP1) [Daucus carota]

Seq. No.	278613
Contig ID	86956_1.R1011
5'-most EST	LIB3069-049-Q1-K1-C7

Seq. No.	278614
Contig ID	86961_1.R1011
5'-most EST	uC-zmflmo17235c06b1
Method	BLASTX
NCBI GI	g100226
BLAST score	599
E value	8.0e-62
Match length	313
% identity	39
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	278615
Contig ID	86965_1.R1011
5'-most EST	xjt700096933.h1
Method	BLASTX
NCBI GI	g3341676
BLAST score	424
E value	2.0e-41
Match length	150
% identity	54
NCBI Description	(AC003672) putative glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	278616
Contig ID	86970_1.R1011
5'-most EST	uC-zmromo17028e05a1

Seq. No.	278617
Contig ID	86974_1.R1011
5'-most EST	LIB3069-049-Q1-K1-F2

Seq. No.	278618
Contig ID	86990_1.R1011
5'-most EST	uC-zmromo17009g08a1

Seq. No.	278619
Contig ID	87018_1.R1011
5'-most EST	LIB3069-050-Q1-K1-C3

Seq. No.	278620
Contig ID	87023_1.R1011
5'-most EST	ceu700430176.h1

Seq. No.	278621
Contig ID	87032_1.R1011
5'-most EST	wty700166774.h1
Method	BLASTX
NCBI GI	g1209756
BLAST score	1160
E value	1.0e-127
Match length	316
% identity	69
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	278622
Contig ID	87034_1.R1011
5'-most EST	qmh700030038.f1
Method	BLASTX
NCBI GI	g3775997
BLAST score	774
E value	1.0e-82
Match length	219
% identity	67
NCBI Description	(AJ010462) RNA helicase [Arabidopsis thaliana]

Seq. No.	278623
Contig ID	87036_1.R1011
5'-most EST	uC-zmflmo17289f05b1
Method	BLASTX
NCBI GI	g629774
BLAST score	778
E value	6.0e-83
Match length	219
% identity	70
NCBI Description	beta-ketoacyl-ACP synthase - barley >gi_498742_emb_CAA84023_ (Z34269) beta-ketoacyl-ACP synthase [Hordeum vulgare]

Seq. No.	278624
Contig ID	87036_2.R1011
5'-most EST	LIB3069-050-Q1-K1-E1
Method	BLASTX
NCBI GI	g629774
BLAST score	628
E value	1.0e-65
Match length	146
% identity	78
NCBI Description	beta-ketoacyl-ACP synthase - barley >gi_498742_emb_CAA84023_ (Z34269) beta-ketoacyl-ACP synthase [Hordeum vulgare]

Seq. No.	278625
Contig ID	87048_1.R1011
5'-most EST	LIB3069-050-Q1-K1-F4

Seq. No.	278626
Contig ID	87056_1.R1011
5'-most EST	LIB3069-050-Q1-K1-G12

Seq. No.	278627
Contig ID	87101_1.R1011
5'-most EST	cyk700048795.f1

Seq. No.	278628
Contig ID	87101_2.R1011
5'-most EST	LIB3137-058-Q1-K1-C3

Seq. No.	278629
Contig ID	87102_1.R1011
5'-most EST	wyr700235237.h1

Method	BLASTX
NCBI GI	g3913789
BLAST score	508
E value	5.0e-62
Match length	140
% identity	88
NCBI Description	NONLEGUME HEMOGLOBIN >gi_1076720_pir__S46502 hemoglobin - barley >gi_508204 (U01228) haemoglobin apoprotein [Hordeum vulgare] >gi_2071976 (U94968) hemoglobin [Hordeum vulgare]

Seq. No.	278630
Contig ID	87102_3.R1011
5'-most EST	wty700170736.h1
Method	BLASTX
NCBI GI	g2058496
BLAST score	193
E value	2.0e-21
Match length	71
% identity	82
NCBI Description	(U76028) hemoglobin 2 [Oryza sativa] >gi_2058502 (U76031) hemoglobin 2 [Oryza sativa]

Seq. No.	278631
Contig ID	87116_1.R1011
5'-most EST	uC-zmroteosinte033d10b1
Method	BLASTX
NCBI GI	g2072986
BLAST score	1070
E value	1.0e-117
Match length	301
% identity	66
NCBI Description	(U95142) putative G-protein-coupled receptor [Arabidopsis thaliana] >gi_2072988 (U95143) putative G-protein-coupled receptor [Arabidopsis thaliana]

Seq. No.	278632
Contig ID	87130_1.R1011
5'-most EST	uC-zmflmo17276g01a1

Seq. No.	278633
Contig ID	87143_1.R1011
5'-most EST	LIB3069-051-Q1-K1-H2
Method	BLASTX
NCBI GI	g2809259
BLAST score	309
E value	3.0e-28
Match length	203
% identity	28
NCBI Description	(AC002560) F21B7.28 [Arabidopsis thaliana]

Seq. No.	278634
Contig ID	87170_1.R1011
5'-most EST	uC-zmflb73149d01b1

Seq. No.	278635
Contig ID	87176_1.R1011
5'-most EST	LIB3069-052-Q1-K1-D5

09054500 - 450800

Method	BLASTX
NCBI GI	g3892652
BLAST score	708
E value	5.0e-75
Match length	149
% identity	95
NCBI Description	(Y09303) putative MADS-domain transcription factor [Zea mays]

Seq. No.	278636
Contig ID	87185_1.R1011
5'-most EST	LIB3069-052-Q1-K1-E7

Seq. No.	278637
Contig ID	87192_1.R1011
5'-most EST	LIB3069-052-Q1-K1-F8
Method	BLASTN
NCBI GI	g533251
BLAST score	207
E value	1.0e-113
Match length	367
% identity	96
NCBI Description	Zea mays (clone pSM8) sucrose synthase 2 (Sus1) gene, complete cds

Seq. No.	278638
Contig ID	87221_1.R1011
5'-most EST	LIB3069-053-Q1-K1-C4
Method	BLASTX
NCBI GI	g4262147
BLAST score	180
E value	5.0e-13
Match length	85
% identity	47
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	278639
Contig ID	87223_1.R1011
5'-most EST	LIB3069-053-Q1-K1-C7
Method	BLASTX
NCBI GI	g2435517
BLAST score	203
E value	1.0e-15
Match length	108
% identity	49
NCBI Description	(AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

Seq. No.	278640
Contig ID	87234_1.R1011
5'-most EST	ceu700433722.h1

Seq. No.	278641
Contig ID	87240_1.R1011
5'-most EST	xyt700342801.h1

Seq. No.	278642
Contig ID	87265_1.R1011
5'-most EST	uC-zmf1Mo17008c04b1

Seq. No.	278643
Contig ID	87274_1.R1011
5'-most EST	LIB3069-054-Q1-K1-A9
Method	BLASTX
NCBI GI	g3644034
BLAST score	527
E value	7.0e-54
Match length	134
% identity	75
NCBI Description	(AF091304) aminoacyl peptidase [Glycine max]

Seq. No.	278644
Contig ID	87282_1.R1011
5'-most EST	gct701175533.h1
Method	BLASTX
NCBI GI	g3413706
BLAST score	144
E value	8.0e-09
Match length	83
% identity	31
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278645
Contig ID	87288_1.R1011
5'-most EST	LIB3069-054-Q1-K1-C12
Method	BLASTX
NCBI GI	g4512616
BLAST score	217
E value	2.0e-17
Match length	103
% identity	52
NCBI Description	(AC004793) Contains similarity to gi_1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb_D90912 and is a member of the Inositol monophophatase family PF_00459. EST gb_AA597395 comes from this gene. [Arabidopsis tha

Seq. No.	278646
Contig ID	87293_1.R1011
5'-most EST	ntr700075821.h1
Method	BLASTX
NCBI GI	g4160280
BLAST score	383
E value	3.0e-70
Match length	181
% identity	69
NCBI Description	(AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No.	278647
Contig ID	87315_1.R1011
5'-most EST	LIB3069-054-Q1-K1-E6
Method	BLASTN
NCBI GI	g2352798
BLAST score	480

E value	0.0e+00
Match length	805
% identity	96
NCBI Description	Zea mays retinoblastoma-related protein 2b (RRB2b) mRNA, partial cds

Seq. No.	278648
Contig ID	87323_1.R1011
5'-most EST	dyk700103977.h1

Seq. No.	278649
Contig ID	87334_1.R1011
5'-most EST	uC-zmflmo17a11b1
Method	BLASTX
NCBI GI	g3927830
BLAST score	1238
E value	1.0e-136
Match length	422
% identity	44
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278650
Contig ID	87354_1.R1011
5'-most EST	LIB3069-055-Q1-K1-A10

Seq. No.	278651
Contig ID	87360_1.R1011
5'-most EST	LIB3069-055-Q1-K1-A7

Seq. No.	278652
Contig ID	87371_1.R1011
5'-most EST	uC-zmflb73169g12b2
Method	BLASTX
NCBI GI	g2583128
BLAST score	164
E value	5.0e-11
Match length	63
% identity	46
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278653
Contig ID	87387_1.R1011
5'-most EST	LIB3069-055-Q1-K1-D5

Seq. No.	278654
Contig ID	87416_1.R1011
5'-most EST	LIB3069-055-Q1-K1-G6
Method	BLASTX
NCBI GI	g2914706
BLAST score	208
E value	3.0e-16
Match length	93
% identity	46
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	278655
Contig ID	87429_1.R1011

5'-most EST	uC-zmf1b73210f06b1
Method	BLASTX
NCBI GI	g3738287
BLAST score	394
E value	8.0e-38
Match length	218
% identity	40
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	278656
Contig ID	87429_2.R1011
5'-most EST	ymt700222656.h1
Method	BLASTX
NCBI GI	g3738287
BLAST score	187
E value	5.0e-14
Match length	72
% identity	47
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	278657
Contig ID	87430_1.R1011
5'-most EST	LIB3070-003-Q1-N1-E7
Method	BLASTX
NCBI GI	g3876863
BLAST score	144
E value	6.0e-09
Match length	122
% identity	30
NCBI Description	(Z81078) predicted using Genefinder; Similarity to Yeast E1-E2 ATPase (SW:YIE8_YEAST); cDNA EST EMBL:D34828 comes from this gene; cDNA EST EMBL:D35545 comes from this gene; cDNA EST EMBL:D35631 comes from this gene; cDNA EST EM... >gi_3880373_emb_CAA16284_ (AL021466) predicted using Genefinder; Similarity to Yeast E1-E2 ATPase (SW:YIE8_YEAST); cDNA EST EMBL:D34828 comes from this gene; cDNA EST EMBL:D35545 comes from this gene; cDNA EST EMBL:D35631 comes from this gene; cDNA EST

Seq. No.	278658
Contig ID	87440_1.R1011
5'-most EST	LIB3069-056-Q1-K1-A9
Method	BLASTX
NCBI GI	g4574141
BLAST score	464
E value	2.0e-46
Match length	105
% identity	86
NCBI Description	(AF073698) cysteine synthase [Oryza sativa]

Seq. No.	278659
Contig ID	87450_1.R1011
5'-most EST	uC-zmf1b73159d06b2
Method	BLASTX
NCBI GI	g4522009

BLAST score	663
E value	1.0e-102
Match length	331
% identity	58
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	278660
Contig ID	87450_2.R1011
5'-most EST	uC-zmflmo17168e04b1
Method	BLASTX
NCBI GI	g4522009
BLAST score	516
E value	2.0e-52
Match length	156
% identity	61
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	278661
Contig ID	87450_3.R1011
5'-most EST	dyk700104977.h1
Method	BLASTX
NCBI GI	g4522009
BLAST score	695
E value	3.0e-73
Match length	264
% identity	52
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	278662
Contig ID	87451_1.R1011
5'-most EST	cyk700050777.f1

Seq. No.	278663
Contig ID	87452_1.R1011
5'-most EST	LIB3069-056-Q1-K1-C11

Seq. No.	278664
Contig ID	87457_1.R1011
5'-most EST	uC-zmrob73066h09b1
Method	BLASTX
NCBI GI	g3402715
BLAST score	207
E value	5.0e-16
Match length	166
% identity	31
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	278665
Contig ID	87462_1.R1011
5'-most EST	LIB3069-056-Q1-K1-D11

Seq. No.	278666
Contig ID	87462_2.R1011
5'-most EST	uC-zmflb73389c02a1

Seq. No.	278667
Contig ID	87466_1.R1011

5'-most EST	rvt700549877.h1
Method	BLASTX
NCBI GI	g1742965
BLAST score	272
E value	1.0e-23
Match length	164
% identity	35
NCBI Description	(Y09562) HAPp48,5 protein [Arabidopsis thaliana]

Seq. No.	278668
Contig ID	87471_1.R1011
5'-most EST	uC-zmflb73301g05b2
Method	BLASTX
NCBI GI	g3252805
BLAST score	183
E value	2.0e-13
Match length	126
% identity	37
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana] >gi_3650027 (AC005396) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278669
Contig ID	87474_1.R1011
5'-most EST	uC-zmflB73042d06b1

Seq. No.	278670
Contig ID	87479_1.R1011
5'-most EST	nbm700471119.h1
Method	BLASTX
NCBI GI	g3738200
BLAST score	229
E value	1.0e-18
Match length	221
% identity	29
NCBI Description	(AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]

Seq. No.	278671
Contig ID	87500_1.R1011
5'-most EST	uC-zmroteosinte075c03b1
Method	BLASTX
NCBI GI	g3176671
BLAST score	810
E value	1.0e-86
Match length	318
% identity	50
NCBI Description	(AC004393) Contains similarity to hypothetical gene B0495.7 gb_687822 from C. elegans cosmid gb_U21317. [Arabidopsis thaliana]

Seq. No.	278672
Contig ID	87504_1.R1011
5'-most EST	uC-zmflmo17015f05b1

Seq. No.	278673
Contig ID	87516_1.R1011

5'-most EST	uC-zmflmo17181g09b1
Seq. No.	278674
Contig ID	87526_1.R1011
5'-most EST	LIB3069-057-Q1-K1-D11
Method	BLASTX
NCBI GI	g4164473
BLAST score	158
E value	2.0e-10
Match length	70
% identity	53
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]
Seq. No.	278675
Contig ID	87539_1.R1011
5'-most EST	uC-zmflmo17138g05b1
Seq. No.	278676
Contig ID	87548_1.R1011
5'-most EST	uC-zmflmo17223d07b1
Method	BLASTX
NCBI GI	g3559807
BLAST score	717
E value	7.0e-76
Match length	164
% identity	81
NCBI Description	(Y15628) HCF136 protein [Arabidopsis thaliana]
Seq. No.	278677
Contig ID	87550_1.R1011
5'-most EST	LIB3069-057-Q1-K1-H4
Method	BLASTX
NCBI GI	g1944575
BLAST score	525
E value	1.0e-53
Match length	128
% identity	73
NCBI Description	(Z94058) pectinesterase [Lycopersicon esculentum]
Seq. No.	278678
Contig ID	87564_1.R1011
5'-most EST	pmx700088594.h1
Method	BLASTX
NCBI GI	g2129630
BLAST score	150
E value	1.0e-09
Match length	64
% identity	41
NCBI Description	lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750_ (X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721) unknown [Arabidopsis thaliana]
Seq. No.	278679
Contig ID	87570_1.R1011
5'-most EST	uC-zmflb73305c04b2
Method	BLASTN

NCBI GI	g3821780
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	278680
Contig ID	87583_1.R1011
5'-most EST	LIB3070-001-Q1-N1-D1

Seq. No.	278681
Contig ID	87590_1.R1011
5'-most EST	gwl700618374.h1
Method	BLASTX
NCBI GI	g1172995
BLAST score	203
E value	4.0e-16
Match length	79
% identity	57
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	278682
Contig ID	87622_1.R1011
5'-most EST	LIB3070-001-Q1-N1-H2

Seq. No.	278683
Contig ID	87662_1.R1011
5'-most EST	LIB3070-002-Q1-N1-E1
Method	BLASTX
NCBI GI	g4218120
BLAST score	300
E value	5.0e-27
Match length	81
% identity	62
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	278684
Contig ID	87675_1.R1011
5'-most EST	wyr700243884.h1
Method	BLASTX
NCBI GI	g3202044
BLAST score	415
E value	1.0e-40
Match length	151
% identity	52
NCBI Description	(AF069492) SONA [Emericella nidulans]

Seq. No.	278685
Contig ID	87678_1.R1011
5'-most EST	cat700017347.r1

Seq. No.	278686
Contig ID	87702_1.R1011
5'-most EST	uC-zmflb73067e05b1
Method	BLASTX
NCBI GI	g4585142
BLAST score	952
E value	1.0e-103
Match length	306
% identity	62
NCBI Description	(AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon esculentum]

Seq. No.	278687
Contig ID	87704_1.R1011
5'-most EST	LIB3070-003-Q1-N1-A9
Method	BLASTX
NCBI GI	g4581111
BLAST score	154
E value	6.0e-10
Match length	139
% identity	32
NCBI Description	(AC005825) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	278688
Contig ID	87722_1.R1011
5'-most EST	wyr700243160.h1

Seq. No.	278689
Contig ID	87746_1.R1011
5'-most EST	LIB3070-003-Q1-N1-F4
Method	BLASTX
NCBI GI	g2149640
BLAST score	740
E value	1.0e-78
Match length	169
% identity	81
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	278690
Contig ID	87754_1.R1011
5'-most EST	uC-zmflb73026h07b1
Method	BLASTX
NCBI GI	g4371280
BLAST score	283
E value	1.0e-45
Match length	154
% identity	66
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278691
Contig ID	87759_1.R1011
5'-most EST	uer700580787.h1

Seq. No.	278692
Contig ID	87773_1.R1011
5'-most EST	LIB84-026-Q1-E1-B6

Seq. No.	278693
Contig ID	87803_1.R1011
5'-most EST	LIB3070-004-Q1-N1-D3

Seq. No.	278694
Contig ID	87823_1.R1011
5'-most EST	LIB3070-004-Q1-N1-F9

Seq. No.	278695
Contig ID	87833_1.R1011
5'-most EST	uC-zmflmo17100h04b1

Seq. No.	278696
Contig ID	87841_1.R1011
5'-most EST	tzu700205154.h1

Seq. No.	278697
Contig ID	87845_1.R1011
5'-most EST	LIB3070-005-Q1-N1-A10
Method	BLASTX
NCBI GI	g3928758
BLAST score	239
E value	4.0e-20
Match length	56
% identity	79
NCBI Description	(AB007987) Lipoic acid synthase [Arabidopsis thaliana] >gi_4454462_gb_AAD20909_ (AC006234) putative lipoic acid synthase [Arabidopsis thaliana]

Seq. No.	278698
Contig ID	87846_1.R1011
5'-most EST	uC-zmflmo17066e04b1
Method	BLASTX
NCBI GI	g2651295
BLAST score	329
E value	6.0e-30
Match length	241
% identity	42
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278699
Contig ID	87846_2.R1011
5'-most EST	LIB3070-005-Q1-N1-A11

Seq. No.	278700
Contig ID	87846_3.R1011
5'-most EST	xmt700259840.h1

Seq. No.	278701
Contig ID	87848_1.R1011
5'-most EST	uC-zmflmo17053a07a1

Seq. No.	278702
Contig ID	87848_2.R1011
5'-most EST	xjt700092950.h1

Seq. No.	278703
Contig ID	87855_1.R1011
5'-most EST	xdb700339924.h1

Seq. No.	278704
Contig ID	87857_1.R1011
5'-most EST	uer700579987.h1
Method	BLASTX
NCBI GI	g4406372
BLAST score	410
E value	1.0e-42
Match length	143
% identity	59
NCBI Description	(AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No.	278705
Contig ID	87864_1.R1011
5'-most EST	pwr700451223.h1

Seq. No.	278706
Contig ID	87873_1.R1011
5'-most EST	vux700158676.h1

Seq. No.	278707
Contig ID	87873_2.R1011
5'-most EST	LIB3070-005-Q1-N1-D12
Method	BLASTX
NCBI GI	g3766365
BLAST score	167
E value	1.0e-11
Match length	137
% identity	30
NCBI Description	(AL031907) putative cystine-rich transcriptional regulator [Schizosaccharomyces pombe]

Seq. No.	278708
Contig ID	87894_1.R1011
5'-most EST	LIB3070-005-Q1-N1-F5
Method	BLASTX
NCBI GI	g2352795
BLAST score	351
E value	4.0e-33
Match length	109
% identity	67
NCBI Description	(AF007793) retinoblastoma-related protein 1 [Zea mays]

Seq. No.	278709
Contig ID	87900_1.R1011
5'-most EST	uer700582875.h1

Seq. No.	278710
Contig ID	87905_1.R1011
5'-most EST	gct701177401.h1

Seq. No.	278711
Contig ID	87909_1.R1011

5'-most EST	hvj700620113.h1
Method	BLASTX
NCBI GI	g4097547
BLAST score	185
E value	7.0e-14
Match length	68
% identity	53
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	278712
Contig ID	87909_2.R1011
5'-most EST	LIB3070-005-Q1-N1-H3

Seq. No.	278713
Contig ID	87914_1.R1011
5'-most EST	LIB3070-005-Q1-N1-H9

Seq. No.	278714
Contig ID	87917_1.R1011
5'-most EST	yyf700349420.h1

Seq. No.	278715
Contig ID	87919_1.R1011
5'-most EST	LIB3070-006-Q1-N1-A2

Seq. No.	278716
Contig ID	87921_1.R1011
5'-most EST	xyt700346357.h1
Method	BLASTX
NCBI GI	g3298537
BLAST score	200
E value	1.0e-15
Match length	107
% identity	46
NCBI Description	(AC004681) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278717
Contig ID	87943_1.R1011
5'-most EST	LIB3070-006-Q1-N1-C8

Seq. No.	278718
Contig ID	87963_1.R1011
5'-most EST	LIB3070-006-Q1-N1-E6
Method	BLASTX
NCBI GI	g4587615
BLAST score	574
E value	2.0e-59
Match length	135
% identity	75
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	278719
Contig ID	87974_1.R1011
5'-most EST	LIB3070-006-Q1-N1-F9
Method	BLASTX
NCBI GI	g2130120

BLAST score	645
E value	1.0e-67
Match length	137
% identity	93
NCBI Description	cyclin Ib - maize >gi_516552 (U10078) cyclin IbZm [Zea mays]

Seq. No.	278720
Contig ID	87979_1.R1011
5'-most EST	LIB3070-006-Q1-N1-G2

Seq. No.	278721
Contig ID	87998_1.R1011
5'-most EST	uC-zmflb73416h05a1

Seq. No.	278722
Contig ID	88007_1.R1011
5'-most EST	LIB3070-007-Q1-N1-B1

Seq. No.	278723
Contig ID	88021_1.R1011
5'-most EST	LIB3070-007-Q1-N1-C4

Seq. No.	278724
Contig ID	88028_1.R1011
5'-most EST	LIB3070-007-Q1-N1-D8
Method	BLASTX
NCBI GI	g4206209
BLAST score	409
E value	5.0e-40
Match length	137
% identity	57
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No.	278725
Contig ID	88032_1.R1011
5'-most EST	LIB3070-007-Q1-N1-E12
Method	BLASTN
NCBI GI	g4416300
BLAST score	86
E value	1.0e-40
Match length	212
% identity	87
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	278726
Contig ID	88043_1.R1011
5'-most EST	tzu700204550.h1
Method	BLASTX
NCBI GI	g4115933
BLAST score	170
E value	7.0e-12
Match length	70
% identity	67

NCBI Description	(AF118223) contains similarity to human RNA polymerase II complex component SRB7 (GB:U52960) [Arabidopsis thaliana]

Seq. No.	278727
Contig ID	88049_1.R1011
5'-most EST	LIB3070-007-Q1-N1-F9
Method	BLASTX
NCBI GI	g4585987
BLAST score	359
E value	5.0e-34
Match length	167
% identity	46
NCBI Description	(AC005287) Similar to nucleolar protein [Arabidopsis thaliana]

Seq. No.	278728
Contig ID	88051_1.R1011
5'-most EST	LIB3070-007-Q1-N1-G10

Seq. No.	278729
Contig ID	88056_1.R1011
5'-most EST	LIB3070-007-Q1-N1-G6
Method	BLASTX
NCBI GI	g2392895
BLAST score	244
E value	1.0e-20
Match length	94
% identity	48
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	278730
Contig ID	88069_1.R1011
5'-most EST	LIB3070-008-Q1-N1-A10
Method	BLASTN
NCBI GI	g56539
BLAST score	103
E value	1.0e-50
Match length	309
% identity	98
NCBI Description	R.norvegicus gene encoding prolactin, exon 5 >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene : exon v and flanks

Seq. No.	278731
Contig ID	88078_1.R1011
5'-most EST	LIB3070-008-Q1-N1-A9

Seq. No.	278732
Contig ID	88088_1.R1011
5'-most EST	fwa70098521.h1
Method	BLASTX
NCBI GI	g2499570
BLAST score	698
E value	7.0e-74
Match length	149
% identity	87

NCBI Description	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) >gi_414332 (L07941) L-isoaspartyl methyltransferase [Triticum aestivum]
Seq. No.	278733
Contig ID	88131_1.R1011
5'-most EST	xsy700209537.h1
Method	BLASTX
NCBI GI	g4033396
BLAST score	752
E value	7.0e-80
Match length	273
% identity	55
NCBI Description	DNA GYRASE SUBUNIT B >gi_2760177_dbj_BAA24187_ (AB010081) B subunit of DNA gyrase [Bacillus sp.]
Seq. No.	278734
Contig ID	88138_1.R1011
5'-most EST	LIB3070-009-Q1-N1-A12
Seq. No.	278735
Contig ID	88143_1.R1011
5'-most EST	fdz701160692.h1
Seq. No.	278736
Contig ID	88155_1.R1011
5'-most EST	LIB3070-009-Q1-N1-C2
Seq. No.	278737
Contig ID	88159_2.R1011
5'-most EST	uer700583594.h1
Method	BLASTX
NCBI GI	g4582434
BLAST score	190
E value	1.0e-14
Match length	48
% identity	77
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.	278738
Contig ID	88159_3.R1011
5'-most EST	cat700018517.r1
Seq. No.	278739
Contig ID	88173_1.R1011
5'-most EST	uC-zmflb73059f02a2
Seq. No.	278740
Contig ID	88176_1.R1011
5'-most EST	uwc700153951.h1
Method	BLASTX
NCBI GI	g4585976
BLAST score	282
E value	5.0e-25
Match length	81

% identity	65
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]
Seq. No.	278741
Contig ID	88181_1.R1011
5'-most EST	vux700159614.h2
Seq. No.	278742
Contig ID	88185_1.R1011
5'-most EST	uer700582359.h1
Seq. No.	278743
Contig ID	88188_1.R1011
5'-most EST	LIB3070-014-Q1-N1-E7
Seq. No.	278744
Contig ID	88205_1.R1011
5'-most EST	uC-zmrob73080f08b1
Method	BLASTX
NCBI GI	g4263517
BLAST score	420
E value	5.0e-41
Match length	190
% identity	47
NCBI Description	(AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]
Seq. No.	278745
Contig ID	88212_1.R1011
5'-most EST	LIB3070-010-Q1-N1-B1
Seq. No.	278746
Contig ID	88222_2.R1011
5'-most EST	ceu700431784.h1
Seq. No.	278747
Contig ID	88239_1.R1011
5'-most EST	uwc700150128.h1
Seq. No.	278748
Contig ID	88245_1.R1011
5'-most EST	LIB3070-010-Q1-N1-E7
Seq. No.	278749
Contig ID	88247_2.R1011
5'-most EST	LIB3070-010-Q1-N1-E9
Method	BLASTX
NCBI GI	g416564
BLAST score	901
E value	1.0e-97
Match length	177
% identity	95
NCBI Description	ABCISIC ACID-INDUCIBLE PROTEIN KINASE >gi_422013_pir__A46408 abscisic acid-inducible serine/threonine protein kinase homolog - wheat (fragment)

>gi_170664 (M94726) protein kinase [Triticum aestivum]

Seq. No.	278750
Contig ID	88264_1.R1011
5'-most EST	nwy700445008.h1
Method	BLASTX
NCBI GI	g3789917
BLAST score	161
E value	7.0e-11
Match length	85
% identity	42
NCBI Description	(AF084928) erythroblast macrophage protein EMP [Homo sapiens]

Seq. No.	278751
Contig ID	88292_1.R1011
5'-most EST	fdz701158674.h1
Method	BLASTX
NCBI GI	g4415933
BLAST score	166
E value	1.0e-11
Match length	71
% identity	44
NCBI Description	(AC006418) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana]

Seq. No.	278752
Contig ID	88310_1.R1011
5'-most EST	cat700019653.r1

Seq. No.	278753
Contig ID	88326_1.R1011
5'-most EST	LIB3070-011-Q1-N1-G3

Seq. No.	278754
Contig ID	88328_1.R1011
5'-most EST	ceu700422280.h1
Method	BLASTX
NCBI GI	g3334739
BLAST score	286
E value	3.0e-25
Match length	154
% identity	45
NCBI Description	(AJ005892) JM23 [Homo sapiens]

Seq. No.	278755
Contig ID	88383_1.R1011
5'-most EST	LIB3070-012-Q1-N1-F1

Seq. No.	278756
Contig ID	88397_1.R1011
5'-most EST	xsy700214109.h1
Method	BLASTX
NCBI GI	g4186184

BLAST score	196
E value	1.0e-14
Match length	134
% identity	29
NCBI Description	(AF111168) unknown [Homo sapiens]

Seq. No.	278757
Contig ID	88406_1.R1011
5'-most EST	LIB3070-012-Q1-N1-H12

Seq. No.	278758
Contig ID	88411_1.R1011
5'-most EST	uC-zmflmo17242a04b1

Seq. No.	278759
Contig ID	88420_1.R1011
5'-most EST	LIB3070-013-Q1-N1-B1

Seq. No.	278760
Contig ID	88434_1.R1011
5'-most EST	uC-zmflb73147a02b1
Method	BLASTX
NCBI GI	g2213594
BLAST score	451
E value	1.0e-44
Match length	195
% identity	45
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	278761
Contig ID	88434_2.R1011
5'-most EST	uC-zmroteosinte008e06b1
Method	BLASTX
NCBI GI	g2213594
BLAST score	172
E value	4.0e-12
Match length	110
% identity	36
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	278762
Contig ID	88437_1.R1011
5'-most EST	uwc700150284.h1

Seq. No.	278763
Contig ID	88437_2.R1011
5'-most EST	qmh700030667.f1

Seq. No.	278764
Contig ID	88442_1.R1011
5'-most EST	LIB3070-013-Q1-N1-D7
Method	BLASTX
NCBI GI	g4538948
BLAST score	374
E value	1.0e-35
Match length	133
% identity	53

NCBI Description	(AL049483) putative protein [Arabidopsis thaliana]
Seq. No.	278765
Contig ID	88449_1.R1011
5'-most EST	LIB3070-013-Q1-N1-E6
Seq. No.	278766
Contig ID	88467_1.R1011
5'-most EST	uC-zmroteosinte120f05b2
Method	BLASTX
NCBI GI	g4566505
BLAST score	374
E value	7.0e-36
Match length	86
% identity	79
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]
Seq. No.	278767
Contig ID	88467_3.R1011
5'-most EST	LIB3070-013-Q1-N1-G9
Method	BLASTN
NCBI GI	g347843
BLAST score	156
E value	2.0e-82
Match length	188
% identity	95
NCBI Description	Zea mays globulin-1 gene, promoter region
Seq. No.	278768
Contig ID	88479_2.R1011
5'-most EST	LIB3070-014-Q1-N1-A2
Method	BLASTX
NCBI GI	g2735008
BLAST score	261
E value	1.0e-22
Match length	61
% identity	90
NCBI Description	(U81960) kinase associated protein phosphatase [Zea mays]
Seq. No.	278769
Contig ID	88485_4.R1011
5'-most EST	yyf700350478.h1
Seq. No.	278770
Contig ID	88500_1.R1011
5'-most EST	LIB3070-014-Q1-N1-C7
Seq. No.	278771
Contig ID	88501_1.R1011
5'-most EST	uC-zmflmo17068g11b2
Seq. No.	278772
Contig ID	88501_2.R1011
5'-most EST	hbs701182279.h1
Seq. No.	278773

Contig ID	88506_1.R1011
5'-most EST	uC-zmflmo17044d05a1
Method	BLASTX
NCBI GI	g2623300
BLAST score	307
E value	5.0e-28
Match length	71
% identity	85
NCBI Description	(AC002409) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	278774
Contig ID	88529_1.R1011
5'-most EST	qmh700028444.f1
Method	BLASTX
NCBI GI	g3176687
BLAST score	455
E value	4.0e-45
Match length	138
% identity	65
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	278775
Contig ID	88540_1.R1011
5'-most EST	LIB3070-016-Q1-N1-E9

Seq. No.	278776
Contig ID	88559_1.R1011
5'-most EST	cyk700051035.f1

Seq. No.	278777
Contig ID	88629_1.R1011
5'-most EST	LIB3070-016-Q1-N1-B3

Seq. No.	278778
Contig ID	88639_1.R1011
5'-most EST	LIB3070-016-Q1-N1-C6

Seq. No.	278779
Contig ID	88643_1.R1011
5'-most EST	uC-zmflb73255d12b1
Method	BLASTX
NCBI GI	g3885336
BLAST score	413
E value	4.0e-40
Match length	179
% identity	48
NCBI Description	(AC005623) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	278780
Contig ID	88663_1.R1011
5'-most EST	uC-zmroteosinte099g11b2

Seq. No.	278781
Contig ID	88680_1.R1011
5'-most EST	LIB3070-016-Q1-N1-H12
Method	BLASTX
NCBI GI	g4566505
BLAST score	395
E value	4.0e-64
Match length	219
% identity	58
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	278782
Contig ID	88682_1.R1011
5'-most EST	ymt700219829.h1
Method	BLASTX
NCBI GI	g2950478
BLAST score	168
E value	1.0e-11
Match length	77
% identity	45
NCBI Description	(AL022070) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	278783
Contig ID	88682_2.R1011
5'-most EST	wyr700239771.h1

Seq. No.	278784
Contig ID	88686_1.R1011
5'-most EST	uC-zmflb73097f01a2

Seq. No.	278785
Contig ID	88690_1.R1011
5'-most EST	wyr700244078.h1
Method	BLASTX
NCBI GI	g4539383
BLAST score	479
E value	2.0e-98
Match length	331
% identity	54
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	278786
Contig ID	88726_1.R1011
5'-most EST	LIB3117-001-Q1-K1-D7

Seq. No.	278787
Contig ID	88728_1.R1011
5'-most EST	LIB3117-001-Q1-K1-D9

Seq. No.	278788
Contig ID	88734_1.R1011
5'-most EST	LIB3117-001-Q1-K1-E5

Seq. No.	278789
Contig ID	88737_1.R1011

5'-most EST	LIB3117-001-Q1-K1-F12
Method	BLASTX
NCBI GI	g3935168
BLAST score	294
E value	3.0e-26
Match length	90
% identity	67
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	278790
Contig ID	88749_1.R1011
5'-most EST	dyk700106306.h1

Seq. No.	278791
Contig ID	88762_1.R1011
5'-most EST	uC-zmroteosinte061b07b2
Method	BLASTX
NCBI GI	g4539344
BLAST score	351
E value	4.0e-66
Match length	256
% identity	57
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	278792
Contig ID	88765_1.R1011
5'-most EST	LIB3117-002-Q1-K1-B5
Method	BLASTX
NCBI GI	g3776011
BLAST score	289
E value	6.0e-26
Match length	141
% identity	45
NCBI Description	(AJ010469) RNA helicase [Arabidopsis thaliana]

Seq. No.	278793
Contig ID	88780_1.R1011
5'-most EST	uwc700152296.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	278794
Contig ID	88785_1.R1011
5'-most EST	xsy700213002.h1

Seq. No.	278795
Contig ID	88785_2.R1011
5'-most EST	LIB3117-002-Q1-K1-D9

Seq. No.	278796
Contig ID	88793_1.R1011
5'-most EST	LIB3117-002-Q1-K1-F10

Method	BLASTX
NCBI GI	g4586061
BLAST score	584
E value	4.0e-60
Match length	136
% identity	78
NCBI Description	(AC007020) putative BOP1 protein [Arabidopsis thaliana]

Seq. No.	278797
Contig ID	88814_1.R1011
5'-most EST	LIB3117-002-Q1-K1-H12
Method	BLASTX
NCBI GI	g100226
BLAST score	176
E value	2.0e-12
Match length	84
% identity	40
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	278798
Contig ID	88815_1.R1011
5'-most EST	LIB3117-002-Q1-K1-H3

Seq. No.	278799
Contig ID	88845_1.R1011
5'-most EST	uC-zmflmo17186f11b1
Method	BLASTX
NCBI GI	g2828280
BLAST score	357
E value	7.0e-34
Match length	79
% identity	82
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana] >gi_2832633_emb_CAA16762_ (AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	278800
Contig ID	88847_1.R1011
5'-most EST	wyr700241060.h1

Seq. No.	278801
Contig ID	88875_1.R1011
5'-most EST	wyr700240236.h1

Seq. No.	278802
Contig ID	88891_1.R1011
5'-most EST	wty700167518.h1
Method	BLASTX
NCBI GI	g3834307
BLAST score	312
E value	2.0e-28
Match length	157
% identity	42
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679

putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	278803
Contig ID	88901_1.R1011
5'-most EST	pwr700451016.h1

Seq. No.	278804
Contig ID	88908_1.R1011
5'-most EST	LIB3117-004-Q1-K1-D2

Seq. No.	278805
Contig ID	88948_1.R1011
5'-most EST	LIB3117-005-Q1-K1-D10
Method	BLASTX
NCBI GI	g3047083
BLAST score	608
E value	6.0e-63
Match length	141
% identity	80
NCBI Description	(AF058914) similar to FLAP endonuclease-1 (SW:P39748) [Arabidopsis thaliana]

Seq. No.	278806
Contig ID	88952_1.R1011
5'-most EST	LIB3117-005-Q1-K1-E2

Seq. No.	278807
Contig ID	88962_1.R1011
5'-most EST	hvj700624244.h1
Method	BLASTN
NCBI GI	g4519188
BLAST score	53
E value	1.0e-20
Match length	155
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	278808
Contig ID	88966_1.R1011
5'-most EST	uC-zmf1b73071g02b3

Seq. No.	278809
Contig ID	88971_1.R1011
5'-most EST	LIB3117-007-Q1-K1-A11

Seq. No.	278810
Contig ID	88976_1.R1011
5'-most EST	uC-zmf1mo17038b04b1
Method	BLASTX
NCBI GI	g2911075
BLAST score	505
E value	4.0e-51
Match length	157
% identity	64

NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]
Seq. No.	278811
Contig ID	89011_1.R1011
5'-most EST	LIB3117-006-Q1-K1-F1
Seq. No.	278812
Contig ID	89067_1.R1011
5'-most EST	cat700016849.r1
Seq. No.	278813
Contig ID	89103_1.R1011
5'-most EST	pmx700087636.h1
Method	BLASTX
NCBI GI	g3860273
BLAST score	145
E value	5.0e-09
Match length	48
% identity	67
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana] >gi_4314398_gb_AAD15608_ (AC006232) hypothetical protein [Arabidopsis thaliana]
Seq. No.	278814
Contig ID	89159_1.R1011
5'-most EST	LIB3117-009-Q1-K1-G4
Seq. No.	278815
Contig ID	89176_1.R1011
5'-most EST	LIB3117-010-Q1-K1-E11
Method	BLASTX
NCBI GI	g3063449
BLAST score	639
E value	8.0e-67
Match length	188
% identity	67
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]
Seq. No.	278816
Contig ID	89202_1.R1011
5'-most EST	rvt700550662.h1
Method	BLASTX
NCBI GI	g3021270
BLAST score	339
E value	2.0e-31
Match length	207
% identity	38
NCBI Description	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]
Seq. No.	278817
Contig ID	89210_1.R1011
5'-most EST	afb700381519.h1
Seq. No.	278818
Contig ID	89246_1.R1011
5'-most EST	ceu700432266.h1

Seq. No.	278819
Contig ID	89254_1.R1011
5'-most EST	yyf700349579.h1
Method	BLASTX
NCBI GI	g4584255
BLAST score	144
E value	7.0e-09
Match length	43
% identity	60
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	278820
Contig ID	89270_1.R1011
5'-most EST	LIB3117-012-Q1-K1-C1
Method	BLASTX
NCBI GI	g1666096
BLAST score	273
E value	5.0e-24
Match length	143
% identity	38
NCBI Description	(Y09113) dioxygenase [Marah macrocarpus]

Seq. No.	278821
Contig ID	89283_1.R1011
5'-most EST	LIB3117-012-Q1-K1-D5
Method	BLASTX
NCBI GI	g3087737
BLAST score	497
E value	2.0e-50
Match length	125
% identity	72
NCBI Description	(AJ001158) ABC1 protein [Arabidopsis thaliana]

Seq. No.	278822
Contig ID	89286_1.R1011
5'-most EST	uC-zmflmo17111b02a1

Seq. No.	278823
Contig ID	89318_1.R1011
5'-most EST	yne700379503.h1
Method	BLASTX
NCBI GI	g4432846
BLAST score	252
E value	2.0e-21
Match length	87
% identity	55
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	278824
Contig ID	89339_1.R1011
5'-most EST	LIB3117-013-Q1-K1-E5
Method	BLASTX
NCBI GI	g4585708
BLAST score	594
E value	2.0e-61
Match length	130

% identity	82
NCBI Description	(AJ238117) putative phospholipase A2 [Oryza sativa]
Seq. No.	278825
Contig ID	89397_1.R1011
5'-most EST	uC-zmflb73264d05b1
Seq. No.	278826
Contig ID	89415_1.R1011
5'-most EST	hvj700619633.h1
Method	BLASTX
NCBI GI	g3212852
BLAST score	208
E value	2.0e-34
Match length	171
% identity	51
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	278827
Contig ID	89415_3.R1011
5'-most EST	LIB3136-058-Q1-K1-A2
Method	BLASTX
NCBI GI	g3212852
BLAST score	315
E value	8.0e-29
Match length	174
% identity	41
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	278828
Contig ID	89419_1.R1011
5'-most EST	ypc700799551.h1
Seq. No.	278829
Contig ID	89423_1.R1011
5'-most EST	LIB3117-015-Q1-K1-C1
Seq. No.	278830
Contig ID	89431_1.R1011
5'-most EST	LIB3117-015-Q1-K1-D10
Seq. No.	278831
Contig ID	89439_1.R1011
5'-most EST	uC-zmflb73185b05b1
Method	BLASTX
NCBI GI	g4585995
BLAST score	264
E value	5.0e-23
Match length	89
% identity	62
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	278832
Contig ID	89448_1.R1011
5'-most EST	uC-zmflb73299g10b1
Seq. No.	278833

Contig ID	89454_1.R1011
5'-most EST	LIB3117-015-Q1-K1-G1

Seq. No.	278834
Contig ID	89464_1.R1011
5'-most EST	LIB3118-001-Q1-K1-C9
Method	BLASTN
NCBI GI	g4106527
BLAST score	77
E value	3.0e-35
Match length	324
% identity	56
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	278835
Contig ID	89580_1.R1011
5'-most EST	ceu700434265.h1

Seq. No.	278836
Contig ID	89580_2.R1011
5'-most EST	uC-zmflmo17052b08a1

Seq. No.	278837
Contig ID	89589_1.R1011
5'-most EST	uC-zmflmo17310c10a1

Seq. No.	278838
Contig ID	89594_1.R1011
5'-most EST	LIB3118-003-Q1-K1-F5
Method	BLASTX
NCBI GI	g3925277
BLAST score	170
E value	5.0e-12
Match length	78
% identity	42
NCBI Description	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	278839
Contig ID	89623_1.R1011
5'-most EST	dyk700102225.h1
Method	BLASTX
NCBI GI	g3269288
BLAST score	303
E value	6.0e-50
Match length	163
% identity	64
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	278840
Contig ID	89623_2.R1011
5'-most EST	uC-zmf1b73130f07b2
Method	BLASTX
NCBI GI	g3269288
BLAST score	311

E value	3.0e-28
Match length	74
% identity	76
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	278841
Contig ID	89629_1.R1011
5'-most EST	uC-zmroteosinte009a07b1
Method	BLASTX
NCBI GI	g4150963
BLAST score	252
E value	5.0e-21
Match length	163
% identity	37
NCBI Description	(Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No.	278842
Contig ID	89635_1.R1011
5'-most EST	pwr700449332.h1
Method	BLASTX
NCBI GI	g2495724
BLAST score	376
E value	1.0e-35
Match length	169
% identity	47
NCBI Description	HYPOTHETICAL PROTEIN KIAA0249 >gi_1665767_dbj_BAA13380_ (D87436) Similar to Human KIAA0188 protein [Homo sapiens]

Seq. No.	278843
Contig ID	89670_1.R1011
5'-most EST	LIB3118-006-Q1-K1-C5
Method	BLASTX
NCBI GI	g4588758
BLAST score	221
E value	5.0e-18
Match length	56
% identity	77
NCBI Description	(AF115476) rac-like GTP binding protein [Physcomitrella patens]

Seq. No.	278844
Contig ID	89680_1.R1011
5'-most EST	LIB3118-006-Q1-K1-D7
Method	BLASTX
NCBI GI	g3250692
BLAST score	246
E value	4.0e-21
Match length	56
% identity	77
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	278845
Contig ID	89696_2.R1011
5'-most EST	LIB3118-006-Q1-K1-G7

Seq. No.	278846
Contig ID	89710_1.R1011

5'-most EST	uC-zmf1b73008c07b1
Method	BLASTX
NCBI GI	g2653885
BLAST score	274
E value	2.0e-46
Match length	160
% identity	58
NCBI Description	(AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis thaliana]

Seq. No.	278847
Contig ID	89720_1.R1011
5'-most EST	LIB3118-007-Q1-K1-D2

Seq. No.	278848
Contig ID	89735_1.R1011
5'-most EST	uer700580846.h1
Method	BLASTX
NCBI GI	g731651
BLAST score	233
E value	5.0e-19
Match length	133
% identity	39
NCBI Description	HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN PUT2-SRB2 INTERGENIC REGION >gi_626608_pir__S46746 hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) >gi_488180 (U00062) Yhr039cp [Saccharomyces cerevisiae]

Seq. No.	278849
Contig ID	89746_1.R1011
5'-most EST	fdz701158596.h1

Seq. No.	278850
Contig ID	89752_1.R1011
5'-most EST	uC-zmflmo17323f02a1
Method	BLASTN
NCBI GI	g1657763
BLAST score	193
E value	1.0e-104
Match length	387
% identity	88
NCBI Description	Zea mays retrotransposon Ji-3 5' LTR and primer binding site DNA sequence

Seq. No.	278851
Contig ID	89752_2.R1011
5'-most EST	uC-zmflmo17128d12b1
Method	BLASTN
NCBI GI	g1213278
BLAST score	262
E value	1.0e-145
Match length	438
% identity	90
NCBI Description	Z.mays ZEMb gene

Seq. No. 278852

Contig ID	89752_3.R1011
5'-most EST	LIB3118-008-Q1-K1-A1
Method	BLASTN
NCBI GI	g3452296
BLAST score	263
E value	1.0e-146
Match length	493
% identity	89
NCBI Description	Zea mays retrotransposon Ji-4 3' LTR, partial sequence

Seq. No.	278853
Contig ID	89778_1.R1011
5'-most EST	LIB3118-008-Q1-K1-C7

Seq. No.	278854
Contig ID	89795_1.R1011
5'-most EST	fdz701158426.h1

Seq. No.	278855
Contig ID	89805_1.R1011
5'-most EST	LIB3118-008-Q1-K1-G2

Seq. No.	278856
Contig ID	89811_1.R1011
5'-most EST	LIB3118-011-Q1-K1-G12

Seq. No.	278857
Contig ID	89901_2.R1011
5'-most EST	LIB3118-010-Q1-K1-F8

Seq. No.	278858
Contig ID	89922_1.R1011
5'-most EST	LIB3118-011-Q1-K1-B4

Seq. No.	278859
Contig ID	89937_1.R1011
5'-most EST	LIB3137-002-Q1-K1-H8

Seq. No.	278860
Contig ID	89970_1.R1011
5'-most EST	LIB3118-011-Q1-K1-H5
Method	BLASTX
NCBI GI	g3176709
BLAST score	247
E value	1.0e-20
Match length	184
% identity	30
NCBI Description	(AC002392) putative anthranilate N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana]

Seq. No.	278861
Contig ID	90011_1.R1011
5'-most EST	LIB3118-012-Q1-K1-E2
Method	BLASTX
NCBI GI	g4432870
BLAST score	447

E value	2.0e-44
Match length	151
% identity	54
NCBI Description	(AC006300) putative selenium-binding protein, 3' partial [Arabidopsis thaliana]

Seq. No.	278862
Contig ID	90024_1.R1011
5'-most EST	LIB3118-012-Q1-K1-G3

Seq. No.	278863
Contig ID	90082_1.R1011
5'-most EST	ymt700219619.h1

Seq. No.	278864
Contig ID	90103_1.R1011
5'-most EST	LIB3118-014-Q1-K1-D9

Seq. No.	278865
Contig ID	90104_1.R1011
5'-most EST	LIB3118-014-Q1-K1-E1

Seq. No.	278866
Contig ID	90112_1.R1011
5'-most EST	LIB3118-014-Q1-K1-G1
Method	BLASTX
NCBI GI	g4138290
BLAST score	214
E value	4.0e-17
Match length	57
% identity	67
NCBI Description	(AJ005841) thioredoxin M [Oryza sativa]

Seq. No.	278867
Contig ID	90121_1.R1011
5'-most EST	LIB3118-014-Q1-K1-H5
Method	BLASTX
NCBI GI	g2781345
BLAST score	185
E value	2.0e-13
Match length	84
% identity	50
NCBI Description	(AC003113) F24O1.2 [Arabidopsis thaliana]

Seq. No.	278868
Contig ID	90130_1.R1011
5'-most EST	uC-zmflmo17126c04b1

Seq. No.	278869
Contig ID	90135_1.R1011
5'-most EST	LIB3136-001-P1-K1-B12

Seq. No.	278870
Contig ID	90135_2.R1011
5'-most EST	xmt700264714.h1

Seq. No.	278871

Contig ID	90138_1.R1011
5'-most EST	LIB3136-001-P1-K1-B4
Seq. No.	278872
Contig ID	90172_1.R1011
5'-most EST	LIB3136-001-P1-K1-F10
Seq. No.	278873
Contig ID	90193_1.R1011
5'-most EST	LIB3136-001-P1-K1-H8
Seq. No.	278874
Contig ID	90196_1.R1011
5'-most EST	xmt700263249.h1
Seq. No.	278875
Contig ID	90204_1.R1011
5'-most EST	LIB3136-002-P1-K1-A4
Method	BLASTX
NCBI GI	g4063751
BLAST score	222
E value	7.0e-18
Match length	153
% identity	34
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]
Seq. No.	278876
Contig ID	90222_1.R1011
5'-most EST	LIB3136-002-P1-K1-C11
Method	BLASTX
NCBI GI	g2245064
BLAST score	150
E value	8.0e-10
Match length	62
% identity	55
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.	278877
Contig ID	90223_1.R1011
5'-most EST	uC-zmf1b73116b10b2
Method	BLASTX
NCBI GI	g2702277
BLAST score	338
E value	4.0e-31
Match length	310
% identity	38
NCBI Description	(AC003033) putative cyclin g-associated kinase [Arabidopsis thaliana] >gi_2914689 (AC003974) putative cyclin g-associated kinase [Arabidopsis thaliana]
Seq. No.	278878
Contig ID	90236_1.R1011
5'-most EST	LIB3136-002-P1-K1-D3
Method	BLASTX
NCBI GI	g3482921

BLAST score	260
E value	2.0e-22
Match length	78
% identity	60
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana]

Seq. No.	278879
Contig ID	90253_1.R1011
5'-most EST	LIB3136-002-P1-K1-F1
Method	BLASTN
NCBI GI	g2340107
BLAST score	40
E value	3.0e-13
Match length	56
% identity	93
NCBI Description	Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial cds

Seq. No.	278880
Contig ID	90255_1.R1011
5'-most EST	LIB3136-002-P1-K1-F11
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	278881
Contig ID	90277_1.R1011
5'-most EST	uC-zmflmo17035g10b1
Method	BLASTX
NCBI GI	g4539423
BLAST score	446
E value	5.0e-44
Match length	121
% identity	72
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	278882
Contig ID	90277_2.R1011
5'-most EST	xmt700258071.h1

Seq. No.	278883
Contig ID	90278_1.R1011
5'-most EST	xsy700217770.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	278884

Contig ID	90281_2.R1011
5'-most EST	yyf700348973.h1
Method	BLASTX
NCBI GI	g2760844
BLAST score	200
E value	1.0e-25
Match length	118
% identity	54
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278885
Contig ID	90286_1.R1011
5'-most EST	LIB3136-003-Q1-K1-A2

Seq. No.	278886
Contig ID	90289_1.R1011
5'-most EST	LIB3136-003-Q1-K1-A5
Method	BLASTX
NCBI GI	g3287693
BLAST score	704
E value	2.0e-74
Match length	155
% identity	80
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	278887
Contig ID	90292_1.R1011
5'-most EST	gct701173885.h1
Method	BLASTX
NCBI GI	g4539437
BLAST score	232
E value	2.0e-19
Match length	100
% identity	46
NCBI Description	(AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	278888
Contig ID	90299_1.R1011
5'-most EST	uC-zmroteosinte011d11b1

Seq. No.	278889
Contig ID	90302_1.R1011
5'-most EST	uC-zmflmo17017f01b1
Method	BLASTX
NCBI GI	g3901268
BLAST score	239
E value	8.0e-20
Match length	149
% identity	36
NCBI Description	(AF060173) SV2 related protein [Rattus norvegicus]

Seq. No.	278890
Contig ID	90304_1.R1011
5'-most EST	LIB3136-003-Q1-K1-B9
Method	BLASTX

NCBI GI	g2224547
BLAST score	361
E value	2.0e-41
Match length	168
% identity	51
NCBI Description	(AB002301) KIAA0303 [Homo sapiens]

Seq. No.	278891
Contig ID	90304_2.R1011
5'-most EST	pmx700085123.h1
Method	BLASTX
NCBI GI	g3874215
BLAST score	185
E value	8.0e-20
Match length	76
% identity	66
NCBI Description	(Z83217) predicted using Genefinder; Similarity with Mouse protein kinase (TR:G406058); cDNA EST EMBL:D27750 comes from this gene; cDNA EST EMBL:D27749 comes from this gene; cDNA EST EMBL:D33894 comes from this gene; cDNA EST E

Seq. No.	278892
Contig ID	90309_1.R1011
5'-most EST	LIB3136-003-Q1-K1-D10

Seq. No.	278893
Contig ID	90310_1.R1011
5'-most EST	LIB3136-003-Q1-K1-C4
Method	BLASTX
NCBI GI	g4235646
BLAST score	153
E value	3.0e-10
Match length	81
% identity	41
NCBI Description	(AF119041) SC0A [Lycopersicon esculentum]

Seq. No.	278894
Contig ID	90312_1.R1011
5'-most EST	rvl700457507.h1

Seq. No.	278895
Contig ID	90341_1.R1011
5'-most EST	LIB3136-003-Q1-K1-F11
Method	BLASTX
NCBI GI	g3150406
BLAST score	385
E value	3.0e-37
Match length	125
% identity	55
NCBI Description	(AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	278896
Contig ID	90342_1.R1011
5'-most EST	uC-zmflmo17263h04b1
Method	BLASTX
NCBI GI	g4512263

BLAST score	691
E value	8.0e-73
Match length	153
% identity	90
NCBI Description	(AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]

Seq. No.	278897
Contig ID	90345_1.R1011
5'-most EST	uC-zmflmo170113g04b1
Method	BLASTX
NCBI GI	g3287696
BLAST score	521
E value	1.0e-62
Match length	214
% identity	57
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	278898
Contig ID	90358_1.R1011
5'-most EST	LIB3136-003-Q1-K1-H10

Seq. No.	278899
Contig ID	90359_1.R1011
5'-most EST	xjt700092561.h1
Method	BLASTX
NCBI GI	g2245378
BLAST score	571
E value	2.0e-58
Match length	328
% identity	45
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	278900
Contig ID	90380_1.R1011
5'-most EST	LIB3136-004-Q1-K1-A9

Seq. No.	278901
Contig ID	90382_1.R1011
5'-most EST	yyf700351984.h1

Seq. No.	278902
Contig ID	90384_1.R1011
5'-most EST	LIB3136-004-Q1-K1-B12
Method	BLASTX
NCBI GI	g4325342
BLAST score	753
E value	8.0e-80
Match length	215
% identity	68
NCBI Description	(AF128393) No definition line found [Arabidopsis thaliana]

Seq. No.	278903
Contig ID	90390_1.R1011
5'-most EST	LIB3136-004-Q1-K1-B9

Seq. No.	278904
Contig ID	90404_1.R1011
5'-most EST	LIB3136-004-Q1-K1-D11

Seq. No.	278905
Contig ID	90412_1.R1011
5'-most EST	uC-zmroB73028h06b1
Method	BLASTX
NCBI GI	g4204912
BLAST score	674
E value	9.0e-71
Match length	161
% identity	80
NCBI Description	(U58918) MEK kinase [Arabidopsis thaliana]

Seq. No.	278906
Contig ID	90414_1.R1011
5'-most EST	xsy700212054.h1
Method	BLASTX
NCBI GI	g4234941
BLAST score	849
E value	4.0e-91
Match length	289
% identity	58
NCBI Description	(AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No.	278907
Contig ID	90414_2.R1011
5'-most EST	LIB3136-004-Q1-K1-E10
Method	BLASTX
NCBI GI	g1408296
BLAST score	278
E value	2.0e-24
Match length	97
% identity	54
NCBI Description	(U61984) phosphoglucomutase A [Dictyostelium discoideum]

Seq. No.	278908
Contig ID	90438_1.R1011
5'-most EST	LIB3136-004-Q1-K1-G2
Method	BLASTX
NCBI GI	g2462762
BLAST score	1116
E value	1.0e-122
Match length	301
% identity	70
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	278909
Contig ID	90465_1.R1011
5'-most EST	vux700160943.h1

Seq. No.	278910
Contig ID	90477_1.R1011

5'-most EST	uC-zmflmo17271g11b1
Method	BLASTX
NCBI GI	g1737222
BLAST score	1548
E value	1.0e-173
Match length	352
% identity	79
NCBI Description	(U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

Seq. No.	278911
Contig ID	90488_1.R1011
5'-most EST	yyf700350350.h1

Seq. No.	278912
Contig ID	90491_1.R1011
5'-most EST	uer700582609.h1
Method	BLASTX
NCBI GI	g4056438
BLAST score	223
E value	8.0e-18
Match length	179
% identity	30
NCBI Description	(AC005990) F5O8.11 [Arabidopsis thaliana]

Seq. No.	278913
Contig ID	90502_1.R1011
5'-most EST	xmt700268144.h1

Seq. No.	278914
Contig ID	90503_1.R1011
5'-most EST	ymt700219678.h1
Method	BLASTX
NCBI GI	g4455199
BLAST score	376
E value	6.0e-36
Match length	129
% identity	60
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	278915
Contig ID	90521_1.R1011
5'-most EST	LIB3136-030-Q1-K1-A7

Seq. No.	278916
Contig ID	90524_1.R1011
5'-most EST	uC-zmflb73125e04b2

Seq. No.	278917
Contig ID	90524_2.R1011
5'-most EST	LIB3136-005-Q1-K1-G11

Seq. No.	278918
Contig ID	90525_1.R1011
5'-most EST	LIB3136-005-Q1-K1-G12

Seq. No.	278919
Contig ID	90533_1.R1011

5'-most EST	LIB3136-023-Q1-K1-B2
Method	BLASTX
NCBI GI	g1076422
BLAST score	318
E value	5.0e-29
Match length	108
% identity	66
NCBI Description	transcription factor OBF4 - Arabidopsis thaliana >gi_414613_emb_CAA49524_ (X69899) ocs-element binding factor 4 [Arabidopsis thaliana]

Seq. No.	278920
Contig ID	90533_2.R1011
5'-most EST	uC-zmflmo17031a07b1
Method	BLASTX
NCBI GI	g1076421
BLAST score	197
E value	8.0e-15
Match length	49
% identity	82
NCBI Description	transcription factor TGA3 - Arabidopsis thaliana >gi_304113 (L10209) transcription factor [Arabidopsis thaliana]

Seq. No.	278921
Contig ID	90538_1.R1011
5'-most EST	uC-zmflmo17060h05b1

Seq. No.	278922
Contig ID	90565_1.R1011
5'-most EST	LIB3136-006-Q1-K1-C1

Seq. No.	278923
Contig ID	90566_1.R1011
5'-most EST	ymt700219374.h1
Method	BLASTX
NCBI GI	g479413
BLAST score	802
E value	7.0e-86
Match length	188
% identity	85
NCBI Description	myosin-like protein - Arabidopsis thaliana

Seq. No.	278924
Contig ID	90572_1.R1011
5'-most EST	wyr700236437.h1

Seq. No.	278925
Contig ID	90574_1.R1011
5'-most EST	uwc700151829.h1
Method	BLASTX
NCBI GI	g2827699
BLAST score	196
E value	6.0e-15
Match length	144
% identity	40
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	278926
Contig ID	90580_1.R1011
5'-most EST	fC-zmst700620624a1
Method	BLASTX
NCBI GI	g399307
BLAST score	576
E value	3.0e-59
Match length	190
% identity	57
NCBI Description	PRENYL TRANSFERASE >gi_99282_pir__A40433 prephytoene pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora paradoxa >gi_336639 (M37111) prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] >gi_1016130 (U30821) prenyl transferase [Cyanophora paradoxa]

Seq. No.	278927
Contig ID	90580_2.R1011
5'-most EST	uwc700156126.h2

Seq. No.	278928
Contig ID	90602_1.R1011
5'-most EST	LIB3136-008-Q1-K1-F10

Seq. No.	278929
Contig ID	90618_1.R1011
5'-most EST	ceu700421620.h1

Seq. No.	278930
Contig ID	90629_1.R1011
5'-most EST	LIB3136-006-Q1-K1-H8

Seq. No.	278931
Contig ID	90632_1.R1011
5'-most EST	LIB3136-007-Q1-K1-A12

Seq. No.	278932
Contig ID	90635_1.R1011
5'-most EST	LIB3136-007-Q1-K1-B11

Seq. No.	278933
Contig ID	90644_1.R1011
5'-most EST	uC-zmflb73151f06b1
Method	BLASTX
NCBI GI	g2462822
BLAST score	198
E value	3.0e-15
Match length	70
% identity	51
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278934
Contig ID	90649_1.R1011
5'-most EST	tzu700205091.h1
Method	BLASTX
NCBI GI	g3393019
BLAST score	459
E value	5.0e-62

Match length	236
% identity	49
NCBI Description	(AL031174) beta-transducin [Schizosaccharomyces pombe]

Seq. No.	278935
Contig ID	90656_1.R1011
5'-most EST	LIB3136-007-Q1-K1-E8
Method	BLASTX
NCBI GI	g3377800
BLAST score	344
E value	2.0e-32
Match length	89
% identity	71
NCBI Description	(AF075597) similar to glycosyl hydrolases family 9 (PFam:glycosyl_hydro5.hmm, score: 100.70) [Arabidopsis thaliana]

Seq. No.	278936
Contig ID	90678_1.R1011
5'-most EST	LIB3136-008-Q1-K1-A1
Method	BLASTX
NCBI GI	g4544409
BLAST score	620
E value	1.0e-64
Match length	169
% identity	68
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana] >gi_4585920_gb_AAD25580.1_AC007211_2 (AC007211) putative scarecrow homolog [Arabidopsis thaliana]

Seq. No.	278937
Contig ID	90699_1.R1011
5'-most EST	LIB3137-021-Q1-K1-A4
Method	BLASTX
NCBI GI	g3928543
BLAST score	299
E value	5.0e-29
Match length	106
% identity	58
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	278938
Contig ID	90701_1.R1011
5'-most EST	uC-zmflmo17156b08b1
Method	BLASTX
NCBI GI	g4589961
BLAST score	183
E value	2.0e-13
Match length	115
% identity	11
NCBI Description	(AC007169) unknown protein [Arabidopsis thaliana]

Seq. No.	278939
Contig ID	90711_1.R1011
5'-most EST	xmt700264721.h1
Method	BLASTX

NCBI GI	g2191149
BLAST score	209
E value	3.0e-33
Match length	230
% identity	37
NCBI Description	(AF007269) Similar to protein kinase [Arabidopsis thaliana]

Seq. No.	278940
Contig ID	90737_1.R1011
5'-most EST	uC-zmflb73012e06b1
Method	BLASTX
NCBI GI	g4566505
BLAST score	323
E value	1.0e-29
Match length	112
% identity	62
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	278941
Contig ID	90737_2.R1011
5'-most EST	uC-zmroB73015c05b1
Method	BLASTX
NCBI GI	g4566505
BLAST score	185
E value	1.0e-13
Match length	77
% identity	55
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	278942
Contig ID	90755_1.R1011
5'-most EST	xdg700405223.h1

Seq. No.	278943
Contig ID	90771_1.R1011
5'-most EST	LIB3136-009-Q1-K1-A5
Method	BLASTX
NCBI GI	g2183249
BLAST score	645
E value	2.0e-67
Match length	141
% identity	85
NCBI Description	(AF002211) glutathione-S-transferase [Triticum aestivum] >gi_4185800 (AF109714) glutathione S-transferase [Triticum aestivum]

Seq. No.	278944
Contig ID	90783_1.R1011
5'-most EST	uC-zmroteosinte083e06b1
Method	BLASTX
NCBI GI	g3355490
BLAST score	729
E value	4.0e-94
Match length	244
% identity	70

NCBI Description	(AC004218) putative dolichyl-phosphate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	278945
Contig ID	90785_1.R1011
5'-most EST	LIB3136-009-Q1-K1-B8
Method	BLASTX
NCBI GI	g3063448
BLAST score	443
E value	4.0e-44
Match length	124
% identity	64
NCBI Description	(AC003981) F22O13.10 [Arabidopsis thaliana]

Seq. No.	278946
Contig ID	90792_1.R1011
5'-most EST	uer700578551.h1
Method	BLASTX
NCBI GI	g4115946
BLAST score	451
E value	1.0e-44
Match length	249
% identity	41
NCBI Description	(AF118223) contains similarity to Ipomoea nil leaf protein (GB: D85101) [Arabidopsis thaliana]

Seq. No.	278947
Contig ID	90809_1.R1011
5'-most EST	cyk700049421.f1
Method	BLASTX
NCBI GI	g2081612
BLAST score	296
E value	9.0e-27
Match length	76
% identity	80
NCBI Description	(D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza sativa]

Seq. No.	278948
Contig ID	90817_1.R1011
5'-most EST	LIB3136-009-Q1-K1-G1

Seq. No.	278949
Contig ID	90854_1.R1011
5'-most EST	LIB3136-010-Q1-K1-B5
Method	BLASTX
NCBI GI	g3236259
BLAST score	499
E value	8.0e-83
Match length	247
% identity	65
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	278950
Contig ID	90857_1.R1011
5'-most EST	LIB3136-010-Q1-K1-B8

Method	BLASTX
NCBI GI	g1077378
BLAST score	277
E value	2.0e-24
Match length	145
% identity	40
NCBI Description	probable membrane protein YLR222c - yeast (Saccharomyces cerevisiae) >gi_609371 (U19027) Ylr222cp [Saccharomyces cerevisiae]

Seq. No.	278951
Contig ID	90878_1.R1011
5'-most EST	LIB3136-010-Q1-K1-D8
Method	BLASTX
NCBI GI	g3004551
BLAST score	177
E value	8.0e-13
Match length	119
% identity	38
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278952
Contig ID	90910_1.R1011
5'-most EST	LIB3136-021-Q1-K1-D5

Seq. No.	278953
Contig ID	90912_1.R1011
5'-most EST	LIB3136-010-Q1-K1-H10

Seq. No.	278954
Contig ID	90938_1.R1011
5'-most EST	LIB3136-011-Q1-K1-B5
Method	BLASTN
NCBI GI	g733457
BLAST score	45
E value	3.0e-16
Match length	57
% identity	95
NCBI Description	Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1) mRNA, complete cds

Seq. No.	278955
Contig ID	90943_1.R1011
5'-most EST	LIB3136-011-Q1-K1-B9
Method	BLASTX
NCBI GI	g4567312
BLAST score	306
E value	2.0e-28
Match length	120
% identity	57
NCBI Description	(AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278956
Contig ID	90945_2.R1011
5'-most EST	uC-zmf1b73160b06b2

Seq. No.	278957

Contig ID	90953_1.R1011
5'-most EST	LIB83-003-Q1-E1-B3
Method	BLASTX
NCBI GI	g3219782
BLAST score	257
E value	3.0e-22
Match length	86
% identity	57
NCBI Description	CCR4-ASSOCIATED FACTOR 1 (CAF1) >gi_726136 (U21855) mCAF1 protein [Mus musculus]

Seq. No.	278958
Contig ID	90971_1.R1011
5'-most EST	LIB3136-016-Q1-K1-B10

Seq. No.	278959
Contig ID	90973_1.R1011
5'-most EST	LIB3136-011-Q1-K1-E8
Method	BLASTX
NCBI GI	g4455359
BLAST score	149
E value	9.0e-10
Match length	47
% identity	79
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	278960
Contig ID	90975_1.R1011
5'-most EST	rvl700457437.h1
Method	BLASTN
NCBI GI	g1906603
BLAST score	69
E value	2.0e-30
Match length	112
% identity	91
NCBI Description	Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence

Seq. No.	278961
Contig ID	90977_1.R1011
5'-most EST	LIB3153-011-Q1-K1-G8

Seq. No.	278962
Contig ID	90980_1.R1011
5'-most EST	LIB3136-018-Q1-K1-C10
Method	BLASTN
NCBI GI	g309558
BLAST score	201
E value	1.0e-109
Match length	262
% identity	94
NCBI Description	Corn nuclear-encoded mitochondrial chaperonin 60 (cpn60II) gene, complete cds

Seq. No.	278963
Contig ID	91019_1.R1011

5'-most EST	LIB3136-012-Q1-K1-B4
Method	BLASTX
NCBI GI	g1723480
BLAST score	203
E value	6.0e-16
Match length	130
% identity	44
NCBI Description	HYPOTHETICAL 31.3 KD PROTEIN C17G8.08C IN CHROMOSOME I >gi_1213257_emb_CAA93691_ (Z69795) unknown [Schizosaccharomyces pombe]

Seq. No.	278964
Contig ID	91039_1.R1011
5'-most EST	uC-zmroteosinte090b11b2

Seq. No.	278965
Contig ID	91074_1.R1011
5'-most EST	ymt700220390.h1
Method	BLASTX
NCBI GI	g3355471
BLAST score	520
E value	6.0e-53
Match length	160
% identity	59
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	278966
Contig ID	91075_1.R1011
5'-most EST	fdz701165163.h1
Method	BLASTX
NCBI GI	g3297816
BLAST score	440
E value	3.0e-43
Match length	157
% identity	57
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	278967
Contig ID	91078_1.R1011
5'-most EST	LIB3136-012-Q1-K1-H5

Seq. No.	278968
Contig ID	91079_1.R1011
5'-most EST	LIB3136-012-Q1-K1-H8
Method	BLASTX
NCBI GI	g2760839
BLAST score	165
E value	1.0e-11
Match length	84
% identity	39
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	278969
Contig ID	91094_1.R1011
5'-most EST	LIB3136-013-Q1-K1-B1

Seq. No.	278970
Contig ID	91108_1.R1011
5'-most EST	ntr700075357.h1

Seq. No.	278971
Contig ID	91128_1.R1011
5'-most EST	uC-zmroteosinte061f09b2

Seq. No.	278972
Contig ID	91131_1.R1011
5'-most EST	uC-zmflb73266d01b2
Method	BLASTX
NCBI GI	g731651
BLAST score	606
E value	2.0e-62
Match length	337
% identity	41
NCBI Description	HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN PUT2-SRB2 INTERGENIC REGION >gi_626608_pir__S46746 hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) >gi_488180 (U00062) Yhr039cp [Saccharomyces cerevisiae]

Seq. No.	278973
Contig ID	91131_2.R1011
5'-most EST	uC-zmroteosinte002g08b1
Method	BLASTX
NCBI GI	g1708424
BLAST score	325
E value	9.0e-30
Match length	117
% identity	60
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

Seq. No.	278974
Contig ID	91131_3.R1011
5'-most EST	uC-zmroteosinte072b02b2
Method	BLASTX
NCBI GI	g1708424
BLAST score	602
E value	2.0e-62
Match length	174
% identity	68
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

Seq. No.	278975
Contig ID	91131_4.R1011
5'-most EST	xsy700214295.h1

Seq. No.	278976
Contig ID	91174_1.R1011
5'-most EST	uC-zmflMo17002b07b1
Method	BLASTX
NCBI GI	g1753085
BLAST score	332

E value	1.0e-30
Match length	182
% identity	46
NCBI Description	(U25283) leucine zipper protein [Oryza sativa]

Seq. No.	278977
Contig ID	91174_2.R1011
5'-most EST	LIB3136-014-Q1-K2-A8

Seq. No.	278978
Contig ID	91175_1.R1011
5'-most EST	uC-zmflmo17044e06b1
Method	BLASTX
NCBI GI	g118719
BLAST score	513
E value	1.0e-51
Match length	291
% identity	38
NCBI Description	DNAJ PROTEIN >gi_72228_pir__HHECDJ heat shock protein dnaJ - Escherichia coli >gi_145769 (M12565) heat shock protein dnaJ [Escherichia coli] >gi_216441_dbj_BAA01292_ (D10483) DnaJ [Escherichia coli] >gi_1786197 (AE000112) chaperone with DnaK; heat shock protein [Escherichia coli]

Seq. No.	278979
Contig ID	91177_1.R1011
5'-most EST	LIB3136-014-Q1-K1-B12
Method	BLASTX
NCBI GI	g2864625
BLAST score	546
E value	8.0e-66
Match length	146
% identity	88
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	278980
Contig ID	91180_1.R1011
5'-most EST	LIB3136-014-Q1-K2-B4

Seq. No.	278981
Contig ID	91186_1.R1011
5'-most EST	tfd700572487.h1

Seq. No.	278982
Contig ID	91188_1.R1011
5'-most EST	LIB3136-014-Q1-K1-C11
Method	BLASTX
NCBI GI	g4490330
BLAST score	770
E value	2.0e-82
Match length	145
% identity	96
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	278983
Contig ID	91194_1.R1011

5'-most EST	LIB3136-014-Q1-K1-C6
Seq. No.	278984
Contig ID	91199_1.R1011
5'-most EST	LIB3136-014-Q1-K1-D10
Method	BLASTX
NCBI GI	g4240207
BLAST score	163
E value	4.0e-11
Match length	79
% identity	35
NCBI Description	(AB020666) KIAA0859 protein [Homo sapiens]
Seq. No.	278985
Contig ID	91215_1.R1011
5'-most EST	wty700167170.h1
Seq. No.	278986
Contig ID	91229_1.R1011
5'-most EST	uC-zmrob73011f09b1
Method	BLASTX
NCBI GI	g1514643
BLAST score	608
E value	3.0e-63
Match length	166
% identity	72
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
Seq. No.	278987
Contig ID	91249_1.R1011
5'-most EST	LIB3136-014-Q1-K2-H6
Seq. No.	278988
Contig ID	91265_1.R1011
5'-most EST	tzu700206461.h1
Seq. No.	278989
Contig ID	91274_1.R1011
5'-most EST	uC-zmflmo17333g02b1
Method	BLASTX
NCBI GI	g1168654
BLAST score	1771
E value	0.0e+00
Match length	400
% identity	79
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) - garden asparagus >gi_452712_emb_CAA54525_ (X77319) beta-galactosidase [Asparagus officinalis]
Seq. No.	278990
Contig ID	91283_1.R1011
5'-most EST	LIB3136-014-Q1-K2-C8
Method	BLASTX
NCBI GI	g1084335
BLAST score	872
E value	4.0e-94

Match length	202
% identity	79
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) 2 - Arabidopsis thaliana >gi_604881_dbj_BAA04830_ (D21806) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	278991
Contig ID	91341_2.R1011
5'-most EST	ymt700221888.h1
Method	BLASTX
NCBI GI	g3236249
BLAST score	503
E value	3.0e-72
Match length	247
% identity	51
NCBI Description	(AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No.	278992
Contig ID	91352_1.R1011
5'-most EST	uC-zmflmo17294g04b1
Method	BLASTX
NCBI GI	g3169174
BLAST score	412
E value	1.0e-63
Match length	304
% identity	42
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	278993
Contig ID	91392_1.R1011
5'-most EST	nbm700469148.h1
Method	BLASTX
NCBI GI	g4006855
BLAST score	576
E value	2.0e-59
Match length	182
% identity	63
NCBI Description	(Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	278994
Contig ID	91395_1.R1011
5'-most EST	fwa700100522.h1
Method	BLASTX
NCBI GI	g586038
BLAST score	212
E value	9.0e-17
Match length	88
% identity	53
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN CHLOROPLAST PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC) >gi_480296_pir__S36637 signal recognition particle 54CP protein precursor - Arabidopsis thaliana >gi_396701_emb_CAA79981_ (Z21970) 54CP [Arabidopsis thaliana]

Seq. No.	278995
Contig ID	91402_1.R1011
5'-most EST	LIB3136-015-Q1-K1-G10

Seq. No.	278996
Contig ID	91410_1.R1011
5'-most EST	LIB3136-015-Q1-K1-G7
Method	BLASTX
NCBI GI	g1174718
BLAST score	387
E value	3.0e-37
Match length	202
% identity	39
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	278997
Contig ID	91411_1.R1011
5'-most EST	LIB3136-015-Q1-K1-G8

Seq. No.	278998
Contig ID	91415_1.R1011
5'-most EST	uC-zmflmo17042e01b1
Method	BLASTX
NCBI GI	g3522929
BLAST score	179
E value	6.0e-13
Match length	144
% identity	36
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	278999
Contig ID	91418_2.R1011
5'-most EST	uC-zmflmo17186c07b1

Seq. No.	279000
Contig ID	91431_1.R1011
5'-most EST	ceu700421759.h1

Seq. No.	279001
Contig ID	91442_1.R1011
5'-most EST	LIB3136-016-Q1-K1-B4

Seq. No.	279002
Contig ID	91443_1.R1011
5'-most EST	uC-zmflb73287d03b1

Seq. No.	279003
Contig ID	91445_1.R1011
5'-most EST	uC-zmflb73091f09a1

Seq. No.	279004
Contig ID	91465_1.R1011

5'-most EST	LIB3136-016-Q1-K1-D4
Method	BLASTX
NCBI GI	g3522956
BLAST score	388
E value	1.0e-37
Match length	132
% identity	51
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	279005
Contig ID	91476_1.R1011
5'-most EST	uC-zmflb73197h09b1
Method	BLASTX
NCBI GI	g3461817
BLAST score	1210
E value	1.0e-133
Match length	349
% identity	63
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	279006
Contig ID	91487_1.R1011
5'-most EST	LIB3136-016-Q1-K1-F8

Seq. No.	279007
Contig ID	91490_2.R1011
5'-most EST	LIB3136-016-Q1-K1-F9

Seq. No.	279008
Contig ID	91494_1.R1011
5'-most EST	uC-zmflmo17292a10b1

Seq. No.	279009
Contig ID	91509_1.R1011
5'-most EST	LIB3136-055-Q1-K1-C12
Method	BLASTX
NCBI GI	g2505876
BLAST score	255
E value	4.0e-22
Match length	66
% identity	76
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	279010
Contig ID	91516_1.R1011
5'-most EST	hvj700622931.h1

Seq. No.	279011
Contig ID	91520_1.R1011
5'-most EST	wyr700238884.h1
Method	BLASTN
NCBI GI	g1245938
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100

NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	279012
Contig ID	91541_1.R1011
5'-most EST	uer700582851.h1
Method	BLASTX
NCBI GI	g4580468
BLAST score	544
E value	2.0e-55
Match length	199
% identity	53
NCBI Description	(AC006081) putative protein kinase; similar to human PKX1 and Drosophila DC2 [Arabidopsis thaliana]

Seq. No.	279013
Contig ID	91554_1.R1011
5'-most EST	LIB3136-017-Q1-K1-E12

Seq. No.	279014
Contig ID	91559_1.R1011
5'-most EST	uC-zmroB73014f12b1
Method	BLASTX
NCBI GI	g3702352
BLAST score	850
E value	3.0e-91
Match length	257
% identity	65
NCBI Description	(AC005397) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	279015
Contig ID	91559_2.R1011
5'-most EST	uC-zmflb73065b06b1
Method	BLASTX
NCBI GI	g4455353
BLAST score	268
E value	4.0e-23
Match length	124
% identity	47
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	279016
Contig ID	91579_1.R1011
5'-most EST	uer700577321.h1

Seq. No.	279017
Contig ID	91592_1.R1011
5'-most EST	uC-zmflmo17139c05b1

Seq. No.	279018
Contig ID	91615_1.R1011
5'-most EST	LIB3136-018-Q1-K1-C8

Seq. No.	279019
Contig ID	91619_1.R1011
5'-most EST	LIB3136-018-Q1-K1-D11

Seq. No.	279020
Contig ID	91639_1.R1011
5'-most EST	LIB3136-018-Q1-K1-F11
Method	BLASTX
NCBI GI	g3935168
BLAST score	257
E value	4.0e-22
Match length	158
% identity	41
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	279021
Contig ID	91645_1.R1011
5'-most EST	LIB3136-018-Q1-K1-F9
Method	BLASTX
NCBI GI	g2853083
BLAST score	235
E value	2.0e-19
Match length	187
% identity	35
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	279022
Contig ID	91649_1.R1011
5'-most EST	LIB3136-018-Q1-K1-G2
Method	BLASTX
NCBI GI	g4079809
BLAST score	176
E value	1.0e-12
Match length	152
% identity	4
NCBI Description	(AF071172) HERC2 [Homo sapiens]

Seq. No.	279023
Contig ID	91653_2.R1011
5'-most EST	xjt700092423.h1
Method	BLASTX
NCBI GI	g2213594
BLAST score	757
E value	1.0e-80
Match length	216
% identity	65
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	279024
Contig ID	91654_1.R1011
5'-most EST	xdb700338447.h1
Method	BLASTX
NCBI GI	g4337176
BLAST score	310
E value	5.0e-28
Match length	136
% identity	17
NCBI Description	(AC006416) T31J12.4 [Arabidopsis thaliana]

Seq. No.	279025

Contig ID	91656_1.R1011
5'-most EST	LIB3136-018-Q1-K1-G9

Seq. No.	279026
Contig ID	91661_1.R1011
5'-most EST	LIB3136-018-Q1-K1-H4
Method	BLASTX
NCBI GI	g4586114
BLAST score	179
E value	8.0e-13
Match length	79
% identity	41
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	279027
Contig ID	91666_1.R1011
5'-most EST	LIB3136-019-Q1-K1-A10

Seq. No.	279028
Contig ID	91668_1.R1011
5'-most EST	LIB3136-019-Q1-K1-A2

Seq. No.	279029
Contig ID	91671_1.R1011
5'-most EST	xsy700211901.h1
Method	BLASTX
NCBI GI	g4490736
BLAST score	737
E value	3.0e-78
Match length	223
% identity	40
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	279030
Contig ID	91693_1.R1011
5'-most EST	uC-zmflmo17321h10b1

Seq. No.	279031
Contig ID	91704_1.R1011
5'-most EST	LIB3136-019-Q1-K1-D5
Method	BLASTX
NCBI GI	g1935912
BLAST score	757
E value	7.0e-81
Match length	138
% identity	100
NCBI Description	(U77346) LLS1 [Zea mays]

Seq. No.	279032
Contig ID	91706_1.R1011
5'-most EST	LIB3136-019-Q1-K1-D7
Method	BLASTX
NCBI GI	g4204265
BLAST score	397
E value	1.0e-38
Match length	135
% identity	60

NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	279033
Contig ID	91707_1.R1011
5'-most EST	LIB83-003-Q1-E1-F2

Seq. No.	279034
Contig ID	91709_1.R1011
5'-most EST	uC-zmflb73020c04b1
Method	BLASTX
NCBI GI	g1621268
BLAST score	594
E value	2.0e-61
Match length	172
% identity	67
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	279035
Contig ID	91718_1.R1011
5'-most EST	uC-zmroteosinte029c10b1
Method	BLASTX
NCBI GI	g3785978
BLAST score	352
E value	2.0e-33
Match length	103
% identity	64
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	279036
Contig ID	91758_1.R1011
5'-most EST	LIB3136-020-Q1-K1-A2

Seq. No.	279037
Contig ID	91764_1.R1011
5'-most EST	cyk700047887.f1
Method	BLASTX
NCBI GI	g3152613
BLAST score	316
E value	5.0e-29
Match length	166
% identity	40
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279038
Contig ID	91769_1.R1011
5'-most EST	uC-zmflmo17007c06a1
Method	BLASTX
NCBI GI	g3252900
BLAST score	294
E value	7.0e-26
Match length	342
% identity	25
NCBI Description	(AF055482) galactose-1-phosphate uridyl transferase [Thermotoga neapolitana]

Seq. No.	279039
Contig ID	91774_1.R1011

5'-most EST	pmx700084371.h1
Method	BLASTX
NCBI GI	g2960216
BLAST score	1293
E value	1.0e-143
Match length	322
% identity	78
NCBI Description	(AJ223384) 26S proteasome regulatory ATPase subunit 10b (S10b) [Manduca sexta]

Seq. No.	279040
Contig ID	91789_1.R1011
5'-most EST	LIB3136-020-Q1-K1-D10
Method	BLASTX
NCBI GI	g4138912
BLAST score	320
E value	1.0e-29
Match length	90
% identity	64
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No.	279041
Contig ID	91791_1.R1011
5'-most EST	uC-zmf1Mo17092a03b1
Method	BLASTX
NCBI GI	g4510401
BLAST score	719
E value	5.0e-76
Match length	224
% identity	59
NCBI Description	(AC006587) putative general negative regulator of transcription [Arabidopsis thaliana]

Seq. No.	279042
Contig ID	91797_1.R1011
5'-most EST	cat700019707.r1

Seq. No.	279043
Contig ID	91799_1.R1011
5'-most EST	LIB3136-020-Q1-K1-E11

Seq. No.	279044
Contig ID	91807_1.R1011
5'-most EST	wyr700235386.h1
Method	BLASTX
NCBI GI	g1841464
BLAST score	477
E value	1.0e-47
Match length	113
% identity	45
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	279045
Contig ID	91809_1.R1011
5'-most EST	uC-zmf1mo17039e07b1
Method	BLASTX
NCBI GI	g4544451

BLAST score	466
E value	2.0e-48
Match length	143
% identity	69
NCBI Description	(AC006592) unknown protein [Arabidopsis thaliana]

Seq. No.	279046
Contig ID	91825_1.R1011
5'-most EST	LIB3136-020-Q1-K1-G7
Method	BLASTX
NCBI GI	g2462927
BLAST score	1041
E value	1.0e-114
Match length	267
% identity	73
NCBI Description	(Y10342) putative amidase [Arabidopsis thaliana]

Seq. No.	279047
Contig ID	91827_1.R1011
5'-most EST	uC-zmflmo17150a06b1

Seq. No.	279048
Contig ID	91847_1.R1011
5'-most EST	LIB3136-021-Q1-K1-B10

Seq. No.	279049
Contig ID	91850_1.R1011
5'-most EST	uC-zmflmo17042c06b1
Method	BLASTX
NCBI GI	g3080398
BLAST score	391
E value	2.0e-37
Match length	222
% identity	43
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	279050
Contig ID	91867_1.R1011
5'-most EST	wty700170732.h1
Method	BLASTX
NCBI GI	g1272505
BLAST score	296
E value	2.0e-30
Match length	131
% identity	56
NCBI Description	(D49551) peroxidase [Oryza sativa]

Seq. No.	279051
Contig ID	91877_1.R1011
5'-most EST	LIB3136-021-Q1-K1-D7
Method	BLASTX
NCBI GI	g3776559
BLAST score	169
E value	1.0e-11
Match length	66
% identity	59
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933

cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	279052
Contig ID	91877_2.R1011
5'-most EST	jfc700968689.h1

Seq. No.	279053
Contig ID	91884_1.R1011
5'-most EST	ntr700076515.h1

Seq. No.	279054
Contig ID	91885_1.R1011
5'-most EST	uC-zmrob73079h05b1

Seq. No.	279055
Contig ID	91886_1.R1011
5'-most EST	LIB84-016-Q1-E1-E5
Method	BLASTX
NCBI GI	g2494075
BLAST score	1111
E value	1.0e-122
Match length	219
% identity	99
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1084478_pir__S43833 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - maize >gi_474408_emb_CAA53075_ (X75326) glyceraldehyde-3-phosphate dehydrogenase (GAPN) [Zea mays]

Seq. No.	279056
Contig ID	91905_1.R1011
5'-most EST	LIB3136-021-Q1-K1-G3
Method	BLASTX
NCBI GI	g2494165
BLAST score	502
E value	6.0e-51
Match length	146
% identity	64
NCBI Description	DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis thaliana]

Seq. No.	279057
Contig ID	91908_1.R1011
5'-most EST	LIB3136-021-Q1-K1-G6
Method	BLASTX
NCBI GI	g2982469
BLAST score	509
E value	2.0e-51
Match length	157
% identity	61

NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]
Seq. No.	279058
Contig ID	91911_1.R1011
5'-most EST	pmx700091793.h1
Method	BLASTX
NCBI GI	g2244807
BLAST score	435
E value	1.0e-42
Match length	127
% identity	68
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	279059
Contig ID	91918_1.R1011
5'-most EST	uC-zmflMo17006h12b1
Seq. No.	279060
Contig ID	91920_1.R1011
5'-most EST	LIB3136-021-Q1-K1-H7
Seq. No.	279061
Contig ID	91928_1.R1011
5'-most EST	LIB3136-022-Q1-K1-A5
Seq. No.	279062
Contig ID	91934_1.R1011
5'-most EST	LIB3136-022-Q1-K1-B11
Seq. No.	279063
Contig ID	91938_1.R1011
5'-most EST	zuv700354455.h1
Method	BLASTX
NCBI GI	g2088650
BLAST score	619
E value	3.0e-64
Match length	238
% identity	55
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]
Seq. No.	279064
Contig ID	91944_1.R1011
5'-most EST	LIB3136-022-Q1-K1-C11
Method	BLASTX
NCBI GI	g3176686
BLAST score	374
E value	7.0e-36
Match length	93
% identity	76
NCBI Description	(AC003671) Similar to high affinity potassium transporter, HAK1 protein gb_U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
Seq. No.	279065
Contig ID	91949_1.R1011
5'-most EST	uC-zmflb73161e02b2

Method	BLASTX
NCBI GI	g282964
BLAST score	770
E value	4.0e-82
Match length	205
% identity	73
NCBI Description	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia x hybrida]

Seq. No.	279066
Contig ID	91952_1.R1011
5'-most EST	qmh700026006.f1
Method	BLASTX
NCBI GI	g3702327
BLAST score	156
E value	2.0e-10
Match length	56
% identity	52
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	279067
Contig ID	91973_1.R1011
5'-most EST	uC-zmflmo17277e04b1

Seq. No.	279068
Contig ID	91975_1.R1011
5'-most EST	uwc700155586.h1
Method	BLASTX
NCBI GI	g4337178
BLAST score	608
E value	6.0e-63
Match length	151
% identity	75
NCBI Description	(AC006416) T31J12.5 [Arabidopsis thaliana]

Seq. No.	279069
Contig ID	91985_1.R1011
5'-most EST	uC-zmflmo17263f10a2

Seq. No.	279070
Contig ID	91990_1.R1011
5'-most EST	LIB3136-022-Q1-K1-G5

Seq. No.	279071
Contig ID	91991_1.R1011
5'-most EST	uC-zmroteosinte061b12b2
Method	BLASTX
NCBI GI	g1742187
BLAST score	250
E value	6.0e-21
Match length	227
% identity	30
NCBI Description	(D90771) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_ (D90772) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1787591 (AE000231)

orf, hypothetical protein [Escherichia coli]

Seq. No.	279072
Contig ID	91998_1.R1011
5'-most EST	ceu700433646.h1

Seq. No.	279073
Contig ID	92023_1.R1011
5'-most EST	LIB3136-023-Q1-K1-B8

Seq. No.	279074
Contig ID	92027_1.R1011
5'-most EST	uC-zmflmo17127d08b1
Method	BLASTX
NCBI GI	g3482978
BLAST score	539
E value	4.0e-55
Match length	128
% identity	79
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	279075
Contig ID	92039_1.R1011
5'-most EST	uC-zmflmo17290f10b1
Method	BLASTX
NCBI GI	g4102600
BLAST score	619
E value	4.0e-64
Match length	236
% identity	57
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	279076
Contig ID	92047_1.R1011
5'-most EST	LIB3136-023-Q1-K1-E10

Seq. No.	279077
Contig ID	92054_1.R1011
5'-most EST	LIB3136-023-Q1-K1-E6
Method	BLASTX
NCBI GI	g3249095
BLAST score	541
E value	3.0e-55
Match length	171
% identity	61
NCBI Description	(AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb_L13703 from Schizosaccharomyces pombe. ESTs gb_N37567 and gb_T43002 come from this gene. [Arabidopsis thaliana]

Seq. No.	279078
Contig ID	92055_1.R1011
5'-most EST	LIB3136-025-Q1-K1-D10

Seq. No.	279079
Contig ID	92059_1.R1011
5'-most EST	nwy700447089.h1

Seq. No.	279080
Contig ID	92068_1.R1011
5'-most EST	LIB3136-023-Q1-K1-G1

Seq. No.	279081
Contig ID	92074_1.R1011
5'-most EST	LIB3136-023-Q1-K1-G5
Method	BLASTX
NCBI GI	g585053
BLAST score	166
E value	1.0e-11
Match length	111
% identity	36
NCBI Description	MITOTIC CONTROL PROTEIN DIS3 >gi_283075_pir__A41944 mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe) >gi_173381 (M74094) mitotic control protein [Schizosaccharomyces pombe] >gi_3650393_emb_CAA21102_ (AL031743) mitotic control protein dis3. [Schizosaccharomyces pombe]

Seq. No.	279082
Contig ID	92081_1.R1011
5'-most EST	rv1700455636.h1
Method	BLASTX
NCBI GI	g2191172
BLAST score	183
E value	2.0e-13
Match length	44
% identity	75
NCBI Description	(AF007270) contains similarity to GATA-type zinc fingers (PS:PS00344) [Arabidopsis thaliana]

Seq. No.	279083
Contig ID	92084_1.R1011
5'-most EST	cyk700049260.f1

Seq. No.	279084
Contig ID	92113_1.R1011
5'-most EST	LIB3136-024-Q1-K1-E7
Method	BLASTX
NCBI GI	g2146740
BLAST score	282
E value	5.0e-25
Match length	111
% identity	50
NCBI Description	inner mitochondrial membrane protein - Arabidopsis thaliana >gi_603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]

Seq. No.	279085
Contig ID	92116_1.R1011
5'-most EST	uC-zmflb73076h11b2

Seq. No.	279086
Contig ID	92116_2.R1011
5'-most EST	uC-zmflb73033d02a1

Seq. No.	279087
Contig ID	92121_1.R1011
5'-most EST	LIB3136-024-Q1-K1-G1
Method	BLASTX
NCBI GI	g1769907
BLAST score	703
E value	3.0e-74
Match length	177
% identity	67
NCBI Description	(X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]

Seq. No.	279088
Contig ID	92128_1.R1011
5'-most EST	uC-zmflb73272e12b1
Method	BLASTX
NCBI GI	g3249072
BLAST score	1130
E value	1.0e-124
Match length	272
% identity	79
NCBI Description	(AC004473) Contains similarity to hypothetical 43.1 KD protein in NDK-GCPE intergenic region gb_493519 from E. coli sequence gb_U02965. [Arabidopsis thaliana]

Seq. No.	279089
Contig ID	92138_1.R1011
5'-most EST	LIB3136-025-Q1-K1-B4
Method	BLASTX
NCBI GI	g3831443
BLAST score	149
E value	2.0e-09
Match length	48
% identity	56
NCBI Description	(AC005819) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	279090
Contig ID	92138_2.R1011
5'-most EST	wyr700241507.h1

Seq. No.	279091
Contig ID	92145_1.R1011
5'-most EST	LIB3136-025-Q1-K1-C11
Method	BLASTX
NCBI GI	g3763928
BLAST score	300
E value	3.0e-27
Match length	151
% identity	47
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279092
Contig ID	92156_1.R1011
5'-most EST	LIB3137-002-Q1-K1-A7

Seq. No.	279093
Contig ID	92156_2.R1011
5'-most EST	qmh700027749.f1

Seq. No.	279094
Contig ID	92158_1.R1011
5'-most EST	tzu700203093.h1

Seq. No.	279095
Contig ID	92165_1.R1011
5'-most EST	pmx700091479.h1
Method	BLASTX
NCBI GI	g4038594
BLAST score	1021
E value	1.0e-111
Match length	283
% identity	71
NCBI Description	(AJ222798) tDET1 protein [Lycopersicon esculentum] >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]

Seq. No.	279096
Contig ID	92165_2.R1011
5'-most EST	uC-zmflb73294e01a1
Method	BLASTX
NCBI GI	g4038594
BLAST score	192
E value	2.0e-14
Match length	64
% identity	59
NCBI Description	(AJ222798) tDET1 protein [Lycopersicon esculentum] >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]

Seq. No.	279097
Contig ID	92185_1.R1011
5'-most EST	rvt700549791.h1
Method	BLASTX
NCBI GI	g3935138
BLAST score	196
E value	5.0e-15
Match length	121
% identity	35
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No.	279098
Contig ID	92208_1.R1011
5'-most EST	rvt700551751.h1
Method	BLASTX
NCBI GI	g3478637
BLAST score	664
E value	2.0e-69
Match length	319
% identity	44
NCBI Description	(AC005546) R29425_1 [Homo sapiens]

Seq. No.	279099

Contig ID	92215_1.R1011
5'-most EST	LIB3136-026-Q1-K1-B11
Method	BLASTX
NCBI GI	g3176686
BLAST score	642
E value	2.0e-67
Match length	143
% identity	83
NCBI Description	(AC003671) Similar to high affinity potassium transporter, HAK1 protein gb_U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	279100
Contig ID	92244_1.R1011
5'-most EST	uC-zmflb73114a12a2

Seq. No.	279101
Contig ID	92246_1.R1011
5'-most EST	LIB3136-026-Q1-K1-H10
Method	BLASTX
NCBI GI	g3850582
BLAST score	856
E value	7.0e-92
Match length	233
% identity	73
NCBI Description	(AC005278) F15K9.14 [Arabidopsis thaliana]

Seq. No.	279102
Contig ID	92248_1.R1011
5'-most EST	pmx700091296.h1
Method	BLASTX
NCBI GI	g1724110
BLAST score	399
E value	9.0e-39
Match length	102
% identity	67
NCBI Description	(U79770) cinnamyl-alcohol dehydrogenase Eli3 [Mesembryanthemum crystallinum]

Seq. No.	279103
Contig ID	92254_1.R1011
5'-most EST	LIB3136-027-P1-K1-A4
Method	BLASTX
NCBI GI	g3367523
BLAST score	320
E value	1.0e-29
Match length	120
% identity	51
NCBI Description	(AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No.	279104
Contig ID	92256_1.R1011
5'-most EST	wty700164010.h1
Method	BLASTX
NCBI GI	g3953458
BLAST score	413

E value	3.0e-40
Match length	130
% identity	65
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	279105
Contig ID	92291_1.R1011
5'-most EST	xmt700265287.h1

Seq. No.	279106
Contig ID	92294_1.R1011
5'-most EST	fC-zmfl700352054a1
Method	BLASTX
NCBI GI	g4512714
BLAST score	256
E value	7.0e-22
Match length	93
% identity	55
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279107
Contig ID	92304_1.R1011
5'-most EST	wyr700238515.h1

Seq. No.	279108
Contig ID	92305_1.R1011
5'-most EST	xmt700257907.h1
Method	BLASTX
NCBI GI	g3540195
BLAST score	192
E value	1.0e-14
Match length	117
% identity	20
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	279109
Contig ID	92349_1.R1011
5'-most EST	xmt700262918.h1

Seq. No.	279110
Contig ID	92353_1.R1011
5'-most EST	uC-zmflmo17095g02b3
Method	BLASTN
NCBI GI	g949979
BLAST score	376
E value	0.0e+00
Match length	452
% identity	96
NCBI Description	Z.mays Glossy2 locus DNA

Seq. No.	279111
Contig ID	92361_2.R1011
5'-most EST	LIB3136-028-Q1-K1-D3

Seq. No.	279112
Contig ID	92367_1.R1011
5'-most EST	wty700166538.h1

Seq. No.	279113
Contig ID	92373_1.R1011
5'-most EST	xsy700217228.h1
Method	BLASTX
NCBI GI	g2829898
BLAST score	316
E value	7.0e-29
Match length	120
% identity	53
NCBI Description	(AC002311) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	279114
Contig ID	92377_1.R1011
5'-most EST	uC-zmflb73270f10a1
Method	BLASTX
NCBI GI	g1931652
BLAST score	254
E value	1.0e-21
Match length	84
% identity	60
NCBI Description	(U95973) phosphatidylinositol-4-phosphate 5-kinase isolog [Arabidopsis thaliana]

Seq. No.	279115
Contig ID	92386_1.R1011
5'-most EST	wyr700237947.h1
Method	BLASTX
NCBI GI	g100226
BLAST score	269
E value	2.0e-32
Match length	171
% identity	44
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	279116
Contig ID	92387_1.R1011
5'-most EST	wyr700244187.h1
Method	BLASTX
NCBI GI	g2853039
BLAST score	357
E value	9.0e-34
Match length	90
% identity	73
NCBI Description	(X94289) phosphoinositide-specific phospholipase C [Solanum tuberosum]

Seq. No.	279117
Contig ID	92402_1.R1011
5'-most EST	LIB3136-028-Q1-K1-H12

Seq. No.	279118
Contig ID	92418_1.R1011
5'-most EST	uer700577487.h1

Method	BLASTX
NCBI GI	g4469011
BLAST score	581
E value	4.0e-60
Match length	150
% identity	76
NCBI Description	(AL035602) carbohydrate kinase-like protein [Arabidopsis thaliana]

Seq. No.	279119
Contig ID	92424_1.R1011
5'-most EST	tfd700572126.h1

Seq. No.	279120
Contig ID	92425_1.R1011
5'-most EST	uC-zmroB73028e03b1

Seq. No.	279121
Contig ID	92438_1.R1011
5'-most EST	ntr700071679.h1
Method	BLASTX
NCBI GI	g2104535
BLAST score	552
E value	1.0e-71
Match length	214
% identity	64
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	279122
Contig ID	92438_2.R1011
5'-most EST	uC-zmroteosinte103d03b2
Method	BLASTX
NCBI GI	g2104535
BLAST score	158
E value	9.0e-12
Match length	66
% identity	59
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	279123
Contig ID	92438_3.R1011
5'-most EST	nbm700469025.h1
Method	BLASTX
NCBI GI	g2104535
BLAST score	380
E value	1.0e-36
Match length	110
% identity	65
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	279124
Contig ID	92449_1.R1011
5'-most EST	LIB3136-034-Q1-K1-A2
Method	BLASTX
NCBI GI	g3914365
BLAST score	451
E value	3.0e-45

Match length	100
% identity	83
NCBI Description	PHOSPHOLIPASE D 2 PRECURSOR (PLD 2) (CHOLINE PHOSPHATASE 2) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 2) >gi_1902901_dbj_BAA19466_ (AB001919) phospholipase D [Oryza sativa]

Seq. No.	279125
Contig ID	92468_1.R1011
5'-most EST	uC-zmflmo17333b08b1

Seq. No.	279126
Contig ID	92470_1.R1011
5'-most EST	LIB3136-029-Q1-K1-G7

Seq. No.	279127
Contig ID	92472_1.R1011
5'-most EST	uC-zmflmo17126e03b1
Method	BLASTX
NCBI GI	g4337192
BLAST score	603
E value	3.0e-62
Match length	275
% identity	47
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279128
Contig ID	92490_1.R1011
5'-most EST	gwl700614936.h1
Method	BLASTX
NCBI GI	g3776559
BLAST score	407
E value	3.0e-39
Match length	122
% identity	59
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	279129
Contig ID	92490_2.R1011
5'-most EST	fC-zmle700445173f6

Seq. No.	279130
Contig ID	92506_1.R1011
5'-most EST	LIB3136-030-Q1-K1-F1

Seq. No.	279131
Contig ID	92521_1.R1011
5'-most EST	uC-zmroteosinte004b11b1

Seq. No.	279132
Contig ID	92523_1.R1011
5'-most EST	LIB3136-044-P1-K1-C11

Seq. No.	279133

Contig ID	92526_1.R1011
5'-most EST	LIB3136-030-Q1-K1-G1
Method	BLASTX
NCBI GI	g1723347
BLAST score	359
E value	2.0e-63
Match length	189
% identity	68
NCBI Description	HYPOTHETICAL 64.2 KD PROTEIN YCF45 (ORF565) >gi_2147571_pir__S73202 hypothetical protein 565 - Porphyra purpurea chloroplast >gi_1276747 (U38804) trnS [Porphyra purpurea]

Seq. No.	279134
Contig ID	92539_1.R1011
5'-most EST	LIB3136-032-Q1-K1-A11

Seq. No.	279135
Contig ID	92543_1.R1011
5'-most EST	LIB3136-032-Q1-K1-A4
Method	BLASTX
NCBI GI	g1710124
BLAST score	394
E value	3.0e-38
Match length	97
% identity	72
NCBI Description	(U62279) leucine-rich repeat-containing extracellular glycoprotein; contains six N-glycosylation sites [NX(S/T)] [Sorghum bicolor]

Seq. No.	279136
Contig ID	92591_1.R1011
5'-most EST	ntr700071637.h1
Method	BLASTX
NCBI GI	g3063710
BLAST score	794
E value	1.0e-84
Match length	265
% identity	55
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	279137
Contig ID	92591_2.R1011
5'-most EST	wty700169649.h1
Method	BLASTX
NCBI GI	g3063710
BLAST score	232
E value	2.0e-19
Match length	122
% identity	43
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	279138
Contig ID	92594_1.R1011
5'-most EST	wty700169954.h1
Method	BLASTX
NCBI GI	g4559346

BLAST score	197
E value	4.0e-15
Match length	94
% identity	41
NCBI Description	(AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No.	279139
Contig ID	92600_1.R1011
5'-most EST	LIB3136-033-Q1-K1-A12
Method	BLASTX
NCBI GI	g1619300
BLAST score	588
E value	1.0e-60
Match length	194
% identity	60
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	279140
Contig ID	92614_1.R1011
5'-most EST	uC-zmflmo17277b03b1
Method	BLASTX
NCBI GI	g1345132
BLAST score	283
E value	6.0e-44
Match length	188
% identity	53
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	279141
Contig ID	92624_1.R1011
5'-most EST	LIB3136-033-Q1-K1-C5

Seq. No.	279142
Contig ID	92626_1.R1011
5'-most EST	nbm700469850.h1
Method	BLASTX
NCBI GI	g1778376
BLAST score	503
E value	4.0e-51
Match length	124
% identity	77
NCBI Description	(U81288) PsRT17-1 [Pisum sativum]

Seq. No.	279143
Contig ID	92632_1.R1011
5'-most EST	nbm700473017.h1

Seq. No.	279144
Contig ID	92636_1.R1011
5'-most EST	hbs701182154.h1

Seq. No.	279145
Contig ID	92649_1.R1011
5'-most EST	LIB3136-033-Q1-K1-F1

Method	BLASTX
NCBI GI	g4455213
BLAST score	525
E value	2.0e-53
Match length	126
% identity	78
NCBI Description	(AL035440) glutamine amidotransferase/cyclase [Arabidopsis thaliana]

Seq. No.	279146
Contig ID	92650_1.R1011
5'-most EST	LIB3136-033-Q1-K1-F11
Method	BLASTX
NCBI GI	g1931652
BLAST score	540
E value	4.0e-55
Match length	214
% identity	55
NCBI Description	(U95973) phosphatidylinositol-4-phosphate 5-kinase isolog [Arabidopsis thaliana]

Seq. No.	279147
Contig ID	92652_1.R1011
5'-most EST	pmx700083924.h1

Seq. No.	279148
Contig ID	92655_1.R1011
5'-most EST	LIB3136-033-Q1-K1-F7
Method	BLASTX
NCBI GI	g4102600
BLAST score	505
E value	5.0e-51
Match length	133
% identity	74
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	279149
Contig ID	92657_1.R1011
5'-most EST	LIB3136-033-Q1-K1-G11
Method	BLASTX
NCBI GI	g4102600
BLAST score	718
E value	2.0e-85
Match length	189
% identity	82
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	279150
Contig ID	92661_1.R1011
5'-most EST	ntr700073572.h1
Method	BLASTX
NCBI GI	g2501499
BLAST score	226
E value	2.0e-18
Match length	111
% identity	44
NCBI Description	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE (IAA-GLU

SYNTHETASE) ((URIDINE 5'-DIPHOSPHATE-GLUCOSE:INDOL-3-YLACETYL)-BETA-D-GLUCOSYL TRANSFERASE) >gi_626043_pir__A54739 indole-3-acetate beta-glucosyltransferase (EC 2.4.1.121) - maize >gi_548195 (L34847) IAA-glu synthetase [Zea mays]

Seq. No.	279151
Contig ID	92671_1.R1011
5'-most EST	uC-zmroteosinte009f06b1
Method	BLASTX
NCBI GI	g3540180
BLAST score	499
E value	3.0e-52
Match length	194
% identity	56
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	279152
Contig ID	92685_1.R1011
5'-most EST	vfk700404891.h1
Method	BLASTX
NCBI GI	g3510253
BLAST score	248
E value	7.0e-21
Match length	130
% identity	37
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279153
Contig ID	92694_1.R1011
5'-most EST	LIB3136-034-Q1-K1-B5

Seq. No.	279154
Contig ID	92707_1.R1011
5'-most EST	gct701175118.h1

Seq. No.	279155
Contig ID	92712_1.R1011
5'-most EST	LIB3136-034-Q1-K1-F6
Method	BLASTX
NCBI GI	g2462927
BLAST score	674
E value	1.0e-70
Match length	168
% identity	76
NCBI Description	(Y10342) putative amidase [Arabidopsis thaliana]

Seq. No.	279156
Contig ID	92715_1.R1011
5'-most EST	rvt700548840.h1
Method	BLASTX
NCBI GI	g123650
BLAST score	281
E value	5.0e-47
Match length	130
% identity	78
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat

shock protein 70 (clone pMON9743) - garden petunia
>gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
[Petunia x hybrida]

Seq. No.	279157
Contig ID	92721_1.R1011
5'-most EST	fC-zmro700453413f1

Seq. No.	279158
Contig ID	92722_1.R1011
5'-most EST	LIB3136-034-Q1-K1-E3

Seq. No.	279159
Contig ID	92725_1.R1011
5'-most EST	uC-zmflb73135e03b2

Seq. No.	279160
Contig ID	92729_1.R1011
5'-most EST	LIB3136-034-Q1-K1-F1
Method	BLASTX
NCBI GI	g3980378
BLAST score	146
E value	5.0e-09
Match length	35
% identity	71
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	279161
Contig ID	92736_1.R1011
5'-most EST	uC-zmflmo17020e10b1
Method	BLASTX
NCBI GI	g2252863
BLAST score	206
E value	4.0e-16
Match length	80
% identity	55
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]

Seq. No.	279162
Contig ID	92736_2.R1011
5'-most EST	uC-zmflB73106d11b1

Seq. No.	279163
Contig ID	92737_1.R1011
5'-most EST	uC-zmflmo17339g04b1
Method	BLASTX
NCBI GI	g1170191
BLAST score	595
E value	2.0e-61
Match length	149
% identity	77
NCBI Description	HOMEOBOX PROTEIN HD1 >gi_1076449_pir__S47535 homeodomain-containing protein - rape >gi_453949_emb_CAA82314_ (Z29073) homeodomain-containing protein [Brassica napus] >gi_1090522_prf__2019252A homeobox

protein [Brassica napus]

Seq. No.	279164
Contig ID	92743_1.R1011
5'-most EST	LIB3136-034-Q1-K1-G3
Method	BLASTX
NCBI GI	g2244813
BLAST score	160
E value	1.0e-10
Match length	68
% identity	50
NCBI Description	(Z97336) acylaminoacyl-peptidase homolog [Arabidopsis thaliana]

Seq. No.	279165
Contig ID	92753_1.R1011
5'-most EST	uC-zmf1Mo17084g06b1
Method	BLASTX
NCBI GI	g4557026
BLAST score	150
E value	4.0e-12
Match length	240
% identity	17
NCBI Description	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 >gi_1477565 (U50078) p532 [Homo sapiens]

Seq. No.	279166
Contig ID	92756_2.R1011
5'-most EST	LIB3137-020-Q1-K1-F4
Method	BLASTX
NCBI GI	g1762144
BLAST score	272
E value	6.0e-24
Match length	79
% identity	65
NCBI Description	(U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No.	279167
Contig ID	92769_1.R1011
5'-most EST	uC-zmrob73060c08a1
Method	BLASTN
NCBI GI	g3342803
BLAST score	98
E value	1.0e-47
Match length	213
% identity	94
NCBI Description	Zea mays strain B73 putative 6-phosphogluconate dehydrogenase mRNA, nuclear gene encoding putative plastid protein, partial cds

Seq. No.	279168
Contig ID	92769_2.R1011
5'-most EST	LIB3136-035-Q1-K1-C12
Method	BLASTX
NCBI GI	g3342804
BLAST score	347

E value	2.0e-32
Match length	66
% identity	100
NCBI Description	(AF061839) putative 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	279169
Contig ID	92776_1.R1011
5'-most EST	uC-zmroteosinte072h03b2
Method	BLASTX
NCBI GI	g4204281
BLAST score	271
E value	2.0e-23
Match length	140
% identity	43
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	279170
Contig ID	92829_1.R1011
5'-most EST	LIB3136-036-Q1-K1-E8

Seq. No.	279171
Contig ID	92834_1.R1011
5'-most EST	wen700334679.h1
Method	BLASTX
NCBI GI	g2642448
BLAST score	786
E value	6.0e-88
Match length	259
% identity	44
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279172
Contig ID	92856_1.R1011
5'-most EST	LIB3136-036-Q1-K1-H7

Seq. No.	279173
Contig ID	92861_1.R1011
5'-most EST	LIB3136-037-P1-K1-A4
Method	BLASTX
NCBI GI	g2660675
BLAST score	358
E value	6.0e-34
Match length	86
% identity	80
NCBI Description	(AC002342) similar to DNA-damage-inducible protein P [Arabidopsis thaliana]

Seq. No.	279174
Contig ID	92862_1.R1011
5'-most EST	uC-zmflb73127h11b2

Seq. No.	279175
Contig ID	92865_1.R1011
5'-most EST	uC-zmflb73027c04b1

Seq. No.	279176
Contig ID	92878_1.R1011
5'-most EST	pmx700083831.h1
Method	BLASTX
NCBI GI	g1125754
BLAST score	261
E value	1.0e-22
Match length	99
% identity	45
NCBI Description	(U42833) coded for by C. elegans cDNA cm16f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]

Seq. No.	279177
Contig ID	92883_1.R1011
5'-most EST	fwa700099639.h1
Method	BLASTX
NCBI GI	g2494280
BLAST score	537
E value	2.0e-54
Match length	297
% identity	64
NCBI Description	ELONGATION FACTOR TS (EF-TS) >gi_1653231_dbj_BAA18146_ (D90912) elongation factor TS [Synechocystis sp.]

Seq. No.	279178
Contig ID	92883_3.R1011
5'-most EST	LIB84-029-Q1-E1-C8
Method	BLASTX
NCBI GI	g2494280
BLAST score	339
E value	5.0e-32
Match length	109
% identity	60
NCBI Description	ELONGATION FACTOR TS (EF-TS) >gi_1653231_dbj_BAA18146_ (D90912) elongation factor TS [Synechocystis sp.]

Seq. No.	279179
Contig ID	92886_1.R1011
5'-most EST	uC-zmroteosinte059f10b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	389
E value	3.0e-37
Match length	149
% identity	54
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	279180
Contig ID	92886_2.R1011
5'-most EST	uC-zmflb73175a07b1
Method	BLASTX
NCBI GI	g4587525

BLAST score	318
E value	8.0e-31
Match length	122
% identity	53
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	279181
Contig ID	92893_1.R1011
5'-most EST	LIB3136-037-P1-K1-E1

Seq. No.	279182
Contig ID	92902_1.R1011
5'-most EST	LIB3136-037-P1-K1-F12

Seq. No.	279183
Contig ID	92905_1.R1011
5'-most EST	LIB3136-037-P1-K1-F6

Seq. No.	279184
Contig ID	92919_1.R1011
5'-most EST	xjt700092553.h1

Seq. No.	279185
Contig ID	92927_1.R1011
5'-most EST	uC-zmflMo17010b10b1

Seq. No.	279186
Contig ID	92930_1.R1011
5'-most EST	uC-zmflmo17259f05b1
Method	BLASTX
NCBI GI	g4582459
BLAST score	644
E value	2.0e-67
Match length	214
% identity	59
NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No.	279187
Contig ID	92956_1.R1011
5'-most EST	LIB3136-038-P1-K1-F9

Seq. No.	279188
Contig ID	92967_1.R1011
5'-most EST	LIB3137-024-Q1-K1-B5
Method	BLASTX
NCBI GI	g1169544
BLAST score	357
E value	7.0e-34
Match length	85
% identity	80
NCBI Description	ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) ERD1 protein [Arabidopsis thaliana]

Seq. No.	279189
Contig ID	92973_1.R1011
5'-most EST	cjh700197008.h1

Seq. No.	279190
Contig ID	92984_1.R1011
5'-most EST	wyr700244001.h1
Method	BLASTX
NCBI GI	g4508083
BLAST score	294
E value	4.0e-26
Match length	241
% identity	35
NCBI Description	(AC005882) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	279191
Contig ID	92990_1.R1011
5'-most EST	uC-zmflmo17109a07b1

Seq. No.	279192
Contig ID	93000_1.R1011
5'-most EST	ceu700433118.h1
Method	BLASTX
NCBI GI	g4558673
BLAST score	367
E value	9.0e-35
Match length	261
% identity	31
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279193
Contig ID	93010_2.R1011
5'-most EST	nbm700476092.h1
Method	BLASTX
NCBI GI	g3643608
BLAST score	317
E value	3.0e-29
Match length	127
% identity	50
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279194
Contig ID	93013_1.R1011
5'-most EST	fdz701164343.h1
Method	BLASTX
NCBI GI	g2654868
BLAST score	675
E value	6.0e-71
Match length	191
% identity	67
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No.	279195
Contig ID	93018_1.R1011
5'-most EST	tfd700569813.h1
Method	BLASTX

NCBI GI g4539452
BLAST score 1037
E value 1.0e-113
Match length 259
% identity 71
NCBI Description (AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No. 279196
Contig ID 93034_1.R1011
5'-most EST uC-zmflb73092b08b2

Seq. No. 279197
Contig ID 93068_1.R1011
5'-most EST xjt700094979.h1

Seq. No. 279198
Contig ID 93068_2.R1011
5'-most EST yyf700352489.h1

Seq. No. 279199
Contig ID 93076_1.R1011
5'-most EST LIB3136-042-P1-K1-A5
Method BLASTX
NCBI GI g4406764
BLAST score 416
E value 2.0e-40
Match length 140
% identity 59
NCBI Description (AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No. 279200
Contig ID 93079_1.R1011
5'-most EST uC-zmflmo17030c08b1
Method BLASTX
NCBI GI g2443870
BLAST score 354
E value 2.0e-33
Match length 170
% identity 45
NCBI Description (AC002985) R27090_2 [Homo sapiens]

Seq. No. 279201
Contig ID 93080_1.R1011
5'-most EST uwc700151727.h1

Seq. No. 279202
Contig ID 93090_1.R1011
5'-most EST LIB3136-042-P1-K1-B9

Seq. No. 279203
Contig ID 93096_1.R1011
5'-most EST afb700381959.h1
Method BLASTX
NCBI GI g2921823
BLAST score 462

E value	8.0e-46
Match length	204
% identity	53
NCBI Description	(AF046934) shoot-forming PKSF1 [Paulownia kawakamii]

Seq. No.	279204
Contig ID	93096_2.R1011
5'-most EST	ymt700222611.h1
Method	BLASTX
NCBI GI	g2651296
BLAST score	287
E value	2.0e-30
Match length	175
% identity	50
NCBI Description	(AC002336) b-zip DNA-binding protein [Arabidopsis thaliana]

Seq. No.	279205
Contig ID	93130_1.R1011
5'-most EST	uC-zmf1b73137b01b1
Method	BLASTX
NCBI GI	g2914703
BLAST score	270
E value	2.0e-33
Match length	190
% identity	48
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	279206
Contig ID	93137_1.R1011
5'-most EST	uC-zmf1b73041f04b1

Seq. No.	279207
Contig ID	93143_1.R1011
5'-most EST	wty700168177.h1
Method	BLASTX
NCBI GI	g3786004
BLAST score	418
E value	7.0e-41
Match length	128
% identity	68
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279208
Contig ID	93163_1.R1011
5'-most EST	LIB3136-044-P1-K1-A1
Method	BLASTX
NCBI GI	g3881381
BLAST score	303
E value	2.0e-27
Match length	102
% identity	60
NCBI Description	(Z68270) Similarity to Yeast Man(0)-alpha-mannosidase (SW:MNS1_YEAST); cDNA EST EMBL:D71247 comes from this gene; cDNA EST EMBL:D73896 comes from this gene [Caenorhabditis elegans]

Seq. No.	279209

Contig ID	93169_1.R1011
5'-most EST	uC-zmflb73223a09b2
Seq. No.	279210
Contig ID	93185_1.R1011
5'-most EST	xjt700092485.h1
Seq. No.	279211
Contig ID	93187_1.R1011
5'-most EST	xmt700264277.h1
Seq. No.	279212
Contig ID	93190_1.R1011
5'-most EST	xyt700342462.h1
Seq. No.	279213
Contig ID	93190_2.R1011
5'-most EST	LIB3136-044-P1-K1-D7
Seq. No.	279214
Contig ID	93200_1.R1011
5'-most EST	LIB3136-044-P1-K1-F3
Method	BLASTX
NCBI GI	g3128168
BLAST score	265
E value	2.0e-39
Match length	124
% identity	63
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]
Seq. No.	279215
Contig ID	93243_1.R1011
5'-most EST	uC-zmflb73256d12b1
Method	BLASTX
NCBI GI	g2842424
BLAST score	1366
E value	1.0e-151
Match length	404
% identity	63
NCBI Description	(AJ223948) RNA helicase [Homo sapiens]
Seq. No.	279216
Contig ID	93243_2.R1011
5'-most EST	LIB3137-049-Q1-K1-E3
Method	BLASTX
NCBI GI	g2842424
BLAST score	486
E value	8.0e-72
Match length	228
% identity	57
NCBI Description	(AJ223948) RNA helicase [Homo sapiens]
Seq. No.	279217
Contig ID	93246_1.R1011
5'-most EST	ceu700422955.h1

Seq. No.	279218
Contig ID	93250_1.R1011
5'-most EST	ntr700073535.h1
Method	BLASTX
NCBI GI	g2224846
BLAST score	526
E value	2.0e-53
Match length	194
% identity	58
NCBI Description	(Y13905) anionic peroxidase [Zea mays]

Seq. No.	279219
Contig ID	93254_1.R1011
5'-most EST	cat700016234.r1
Method	BLASTX
NCBI GI	g728867
BLAST score	281
E value	9.0e-25
Match length	150
% identity	43
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi_99694_pir__S21961 proline-rich protein APG - Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG [Arabidopsis thaliana]

Seq. No.	279220
Contig ID	93274_1.R1011
5'-most EST	wty700172464.h1
Method	BLASTX
NCBI GI	g2262101
BLAST score	188
E value	5.0e-14
Match length	83
% identity	47
NCBI Description	(AC002343) kinesin heavy chain isolog [Arabidopsis thaliana]

Seq. No.	279221
Contig ID	93286_1.R1011
5'-most EST	LIB3136-045-Q1-K1-G5

Seq. No.	279222
Contig ID	93287_1.R1011
5'-most EST	LIB3136-045-Q1-K1-G6

Seq. No.	279223
Contig ID	93315_1.R1011
5'-most EST	uC-zmflm017018c03b1
Method	BLASTX
NCBI GI	g3582333
BLAST score	582
E value	9.0e-60
Match length	180
% identity	62
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279224

Contig ID	93317_1.R1011
5'-most EST	uC-zmroteosinte014d06b1
Method	BLASTX
NCBI GI	g4586260
BLAST score	249
E value	6.0e-21
Match length	210
% identity	34
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	279225
Contig ID	93333_1.R1011
5'-most EST	dyk700102762.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	49
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279226
Contig ID	93337_1.R1011
5'-most EST	LIB3136-047-Q1-K1-C7
Method	BLASTX
NCBI GI	g2576361
BLAST score	245
E value	4.0e-44
Match length	109
% identity	77
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	279227
Contig ID	93337_3.R1011
5'-most EST	tzu700203968.h1
Method	BLASTX
NCBI GI	g2576361
BLAST score	265
E value	2.0e-23
Match length	67
% identity	73
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	279228
Contig ID	93340_1.R1011
5'-most EST	uC-zmflmo17290h08b1
Method	BLASTX
NCBI GI	g1174470
BLAST score	508
E value	2.0e-51
Match length	215
% identity	48
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A

integral membrane protein [Mus musculus]

Seq. No.	279229
Contig ID	93354_1.R1011
5'-most EST	wen700333894.h1

Seq. No.	279230
Contig ID	93376_1.R1011
5'-most EST	fwa700100757.h1
Method	BLASTX
NCBI GI	g4587513
BLAST score	150
E value	1.0e-09
Match length	147
% identity	35
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	279231
Contig ID	93388_1.R1011
5'-most EST	pmx700090261.h1
Method	BLASTN
NCBI GI	g550541
BLAST score	143
E value	2.0e-74
Match length	404
% identity	96
NCBI Description	Z.mays CYP71C4 mRNA for cytochrome P-450

Seq. No.	279232
Contig ID	93390_1.R1011
5'-most EST	uC-zmflmo17073d04b1
Method	BLASTX
NCBI GI	g2244807
BLAST score	332
E value	2.0e-30
Match length	222
% identity	37
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279233
Contig ID	93399_1.R1011
5'-most EST	uC-zmflmo17273e03b1
Method	BLASTX
NCBI GI	g1167953
BLAST score	994
E value	1.0e-108
Match length	315
% identity	61
NCBI Description	(U43496) putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare] >gi_2465426 (AF021256) 32 kDa protein [Hordeum vulgare]

Seq. No.	279234
Contig ID	93407_1.R1011
5'-most EST	LIB3136-048-Q1-K1-E1
Method	BLASTX

NCBI GI	g2392895
BLAST score	268
E value	3.0e-33
Match length	168
% identity	52
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	279235
Contig ID	93441_1.R1011
5'-most EST	uC-zmf1b73013h12b1

Seq. No.	279236
Contig ID	93444_1.R1011
5'-most EST	vux700160875.h1
Method	BLASTX
NCBI GI	g4538929
BLAST score	256
E value	2.0e-21
Match length	321
% identity	32
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	279237
Contig ID	93448_1.R1011
5'-most EST	LIB3136-049-Q1-K1-C11

Seq. No.	279238
Contig ID	93454_1.R1011
5'-most EST	wen700335286.h1
Method	BLASTX
NCBI GI	g112785
BLAST score	288
E value	2.0e-25
Match length	150
% identity	39
NCBI Description	DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1 3-methyladenine DNA glycosylase (EC 3.2.2.-) I - Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa 1-187) [Escherichia coli] >gi_147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432) 3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

Seq. No.	279239
Contig ID	93471_1.R1011
5'-most EST	uC-zmroteosinte015h11b1
Method	BLASTX
NCBI GI	g3513303
BLAST score	463
E value	7.0e-46
Match length	222
% identity	45

NCBI Description	(AC005594) R26984_1 [Homo sapiens]
Seq. No.	279240
Contig ID	93484_1.R1011
5'-most EST	uC-zmflb73130b04b2
Method	BLASTX
NCBI GI	g1653767
BLAST score	162
E value	6.0e-11
Match length	96
% identity	39
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]
Seq. No.	279241
Contig ID	93493_1.R1011
5'-most EST	uC-zmroB73014a12b1
Method	BLASTX
NCBI GI	g100288
BLAST score	293
E value	2.0e-26
Match length	98
% identity	62
NCBI Description	transcription activator TGA1a - tobacco >gi_170285 (M62855) leucine-zipper DNA-binding protein [Nicotiana tabacum]
Seq. No.	279242
Contig ID	93502_1.R1011
5'-most EST	uC-zmroteosinte001h01b1
Method	BLASTX
NCBI GI	g2160694
BLAST score	957
E value	1.0e-104
Match length	261
% identity	68
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
Seq. No.	279243
Contig ID	93507_1.R1011
5'-most EST	ymt700221591.h2
Method	BLASTX
NCBI GI	g3127182
BLAST score	210
E value	2.0e-16
Match length	180
% identity	29
NCBI Description	(AF061758) poly(A) polymerase II [Gallus gallus]
Seq. No.	279244
Contig ID	93510_1.R1011
5'-most EST	LIB3136-050-Q1-K1-D12
Seq. No.	279245
Contig ID	93517_1.R1011
5'-most EST	ymt700224217.h1
Method	BLASTX
NCBI GI	g2145356

BLAST score	720
E value	3.0e-76
Match length	201
% identity	70
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	279246
Contig ID	93519_1.R1011
5'-most EST	wyr700238533.h1

Seq. No.	279247
Contig ID	93529_1.R1011
5'-most EST	LIB3136-050-Q1-K1-H4

Seq. No.	279248
Contig ID	93555_1.R1011
5'-most EST	tzu700201753.h1
Method	BLASTX
NCBI GI	g4539330
BLAST score	355
E value	2.0e-33
Match length	102
% identity	65
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	279249
Contig ID	93560_1.R1011
5'-most EST	LIB3136-051-Q1-K1-E8

Seq. No.	279250
Contig ID	93562_2.R1011
5'-most EST	nbm700471347.h1

Seq. No.	279251
Contig ID	93618_1.R1011
5'-most EST	uC-zmromo17017a05a1

Seq. No.	279252
Contig ID	93637_1.R1011
5'-most EST	xjt700092028.h1

Seq. No.	279253
Contig ID	93642_1.R1011
5'-most EST	uC-zmflb73193f01b1

Seq. No.	279254
Contig ID	93649_1.R1011
5'-most EST	uC-zmflmo17072c10b1
Method	BLASTX
NCBI GI	g4539335
BLAST score	974
E value	1.0e-105
Match length	271
% identity	63
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	279255
Contig ID	93658_1.R1011
5'-most EST	LIB3136-052-Q1-K1-H3

Seq. No.	279256
Contig ID	93661_1.R1011
5'-most EST	LIB3136-052-Q1-K1-H6
Method	BLASTX
NCBI GI	g2190557
BLAST score	208
E value	1.0e-16
Match length	99
% identity	44
NCBI Description	(AC001229) F5I14.11 [Arabidopsis thaliana]

Seq. No.	279257
Contig ID	93663_1.R1011
5'-most EST	uC-zmflb73157f02a1
Method	BLASTN
NCBI GI	g902200
BLAST score	443
E value	0.0e+00
Match length	506
% identity	49
NCBI Description	Z.mays complete chloroplast genome

Seq. No.	279258
Contig ID	93676_1.R1011
5'-most EST	wyr700237267.h1

Seq. No.	279259
Contig ID	93725_1.R1011
5'-most EST	LIB3136-055-Q1-K1-E10

Seq. No.	279260
Contig ID	93728_2.R1011
5'-most EST	uC-zmflb73099c12b1
Method	BLASTX
NCBI GI	g3885328
BLAST score	292
E value	3.0e-26
Match length	107
% identity	54
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	279261
Contig ID	93741_1.R1011
5'-most EST	LIB3136-055-Q1-K1-E9

Seq. No.	279262
Contig ID	93746_1.R1011
5'-most EST	nbm700468212.h1

Seq. No.	279263
Contig ID	93754_1.R1011

5'-most EST	qmh700029803.f1
Method	BLASTX
NCBI GI	g3873710
BLAST score	354
E value	2.0e-33
Match length	126
% identity	52
NCBI Description	(Z73102) predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

Seq. No.	279264
Contig ID	93759_1.R1011
5'-most EST	uwc700155329.h1
Method	BLASTX
NCBI GI	g3355658
BLAST score	183
E value	2.0e-13
Match length	120
% identity	35
NCBI Description	(AJ009691) SMC2orf [Podocoryne carnea]

Seq. No.	279265
Contig ID	93762_1.R1011
5'-most EST	LIB3136-056-Q1-K1-B10
Method	BLASTX
NCBI GI	g2961346
BLAST score	400
E value	5.0e-39
Match length	89
% identity	76
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	279266
Contig ID	93769_1.R1011
5'-most EST	uC-zmf1b73270e12b1

Seq. No.	279267
Contig ID	93776_1.R1011
5'-most EST	LIB3136-056-Q1-K1-C2
Method	BLASTX
NCBI GI	g2335100
BLAST score	494
E value	5.0e-50
Match length	131
% identity	69
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	279268
Contig ID	93778_1.R1011
5'-most EST	uC-zmf1b73159h02b2
Method	BLASTX
NCBI GI	g2341035
BLAST score	738

E value	4.0e-78
Match length	243
% identity	56
NCBI Description	(AC000104) Match to Arabidopsis photolysase (PHH1) gene (gb_X99061) and cryptochrome 2 apoprotein (CRY2) (gb_U43397). ESTs gb_W43661 and gb_Z25638 come from this gene. [Arabidopsis thaliana]

Seq. No.	279269
Contig ID	93802_1.R1011
5'-most EST	tzu700201192.h1
Method	BLASTX
NCBI GI	g4586113
BLAST score	401
E value	5.0e-39
Match length	123
% identity	69
NCBI Description	(AL049638) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	279270
Contig ID	93805_1.R1011
5'-most EST	LIB3136-056-Q1-K1-F3

Seq. No.	279271
Contig ID	93822_1.R1011
5'-most EST	LIB3136-056-Q1-K1-H11

Seq. No.	279272
Contig ID	93831_1.R1011
5'-most EST	uC-zmflmo17268a11b1

Seq. No.	279273
Contig ID	93853_1.R1011
5'-most EST	wty700170321.h1
Method	BLASTX
NCBI GI	g3033400
BLAST score	693
E value	3.0e-74
Match length	162
% identity	85
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	279274
Contig ID	93869_1.R1011
5'-most EST	uC-zmflB73043e02b1

Seq. No.	279275
Contig ID	93891_1.R1011
5'-most EST	uC-zmflmo17241a02b1
Method	BLASTX
NCBI GI	g2464905
BLAST score	274
E value	1.0e-23
Match length	70
% identity	76

NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	279276
Contig ID	93891_2.R1011
5'-most EST	yyf700351509.h1
Method	BLASTX
NCBI GI	g2464905
BLAST score	391
E value	8.0e-38
Match length	118
% identity	69
NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	279277
Contig ID	93901_1.R1011
5'-most EST	uC-zmflb73061e09b1
Method	BLASTX
NCBI GI	g3395431
BLAST score	217
E value	2.0e-17
Match length	75
% identity	51
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	279278
Contig ID	93904_1.R1011
5'-most EST	wty700167673.h1
Method	BLASTX
NCBI GI	g2760830
BLAST score	318
E value	1.0e-29
Match length	70
% identity	79
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	279279
Contig ID	93911_1.R1011
5'-most EST	LIB3136-058-Q1-K1-A5
Method	BLASTX
NCBI GI	g4455174
BLAST score	161
E value	6.0e-11
Match length	45
% identity	64
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	279280
Contig ID	93930_1.R1011
5'-most EST	mwy700442740.h1
Method	BLASTX
NCBI GI	g2642165
BLAST score	156
E value	3.0e-10
Match length	66
% identity	41
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279281
Contig ID	93945_1.R1011
5'-most EST	uC-zmflb73274a02b1

Seq. No.	279282
Contig ID	93949_1.R1011
5'-most EST	LIB3136-058-Q1-K1-E5

Seq. No.	279283
Contig ID	93951_1.R1011
5'-most EST	uC-zmroteosinte037f05b1
Method	BLASTX
NCBI GI	g3915463
BLAST score	203
E value	9.0e-16
Match length	127
% identity	41
NCBI Description	HYPOTHETICAL 33.1 KD PROTEIN SLR1592 >gi_1652063_dbj_BAA16988_ (D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	279284
Contig ID	93964_1.R1011
5'-most EST	uC-zmflmo17310d06b1
Method	BLASTX
NCBI GI	g2832641
BLAST score	290
E value	6.0e-26
Match length	99
% identity	54
NCBI Description	(AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]

Seq. No.	279285
Contig ID	93966_1.R1011
5'-most EST	uC-zmflb73116g05b2
Method	BLASTX
NCBI GI	g4056479
BLAST score	277
E value	2.0e-24
Match length	85
% identity	65
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	279286
Contig ID	93972_1.R1011
5'-most EST	uC-zmflb73222e03b1
Method	BLASTX
NCBI GI	g4538927
BLAST score	418
E value	1.0e-40
Match length	149
% identity	59
NCBI Description	(AL049483) putative peroxidase [Arabidopsis thaliana]

Seq. No.	279287

Contig ID	93974_1.R1011
5'-most EST	LIB3136-058-Q1-K1-H12
Method	BLASTX
NCBI GI	g3319876
BLAST score	177
E value	8.0e-13
Match length	86
% identity	48
NCBI Description	(AJ007791) Msh3 protein [Arabidopsis thaliana]

Seq. No.	279288
Contig ID	93983_1.R1011
5'-most EST	LIB3136-059-Q1-K1-A2

Seq. No.	279289
Contig ID	93985_1.R1011
5'-most EST	LIB3136-059-Q1-K1-A4
Method	BLASTX
NCBI GI	g3912925
BLAST score	342
E value	3.0e-32
Match length	124
% identity	60
NCBI Description	(AF001308) syntaxin-like protein [Arabidopsis thaliana]

Seq. No.	279290
Contig ID	93992_1.R1011
5'-most EST	uC-zmflmo17289e05b1
Method	BLASTX
NCBI GI	g4262226
BLAST score	149
E value	3.0e-09
Match length	35
% identity	74
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	279291
Contig ID	93992_2.R1011
5'-most EST	LIB3136-059-Q1-K1-B10

Seq. No.	279292
Contig ID	94002_1.R1011
5'-most EST	LIB84-021-Q1-E1-E11

Seq. No.	279293
Contig ID	94012_1.R1011
5'-most EST	xyt700344094.h1
Method	BLASTX
NCBI GI	g3775993
BLAST score	1347
E value	1.0e-149
Match length	297
% identity	87
NCBI Description	(AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No.	279294
Contig ID	94032_1.R1011

5'-most EST	LIB3136-059-Q1-K1-F5
Seq. No.	279295
Contig ID	94065_1.R1011
5'-most EST	LIB3136-060-Q1-K1-B2
Method	BLASTX
NCBI GI	g4468986
BLAST score	228
E value	1.0e-18
Match length	153
% identity	32
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]
Seq. No.	279296
Contig ID	94069_1.R1011
5'-most EST	LIB3136-060-Q1-K1-B7
Seq. No.	279297
Contig ID	94076_1.R1011
5'-most EST	LIB3137-016-Q1-K1-F4
Seq. No.	279298
Contig ID	94128_1.R1011
5'-most EST	LIB3137-001-Q1-K1-B8
Seq. No.	279299
Contig ID	94135_1.R1011
5'-most EST	LIB3137-001-Q1-K1-C5
Seq. No.	279300
Contig ID	94139_1.R1011
5'-most EST	LIB3137-001-Q1-K1-C9
Seq. No.	279301
Contig ID	94148_1.R1011
5'-most EST	tzu700204673.h1
Method	BLASTX
NCBI GI	g3702368
BLAST score	609
E value	3.0e-63
Match length	184
% identity	59
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]
Seq. No.	279302
Contig ID	94148_2.R1011
5'-most EST	LIB3137-001-Q1-K1-E10
Method	BLASTX
NCBI GI	g3702368
BLAST score	271
E value	5.0e-24
Match length	90
% identity	54
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No.	279303
Contig ID	94163_1.R1011
5'-most EST	nbm700467967.h1
Method	BLASTX
NCBI GI	g1806617
BLAST score	395
E value	2.0e-44
Match length	194
% identity	47
NCBI Description	(U66167) spindle assembly checkpoint component [Xenopus laevis]

Seq. No.	279304
Contig ID	94171_1.R1011
5'-most EST	LIB3137-001-Q1-K1-G3

Seq. No.	279305
Contig ID	94176_1.R1011
5'-most EST	fC-zmse700614474a1
Method	BLASTX
NCBI GI	g2827715
BLAST score	342
E value	4.0e-32
Match length	151
% identity	50
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	279306
Contig ID	94189_1.R1011
5'-most EST	dyk700106663.h1
Method	BLASTX
NCBI GI	g294845
BLAST score	307
E value	5.0e-28
Match length	91
% identity	66
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	279307
Contig ID	94199_1.R1011
5'-most EST	uC-zmflb73177d08b1
Method	BLASTX
NCBI GI	g2979544
BLAST score	409
E value	7.0e-40
Match length	173
% identity	50
NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	279308
Contig ID	94217_1.R1011
5'-most EST	wty700163954.h1

Seq. No.	279309
Contig ID	94218_1.R1011

5'-most EST	LIB3137-002-Q1-K1-D3
Method	BLASTN
NCBI GI	g257040
BLAST score	57
E value	4.0e-23
Match length	65
% identity	97
NCBI Description	hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No.	279310
Contig ID	94223_1.R1011
5'-most EST	LIB3137-002-Q1-K1-D8
Method	BLASTX
NCBI GI	g3647355
BLAST score	594
E value	3.0e-61
Match length	225
% identity	52
NCBI Description	(Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA

Seq. No.	279311
Contig ID	94229_1.R1011
5'-most EST	LIB3137-002-Q1-K1-E2
Method	BLASTX
NCBI GI	g2104535
BLAST score	628
E value	1.0e-94
Match length	257
% identity	68
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	279312
Contig ID	94229_3.R1011
5'-most EST	tzu700204602.h1
Method	BLASTX
NCBI GI	g3046696
BLAST score	544
E value	7.0e-56
Match length	121
% identity	83
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	279313
Contig ID	94231_1.R1011
5'-most EST	fC-zmf1700381860y1
Method	BLASTX
NCBI GI	g2961371
BLAST score	374
E value	1.0e-35
Match length	217
% identity	41
NCBI Description	(AL022141) hypothetical protein (fragment) [Arabidopsis thaliana]

Seq. No.	279314
Contig ID	94241_1.R1011
5'-most EST	xmt700265273.h1
Method	BLASTX
NCBI GI	g4454471
BLAST score	224
E value	8.0e-27
Match length	123
% identity	52
NCBI Description	(AC006234) putative G protein coupled receptor [Arabidopsis thaliana]

Seq. No.	279315
Contig ID	94242_1.R1011
5'-most EST	uC-zmflb73197b06b1
Method	BLASTX
NCBI GI	g1076385
BLAST score	1911
E value	0.0e+00
Match length	483
% identity	76
NCBI Description	protein kinase (EC 2.7.1.37) tousled - Arabidopsis thaliana >gi_433052 (L23985) protein kinase [Arabidopsis thaliana]

Seq. No.	279316
Contig ID	94260_1.R1011
5'-most EST	uC-zmflMo17065c10b1
Method	BLASTX
NCBI GI	g1076813
BLAST score	1098
E value	1.0e-120
Match length	222
% identity	95
NCBI Description	initiator-binding protein - maize

Seq. No.	279317
Contig ID	94262_1.R1011
5'-most EST	uC-zmflb73226c11b1

Seq. No.	279318
Contig ID	94271_1.R1011
5'-most EST	uwc700150971.h1
Method	BLASTX
NCBI GI	g629561
BLAST score	155
E value	2.0e-15
Match length	127
% identity	39
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	279319
Contig ID	94277_1.R1011
5'-most EST	LIB3137-003-Q1-K1-A6

Seq. No.	279320

Contig ID	94284_1.R1011
5'-most EST	LIB3137-003-Q1-K1-B2

Seq. No.	279321
Contig ID	94295_1.R1011
5'-most EST	uC-zmflmo17168g05b1
Method	BLASTX
NCBI GI	g3142301
BLAST score	198
E value	1.0e-17
Match length	77
% identity	65
NCBI Description	(AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb_M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101, gb_H3630

Seq. No.	279322
Contig ID	94325_1.R1011
5'-most EST	vux700159583.h1
Method	BLASTX
NCBI GI	g882570
BLAST score	278
E value	1.0e-24
Match length	130
% identity	44
NCBI Description	(U28377) ORF_o265; alternate name ygiE; orfB of M77129 [Escherichia coli]

Seq. No.	279323
Contig ID	94329_1.R1011
5'-most EST	xmt700257929.h1
Method	BLASTN
NCBI GI	g22549
BLAST score	56
E value	1.0e-22
Match length	120
% identity	87
NCBI Description	Maize gene for a 27kDa storage protein, zein

Seq. No.	279324
Contig ID	94341_1.R1011
5'-most EST	xjt700093703.h1

Seq. No.	279325
Contig ID	94369_1.R1011
5'-most EST	vux700160737.h1

Seq. No.	279326
Contig ID	94373_1.R1011
5'-most EST	xmt700267951.h1
Method	BLASTX
NCBI GI	g113595
BLAST score	864
E value	3.0e-93
Match length	175

% identity	90
NCBI Description	ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE) >gi_100562_pir__S15024 aldose reductase-related protein - barley >gi_18891_emb_CAA40747_ (X57526) aldose reductase-related protein [Hordeum vulgare]

Seq. No.	279327
Contig ID	94387_1.R1011
5'-most EST	LIB3137-004-Q1-K1-E8
Method	BLASTX
NCBI GI	g1931654
BLAST score	188
E value	4.0e-14
Match length	142
% identity	35
NCBI Description	(U95973) BRCA1-associated RING domain protein isolog [Arabidopsis thaliana]

Seq. No.	279328
Contig ID	94390_1.R1011
5'-most EST	uC-zmromo17111b09a1
Method	BLASTX
NCBI GI	g3913952
BLAST score	159
E value	9.0e-11
Match length	41
% identity	71
NCBI Description	ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi_2351578 (U82330) adenylate kinase homolog [Prunus armeniaca]

Seq. No.	279329
Contig ID	94394_1.R1011
5'-most EST	pmx700087541.h1
Method	BLASTX
NCBI GI	g3421378
BLAST score	519
E value	2.0e-52
Match length	279
% identity	42
NCBI Description	(AF080249) kinesin-like heavy chain [Arabidopsis thaliana]

Seq. No.	279330
Contig ID	94395_1.R1011
5'-most EST	uC-zmrob73055h01b1
Method	BLASTX
NCBI GI	g1171579
BLAST score	410
E value	5.0e-40
Match length	127
% identity	58
NCBI Description	(X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No.	279331
Contig ID	94396_1.R1011
5'-most EST	xjt700095512.h1

Seq. No.	279332

Contig ID	94406_1.R1011
5'-most EST	LIB3137-004-Q1-K1-H3
Method	BLASTX
NCBI GI	g2262101
BLAST score	397
E value	8.0e-39
Match length	109
% identity	78
NCBI Description	(AC002343) kinesin heavy chain isolog [Arabidopsis thaliana]

Seq. No.	279333
Contig ID	94409_1.R1011
5'-most EST	cyk700050915.f1
Method	BLASTX
NCBI GI	g3395425
BLAST score	326
E value	4.0e-30
Match length	117
% identity	40
NCBI Description	(AC004683) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	279334
Contig ID	94457_1.R1011
5'-most EST	LIB3137-005-Q1-K1-E4
Method	BLASTX
NCBI GI	g4409804
BLAST score	182
E value	3.0e-13
Match length	110
% identity	37
NCBI Description	(AF091502) autoaggregation-mediating protein [Lactobacillus reuteri]

Seq. No.	279335
Contig ID	94473_1.R1011
5'-most EST	uC-zmflb73064h04b1
Method	BLASTX
NCBI GI	g2811029
BLAST score	507
E value	2.0e-51
Match length	145
% identity	65
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	279336
Contig ID	94473_2.R1011
5'-most EST	uC-zmflmo17152h02a1
Method	BLASTX
NCBI GI	g3913080
BLAST score	233
E value	8.0e-29
Match length	155

% identity	41
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE (ACOAT) >gi_2650570 (AE001101) acetylornithine aminotransferase (argD-1) [Archaeoglobus fulgidus]
Seq. No.	279337
Contig ID	94474_1.R1011
5'-most EST	LIB3137-005-Q1-K1-G1
Seq. No.	279338
Contig ID	94507_1.R1011
5'-most EST	LIB3137-008-Q1-K1-H8
Seq. No.	279339
Contig ID	94515_1.R1011
5'-most EST	wty700171972.h1
Seq. No.	279340
Contig ID	94516_1.R1011
5'-most EST	LIB3137-006-Q1-K1-G11
Seq. No.	279341
Contig ID	94527_1.R1011
5'-most EST	LIB3137-007-Q1-K1-A6
Seq. No.	279342
Contig ID	94569_1.R1011
5'-most EST	LIB3137-011-Q1-K1-E12
Seq. No.	279343
Contig ID	94577_1.R1011
5'-most EST	mwy700439760.h1
Seq. No.	279344
Contig ID	94586_1.R1011
5'-most EST	LIB3137-008-Q1-K1-A2
Method	BLASTX
NCBI GI	g2252631
BLAST score	377
E value	3.0e-36
Match length	93
% identity	80
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]
Seq. No.	279345
Contig ID	94588_1.R1011
5'-most EST	LIB3137-008-Q1-K1-A4
Seq. No.	279346
Contig ID	94613_1.R1011
5'-most EST	LIB3137-008-Q1-K1-D8
Method	BLASTX
NCBI GI	g3522938
BLAST score	305
E value	1.0e-27
Match length	153
% identity	46

NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.	279347
Contig ID	94629_1.R1011
5'-most EST	ntr700072511.h1
Method	BLASTX
NCBI GI	g1177047
BLAST score	357
E value	8.0e-34
Match length	95
% identity	68
NCBI Description	14 KD ZINC-BINDING PROTEIN (PROTEIN KINASE C INHIBITOR) (PKCI) >gi_629857_pir__S44158 protein kinase C inhibitor - maize >gi_473187_emb_CAA82751_ (Z29643) protein kinase C inhibitor [Zea mays]
Seq. No.	279348
Contig ID	94632_1.R1011
5'-most EST	LIB3137-008-Q1-K1-G7
Seq. No.	279349
Contig ID	94640_2.R1011
5'-most EST	yyf700352425.h1
Seq. No.	279350
Contig ID	94658_1.R1011
5'-most EST	rvt700551538.h1
Seq. No.	279351
Contig ID	94675_1.R1011
5'-most EST	wty700164364.h1
Method	BLASTN
NCBI GI	g1864000
BLAST score	83
E value	1.0e-38
Match length	159
% identity	88
NCBI Description	Maize DNA for Fd III, complete cds
Seq. No.	279352
Contig ID	94690_1.R1011
5'-most EST	LIB3137-009-Q1-K1-E9
Method	BLASTX
NCBI GI	g136125
BLAST score	285
E value	3.0e-25
Match length	92
% identity	61
NCBI Description	PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_ (X05424) ORFa [Zea mays]
Seq. No.	279353
Contig ID	94716_1.R1011
5'-most EST	LIB3137-009-Q1-K1-H5
Method	BLASTX
NCBI GI	g2746086
BLAST score	524

E value	2.0e-53
Match length	128
% identity	76
NCBI Description	(AF025292) putative high-affinity potassium transporter [Hordeum vulgare]

Seq. No.	279354
Contig ID	94720_1.R1011
5'-most EST	fwa700099753.h1
Method	BLASTX
NCBI GI	g3201680
BLAST score	311
E value	4.0e-33
Match length	181
% identity	43
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	279355
Contig ID	94721_1.R1011
5'-most EST	uC-zmflB73005d04b1

Seq. No.	279356
Contig ID	94725_1.R1011
5'-most EST	uC-zmroteosinte009h08b1
Method	BLASTX
NCBI GI	g2506931
BLAST score	206
E value	3.0e-16
Match length	62
% identity	71
NCBI Description	APYRASE PRECURSOR (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE) >gi_2129977_pir__JC4616 apyrase (EC 3.6.1.5) - potato >gi_1381633 (U58597) ATP-diphosphohydrolase [Solanum tuberosum]

Seq. No.	279357
Contig ID	94727_1.R1011
5'-most EST	LIB36-021-Q1-E1-F8
Method	BLASTX
NCBI GI	g4583546
BLAST score	197
E value	6.0e-15
Match length	85
% identity	47
NCBI Description	(AJ010819) GrpE protein [Arabidopsis thaliana]

Seq. No.	279358
Contig ID	94735_1.R1011
5'-most EST	LIB3137-010-Q1-K1-B12

Seq. No.	279359
Contig ID	94744_1.R1011
5'-most EST	wty700168812.h1

Seq. No.	279360
Contig ID	94744_2.R1011

5'-most EST	ceu700432353.h1
Seq. No.	279361
Contig ID	94754_1.R1011
5'-most EST	LIB3137-010-Q1-K1-C9
Method	BLASTX
NCBI GI	g4056420
BLAST score	274
E value	3.0e-24
Match length	112
% identity	52
NCBI Description	(AC005322) ESTs gb_T144077 and gb_T43352 come from this gene. [Arabidopsis thaliana]
Seq. No.	279362
Contig ID	94771_1.R1011
5'-most EST	uC-zmflmo17012c02b1
Method	BLASTX
NCBI GI	g3319357
BLAST score	527
E value	6.0e-82
Match length	236
% identity	67
NCBI Description	(AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
Seq. No.	279363
Contig ID	94795_1.R1011
5'-most EST	LIB3137-010-Q1-K1-G9
Seq. No.	279364
Contig ID	94798_1.R1011
5'-most EST	hbs701182884.h1
Seq. No.	279365
Contig ID	94822_1.R1011
5'-most EST	LIB3137-011-Q1-K1-C10
Method	BLASTX
NCBI GI	g2104535
BLAST score	242
E value	2.0e-20
Match length	68
% identity	72
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]
Seq. No.	279366
Contig ID	94831_1.R1011
5'-most EST	LIB3137-011-Q1-K1-C9
Seq. No.	279367
Contig ID	94833_1.R1011
5'-most EST	uC-zmroteosinte025c07b1
Method	BLASTN
NCBI GI	g287832
BLAST score	60
E value	6.0e-25
Match length	151

% identity	86
NCBI Description	Z.mays yptm1 cDNA
Seq. No.	279368
Contig ID	94834_1.R1011
5'-most EST	LIB3137-011-Q1-K1-D3
Seq. No.	279369
Contig ID	94838_1.R1011
5'-most EST	uC-zmflmo17186a04b1
Seq. No.	279370
Contig ID	94843_2.R1011
5'-most EST	LIB3137-011-Q1-K1-E2
Method	BLASTX
NCBI GI	g2911052
BLAST score	346
E value	1.0e-32
Match length	121
% identity	59
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]
Seq. No.	279371
Contig ID	94845_1.R1011
5'-most EST	uC-zmflb73012a01b1
Seq. No.	279372
Contig ID	94867_1.R1011
5'-most EST	LIB3137-011-Q1-K1-H10
Method	BLASTX
NCBI GI	g2129833
BLAST score	156
E value	3.0e-10
Match length	149
% identity	28
NCBI Description	late embryogenesis abundant protein group 3 (clone pGmPM8) - soybean (fragment)
Seq. No.	279373
Contig ID	94870_1.R1011
5'-most EST	uwc700155414.h1
Method	BLASTX
NCBI GI	g1922242
BLAST score	228
E value	1.0e-18
Match length	74
% identity	65
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]
Seq. No.	279374
Contig ID	94900_1.R1011
5'-most EST	tfd700572649.h1
Method	BLASTX
NCBI GI	g3540201
BLAST score	576
E value	3.0e-59
Match length	150

09604605 - 100600

% identity	73
NCBI Description	(AC004260) Putative nuclear protein [Arabidopsis thaliana]

Seq. No.	279375
Contig ID	94900_2.R1011
5'-most EST	pwr700449927.h1

Seq. No.	279376
Contig ID	94901_1.R1011
5'-most EST	LIB3137-012-Q1-K1-C6

Seq. No.	279377
Contig ID	94904_1.R1011
5'-most EST	uC-zmflmo17312f07b1
Method	BLASTX
NCBI GI	g2832651
BLAST score	274
E value	9.0e-24
Match length	233
% identity	39
NCBI Description	(AL021710) RNA helicase - like protein [Arabidopsis thaliana]

Seq. No.	279378
Contig ID	94926_1.R1011
5'-most EST	LIB3137-012-Q1-K1-F10

Seq. No.	279379
Contig ID	94932_1.R1011
5'-most EST	LIB3137-012-Q1-K1-F5

Seq. No.	279380
Contig ID	94961_1.R1011
5'-most EST	LIB3137-019-Q1-K1-H7
Method	BLASTX
NCBI GI	g4586058
BLAST score	267
E value	2.0e-23
Match length	131
% identity	41
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	279381
Contig ID	94975_1.R1011
5'-most EST	LIB3137-013-Q1-K1-B4
Method	BLASTX
NCBI GI	g505100
BLAST score	231
E value	1.0e-18
Match length	100
% identity	43
NCBI Description	(D31886) KIAA0066 [Homo sapiens]

Seq. No.	279382
Contig ID	94994_1.R1011
5'-most EST	LIB3137-013-Q1-K1-D3
Method	BLASTX

NCBI GI	g3763925
BLAST score	634
E value	4.0e-66
Match length	141
% identity	82
NCBI Description	(AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No.	279383
Contig ID	95013_1.R1011
5'-most EST	uC-zmflmo17333f02b1
Method	BLASTX
NCBI GI	g3695388
BLAST score	176
E value	5.0e-12
Match length	144
% identity	43
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	279384
Contig ID	95028_2.R1011
5'-most EST	gct701168632.h1

Seq. No.	279385
Contig ID	95060_1.R1011
5'-most EST	uC-zmflb73359d08a2

Seq. No.	279386
Contig ID	95060_2.R1011
5'-most EST	LIB3137-014-Q1-K1-C4

Seq. No.	279387
Contig ID	95086_1.R1011
5'-most EST	ymt700221636.h1
Method	BLASTX
NCBI GI	g4220527
BLAST score	174
E value	4.0e-12
Match length	80
% identity	38
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	279388
Contig ID	95102_1.R1011
5'-most EST	LIB3137-060-Q1-K1-D9
Method	BLASTX
NCBI GI	g3777600
BLAST score	290
E value	4.0e-26
Match length	64
% identity	91
NCBI Description	(AF095708) 50S ribosomal protein L5 [Oryza sativa]

Seq. No.	279389
Contig ID	95105_1.R1011
5'-most EST	LIB3137-015-Q1-K1-B4
Method	BLASTX
NCBI GI	g3360289

BLAST score	781
E value	2.0e-83
Match length	185
% identity	81
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	279390
Contig ID	95105_2.R1011
5'-most EST	tfd700571884.h1
Method	BLASTX
NCBI GI	g3360289
BLAST score	546
E value	3.0e-56
Match length	120
% identity	83
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	279391
Contig ID	95111_1.R1011
5'-most EST	LIB3137-015-Q1-K1-C11

Seq. No.	279392
Contig ID	95115_2.R1011
5'-most EST	uC-zmflb73253h09b1

Seq. No.	279393
Contig ID	95129_1.R1011
5'-most EST	LIB3137-015-Q1-K1-E1

Seq. No.	279394
Contig ID	95130_1.R1011
5'-most EST	xjt700092907.h1

Seq. No.	279395
Contig ID	95133_1.R1011
5'-most EST	uC-zmflb73257c08b3
Method	BLASTN
NCBI GI	g2735839
BLAST score	134
E value	3.0e-69
Match length	330
% identity	93
NCBI Description	Sorghum bicolor ADP-glucose pyrophosphorylase subunit SH2, transcriptional regulator, NADPH-dependent reductase A1-a and NADPH-dependent reductase A1-b genes, complete cds

Seq. No.	279396
Contig ID	95134_1.R1011
5'-most EST	uC-zmflmo17054c09b1

Seq. No.	279397
Contig ID	95138_1.R1011
5'-most EST	dyk700106684.h1
Method	BLASTX
NCBI GI	g4490733

BLAST score	375
E value	3.0e-52
Match length	223
% identity	52
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	279398
Contig ID	95150_1.R1011
5'-most EST	LIB3137-015-Q1-K1-G12
Method	BLASTX
NCBI GI	g4538617
BLAST score	185
E value	6.0e-14
Match length	84
% identity	44
NCBI Description	(AJ011316) FolC protein [Methylobacterium sp. CM4]

Seq. No.	279399
Contig ID	95187_1.R1011
5'-most EST	uC-zmflb73223f09b2

Seq. No.	279400
Contig ID	95191_1.R1011
5'-most EST	LIB3137-016-Q1-K1-C3
Method	BLASTX
NCBI GI	g4589852
BLAST score	561
E value	2.0e-65
Match length	216
% identity	58
NCBI Description	(AB025968) cycloartenol synthase [Glycyrrhiza glabra]

Seq. No.	279401
Contig ID	95191_2.R1011
5'-most EST	gct701175404.h1
Method	BLASTX
NCBI GI	g2627181
BLAST score	244
E value	5.0e-21
Match length	86
% identity	53
NCBI Description	(D89619) cycloartenol synthase [Pisum sativum]

Seq. No.	279402
Contig ID	95199_1.R1011
5'-most EST	LIB3137-016-Q1-K1-D12

Seq. No.	279403
Contig ID	95215_1.R1011
5'-most EST	LIB3137-041-Q1-K1-D7
Method	BLASTX
NCBI GI	g746487
BLAST score	147
E value	5.0e-09
Match length	100
% identity	39
NCBI Description	(U23514) No definition line found [Caenorhabditis elegans]

Seq. No.	279404
Contig ID	95228_1.R1011
5'-most EST	uC-zmflmo17071h05b1
Method	BLASTX
NCBI GI	g4586107
BLAST score	263
E value	2.0e-22
Match length	170
% identity	12
NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	279405
Contig ID	95245_1.R1011
5'-most EST	uC-zmflb73151f01b1
Method	BLASTX
NCBI GI	g927577
BLAST score	477
E value	7.0e-48
Match length	119
% identity	73
NCBI Description	(U12927) alpha-galactosidase [Phaseolus vulgaris]

Seq. No.	279406
Contig ID	95263_1.R1011
5'-most EST	LIB3137-017-Q1-K1-B7

Seq. No.	279407
Contig ID	95277_1.R1011
5'-most EST	uC-zmflB73009c10b1

Seq. No.	279408
Contig ID	95284_1.R1011
5'-most EST	LIB3137-059-Q1-K1-E11

Seq. No.	279409
Contig ID	95286_1.R1011
5'-most EST	clt700046217.f1

Seq. No.	279410
Contig ID	95318_1.R1011
5'-most EST	uwc700150364.h1
Method	BLASTX
NCBI GI	g4056427
BLAST score	253
E value	1.0e-21
Match length	129
% identity	50
NCBI Description	(AC005322) Contains similarity to gb_AJ006354 zinc finger protein (ZAC) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	279411
Contig ID	95320_1.R1011
5'-most EST	tzu700202452.h1
Method	BLASTX
NCBI GI	g1871192

BLAST score	641
E value	6.0e-67
Match length	171
% identity	70
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	279412
Contig ID	95362_1.R1011
5'-most EST	wty700172012.h1

Seq. No.	279413
Contig ID	95363_1.R1011
5'-most EST	yne700379581.h1

Seq. No.	279414
Contig ID	95390_1.R1011
5'-most EST	zuv700354507.h1
Method	BLASTX
NCBI GI	g1458245
BLAST score	493
E value	4.0e-49
Match length	266
% identity	41
NCBI Description	(U64834) coded for by C. elegans cDNA cm17a1; coded for by C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis elegans]

Seq. No.	279415
Contig ID	95391_1.R1011
5'-most EST	LIB3137-018-Q1-K1-G11

Seq. No.	279416
Contig ID	95417_2.R1011
5'-most EST	LIB3137-023-Q1-K1-C12

Seq. No.	279417
Contig ID	95423_1.R1011
5'-most EST	xjt700096133.h1
Method	BLASTX
NCBI GI	g3608138
BLAST score	207
E value	3.0e-16
Match length	76
% identity	55
NCBI Description	(AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279418
Contig ID	95427_1.R1011
5'-most EST	LIB3137-019-Q1-K1-B6
Method	BLASTX
NCBI GI	g4586107
BLAST score	685
E value	5.0e-72
Match length	195
% identity	43

NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	279419
Contig ID	95433_1.R1011
5'-most EST	LIB3137-019-Q1-K1-C2
Method	BLASTX
NCBI GI	g2980789
BLAST score	329
E value	1.0e-30
Match length	151
% identity	49
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279420
Contig ID	95436_1.R1011
5'-most EST	pmx700086255.h1

Seq. No.	279421
Contig ID	95451_1.R1011
5'-most EST	LIB3137-019-Q1-K1-E3
Method	BLASTX
NCBI GI	g3201628
BLAST score	1063
E value	1.0e-116
Match length	269
% identity	72
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	279422
Contig ID	95468_1.R1011
5'-most EST	LIB3137-019-Q1-K1-F9
Method	BLASTX
NCBI GI	g537296
BLAST score	175
E value	1.0e-12
Match length	79
% identity	46
NCBI Description	(U13924) chalcone reductase [Medicago sativa subsp. sativa] >gi_1096529_prf__2111449A chalcone reductase [Medicago sativa]

Seq. No.	279423
Contig ID	95476_1.R1011
5'-most EST	LIB3137-019-Q1-K1-G7
Method	BLASTX
NCBI GI	g3135611
BLAST score	319
E value	3.0e-29
Match length	93
% identity	63
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	279424
Contig ID	95487_1.R1011
5'-most EST	yyf700349469.h1
Method	BLASTX

NCBI GI	g2809264
BLAST score	198
E value	7.0e-15
Match length	262
% identity	27
NCBI Description	(AC002560) F21B7.33 [Arabidopsis thaliana]

Seq. No.	279425
Contig ID	95487_2.R1011
5'-most EST	dyk700103918.h1

Seq. No.	279426
Contig ID	95513_1.R1011
5'-most EST	xsy700213637.h1

Seq. No.	279427
Contig ID	95518_1.R1011
5'-most EST	LIB3137-020-Q1-K1-D1
Method	BLASTN
NCBI GI	g312180
BLAST score	67
E value	3.0e-29
Match length	95
% identity	93
NCBI Description	Z.mays GapC4 gene

Seq. No.	279428
Contig ID	95524_1.R1011
5'-most EST	LIB3137-020-Q1-K1-D5
Method	BLASTX
NCBI GI	g4006886
BLAST score	168
E value	5.0e-16
Match length	106
% identity	43
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	279429
Contig ID	95529_1.R1011
5'-most EST	LIB3137-020-Q1-K1-E7

Seq. No.	279430
Contig ID	95536_1.R1011
5'-most EST	LIB3137-020-Q1-K1-E9
Method	BLASTX
NCBI GI	g3806016
BLAST score	173
E value	3.0e-12
Match length	100
% identity	48
NCBI Description	(AF053104) peroxisomal targeting signal 1 receptor; PTS1 receptor; Pex5p [Nicotiana tabacum]

Seq. No.	279431
Contig ID	95551_1.R1011
5'-most EST	nbm700476743.h1
Method	BLASTX

NCBI GI	g4530611
BLAST score	503
E value	5.0e-51
Match length	102
% identity	92
NCBI Description	(AF134552) serine/threonine protein phosphatase PP2A-2 catalytic subunit [Oryza sativa subsp. indica]

Seq. No.	279432
Contig ID	95556_1.R1011
5'-most EST	LIB3137-020-Q1-K1-H1
Method	BLASTX
NCBI GI	g2826786
BLAST score	312
E value	1.0e-28
Match length	90
% identity	74
NCBI Description	(Y10905) RAPB protein [Oryza sativa]

Seq. No.	279433
Contig ID	95590_1.R1011
5'-most EST	LIB3137-043-Q1-K1-D2

Seq. No.	279434
Contig ID	95593_1.R1011
5'-most EST	uC-zmflmo17077a12b1
Method	BLASTX
NCBI GI	g3413511
BLAST score	196
E value	8.0e-15
Match length	71
% identity	52
NCBI Description	(AJ000265) glucose-6-phosphate isomerase [Spinacia oleracea]

Seq. No.	279435
Contig ID	95604_1.R1011
5'-most EST	xjt700096803.h1

Seq. No.	279436
Contig ID	95615_1.R1011
5'-most EST	mwy700438621.h1
Method	BLASTX
NCBI GI	g3582335
BLAST score	646
E value	2.0e-67
Match length	206
% identity	59
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	279437
Contig ID	95618_1.R1011
5'-most EST	xsy700217456.h1

Seq. No.	279438
Contig ID	95625_1.R1011
5'-most EST	uC-zmflmo17077d12b1

Method	BLASTX
NCBI GI	g2288988
BLAST score	171
E value	1.0e-11
Match length	83
% identity	43
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279439
Contig ID	95625_3.R1011
5'-most EST	LIB3137-021-Q1-K1-F8

Seq. No.	279440
Contig ID	95627_1.R1011
5'-most EST	uC-zmflmo17294a01b1
Method	BLASTX
NCBI GI	g1469228
BLAST score	368
E value	5.0e-35
Match length	133
% identity	57
NCBI Description	(Z74841) hypothetical protein [Brassica oleracea]

Seq. No.	279441
Contig ID	95632_1.R1011
5'-most EST	uC-zmflmo17174a09b1
Method	BLASTX
NCBI GI	g4467130
BLAST score	235
E value	2.0e-19
Match length	90
% identity	54
NCBI Description	(AL035538) glycosyltransferase like protein [Arabidopsis thaliana]

Seq. No.	279442
Contig ID	95666_1.R1011
5'-most EST	LIB3137-022-Q1-K1-C9

Seq. No.	279443
Contig ID	95693_1.R1011
5'-most EST	LIB3137-022-Q1-K1-E6

Seq. No.	279444
Contig ID	95697_1.R1011
5'-most EST	LIB3137-022-Q1-K1-F1

Seq. No.	279445
Contig ID	95711_1.R1011
5'-most EST	uC-zmflb73013c02b1
Method	BLASTX
NCBI GI	g1929056
BLAST score	412
E value	2.0e-40
Match length	97
% identity	80
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase

[Lycopersicon esculentum]

Seq. No.	279446
Contig ID	95725_1.R1011
5'-most EST	cjh700196141.h1
Method	BLASTX
NCBI GI	g4544428
BLAST score	255
E value	1.0e-21
Match length	94
% identity	59
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	279447
Contig ID	95725_2.R1011
5'-most EST	xsy700210615.h1
Method	BLASTX
NCBI GI	g4544428
BLAST score	375
E value	5.0e-36
Match length	104
% identity	67
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	279448
Contig ID	95735_1.R1011
5'-most EST	LIB3137-023-Q1-K1-A8

Seq. No.	279449
Contig ID	95735_2.R1011
5'-most EST	ceu700434049.h1

Seq. No.	279450
Contig ID	95738_1.R1011
5'-most EST	tzu700205525.h1
Method	BLASTX
NCBI GI	g3337367
BLAST score	273
E value	6.0e-24
Match length	108
% identity	56
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279451
Contig ID	95752_1.R1011
5'-most EST	xsy700212526.h1
Method	BLASTX
NCBI GI	g2497953
BLAST score	367
E value	5.0e-35
Match length	133
% identity	58
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.	279452
Contig ID	95763_1.R1011
5'-most EST	uC-zmflm017093b12b1
Method	BLASTX
NCBI GI	g2920587
BLAST score	950
E value	1.0e-103
Match length	359
% identity	53
NCBI Description	(AF038362) TBP-associated factor 172 [Homo sapiens] >gi_2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo sapiens]

Seq. No.	279453
Contig ID	95788_1.R1011
5'-most EST	dhd700197950.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	8.0e-11
Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279454
Contig ID	95807_1.R1011
5'-most EST	LIB3137-023-Q1-K1-H10
Method	BLASTX
NCBI GI	g4539295
BLAST score	145
E value	4.0e-09
Match length	58
% identity	53
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	279455
Contig ID	95815_1.R1011
5'-most EST	uC-zmflmo17288e02b1

Seq. No.	279456
Contig ID	95833_1.R1011
5'-most EST	LIB3137-024-Q1-K1-B6

Seq. No.	279457
Contig ID	95839_1.R1011
5'-most EST	LIB3137-024-Q1-K1-C2
Method	BLASTX
NCBI GI	g4559330
BLAST score	462
E value	6.0e-46
Match length	129
% identity	69
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	279458
Contig ID	95865_1.R1011

5'-most EST	uC-zmflb73356h12a2
Method	BLASTX
NCBI GI	g2127717
BLAST score	152
E value	3.0e-09
Match length	125
% identity	29
NCBI Description	2-phosphoglycerate kinase (EC 2.7.2.-) - Methanococcus jannaschii >gi_1592120 (U67589) 2-phosphoglycerate kinase (2pgk) [Methanococcus jannaschii]

Seq. No.	279459
Contig ID	95921_1.R1011
5'-most EST	uC-zmflmo17122a05b1

Seq. No.	279460
Contig ID	95932_1.R1011
5'-most EST	pmx700084239.h1

Seq. No.	279461
Contig ID	95945_1.R1011
5'-most EST	LIB3137-033-Q1-K1-D3

Seq. No.	279462
Contig ID	95946_1.R1011
5'-most EST	LIB3137-027-Q1-K1-E1

Seq. No.	279463
Contig ID	95960_1.R1011
5'-most EST	LIB3137-027-Q1-K1-F11

Seq. No.	279464
Contig ID	95981_1.R1011
5'-most EST	wyr700243169.h1
Method	BLASTX
NCBI GI	g1063666
BLAST score	2352
E value	0.0e+00
Match length	600
% identity	91
NCBI Description	(U38791) unknown [Zea mays]

Seq. No.	279465
Contig ID	95981_4.R1011
5'-most EST	uwc700151089.h1
Method	BLASTN
NCBI GI	g1063665
BLAST score	193
E value	1.0e-104
Match length	319
% identity	55
NCBI Description	Zea mays unknown protein mRNA, complete cds

Seq. No.	279466
Contig ID	95985_1.R1011
5'-most EST	uC-zmroteosinte005f08b1

Seq. No.	279467
Contig ID	95992_1.R1011
5'-most EST	LIB3137-028-Q1-K1-A4
Method	BLASTX
NCBI GI	g2651311
BLAST score	147
E value	2.0e-09
Match length	108
% identity	30
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279468
Contig ID	95994_1.R1011
5'-most EST	LIB3137-028-Q1-K1-A6
Method	BLASTX
NCBI GI	g1076757
BLAST score	249
E value	3.0e-21
Match length	84
% identity	63
NCBI Description	WSI18 protein - rice >gi_537402_dbj_BAA05537_ (D26536) WSI18 protein induced by water stress [Oryza sativa]

Seq. No.	279469
Contig ID	96002_1.R1011
5'-most EST	uC-zmflmo17217g06b1

Seq. No.	279470
Contig ID	96027_1.R1011
5'-most EST	xsy700212254.h1

Seq. No.	279471
Contig ID	96043_1.R1011
5'-most EST	uC-zmflmo17176a11b1

Seq. No.	279472
Contig ID	96044_1.R1011
5'-most EST	uC-zmflb73135h04b2

Seq. No.	279473
Contig ID	96052_1.R1011
5'-most EST	xyt700344715.h1
Method	BLASTX
NCBI GI	g4426607
BLAST score	196
E value	5.0e-15
Match length	94
% identity	47
NCBI Description	(AF092094) AP-4 adaptor complex beta4 subunit [Homo sapiens]

Seq. No.	279474
Contig ID	96066_1.R1011
5'-most EST	LIB3137-062-Q1-K1-G2
Method	BLASTX
NCBI GI	g1488255
BLAST score	412

E value	2.0e-40
Match length	122
% identity	65
NCBI Description	(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana] >gi_2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase (FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574) ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No.	279475
Contig ID	96071_1.R1011
5'-most EST	uC-zmflmo17069f12b1
Method	BLASTX
NCBI GI	g557472
BLAST score	470
E value	1.0e-46
Match length	346
% identity	36
NCBI Description	(U15178) arabinosidase [Bacteroides ovatus]

Seq. No.	279476
Contig ID	96072_1.R1011
5'-most EST	mwy700439374.h1

Seq. No.	279477
Contig ID	96094_1.R1011
5'-most EST	uC-zmflmo17265d07b1

Seq. No.	279478
Contig ID	96094_2.R1011
5'-most EST	LIB3137-029-Q1-K1-C11
Method	BLASTX
NCBI GI	g4006829
BLAST score	468
E value	6.0e-47
Match length	141
% identity	66
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	279479
Contig ID	96096_1.R1011
5'-most EST	LIB3137-029-Q1-K1-C2

Seq. No.	279480
Contig ID	96097_1.R1011
5'-most EST	LIB3137-029-Q1-K1-C3
Method	BLASTX
NCBI GI	g3892709
BLAST score	387
E value	3.0e-37
Match length	147
% identity	57
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	279481
Contig ID	96104_1.R1011
5'-most EST	LIB3137-039-Q1-K1-G11

Seq. No. 279482
Contig ID 96109_1.R1011
5'-most EST uwc700155628.h1

Seq. No. 279483
Contig ID 96110_1.R1011
5'-most EST vux700160889.h1
Method BLASTX
NCBI GI g4314396
BLAST score 171
E value 4.0e-12
Match length 91
% identity 37
NCBI Description (AC006232) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No. 279484
Contig ID 96113_1.R1011
5'-most EST LIB3137-029-Q1-K1-E4

Seq. No. 279485
Contig ID 96114_1.R1011
5'-most EST uC-zmflmo17131e10b1

Seq. No. 279486
Contig ID 96131_1.R1011
5'-most EST LIB3137-029-Q1-K1-F3
Method BLASTX
NCBI GI g3242705
BLAST score 804
E value 4.0e-86
Match length 213
% identity 76
NCBI Description (AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No. 279487
Contig ID 96138_1.R1011
5'-most EST LIB3137-029-Q1-K1-G10

Seq. No. 279488
Contig ID 96150_1.R1011
5'-most EST LIB3137-029-Q1-K1-H12
Method BLASTN
NCBI GI g3819288
BLAST score 46
E value 7.0e-17
Match length 93
% identity 87
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0557.rev

Seq. No. 279489
Contig ID 96153_2.R1011
5'-most EST LIB3137-029-Q1-K1-H4

Seq. No. 279490
Contig ID 96171_1.R1011

5'-most EST	LIB3137-030-Q1-K1-B4
Seq. No.	279491
Contig ID	96187_1.R1011
5'-most EST	uC-zmflb73237e07b2
Seq. No.	279492
Contig ID	96198_1.R1011
5'-most EST	uC-zmflb73116h01b2
Method	BLASTN
NCBI GI	g312180
BLAST score	58
E value	2.0e-23
Match length	137
% identity	86
NCBI Description	Z.mays GapC4 gene
Seq. No.	279493
Contig ID	96204_1.R1011
5'-most EST	xjt700093672.h1
Method	BLASTX
NCBI GI	g3859998
BLAST score	407
E value	1.0e-39
Match length	107
% identity	66
NCBI Description	(AF091080) unknown [Homo sapiens]
Seq. No.	279494
Contig ID	96215_1.R1011
5'-most EST	xsy700211906.h1
Method	BLASTX
NCBI GI	g1899060
BLAST score	554
E value	7.0e-57
Match length	146
% identity	70
NCBI Description	(U79669) endosperm C-24 sterol methyltransferase [Zea mays]
Seq. No.	279495
Contig ID	96215_2.R1011
5'-most EST	fwa700101558.h1
Method	BLASTX
NCBI GI	g3560531
BLAST score	310
E value	3.0e-28
Match length	146
% identity	44
NCBI Description	(AF042332) cycloartenol-C24-methyltransferase [Oryza sativa subsp. japonica]
Seq. No.	279496
Contig ID	96217_1.R1011
5'-most EST	uC-zmflMo17083f12b1
Seq. No.	279497
Contig ID	96221_1.R1011

5'-most EST	LIB3137-030-Q1-K1-G6
Method	BLASTX
NCBI GI	g2746086
BLAST score	808
E value	1.0e-86
Match length	198
% identity	76
NCBI Description	(AF025292) putative high-affinity potassium transporter [Hordeum vulgare]

Seq. No.	279498
Contig ID	96228_1.R1011
5'-most EST	uC-zmflb73234f02b2

Seq. No.	279499
Contig ID	96230_1.R1011
5'-most EST	uC-zmflmo17016d10a1

Seq. No.	279500
Contig ID	96232_1.R1011
5'-most EST	LIB3137-030-Q1-K1-H7

Seq. No.	279501
Contig ID	96240_1.R1011
5'-most EST	uC-zmflm017211g10b1

Seq. No.	279502
Contig ID	96257_1.R1011
5'-most EST	uC-zmroteosinte084d11b1
Method	BLASTX
NCBI GI	g4538920
BLAST score	423
E value	2.0e-41
Match length	114
% identity	75
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	279503
Contig ID	96307_1.R1011
5'-most EST	LIB3137-033-Q1-K1-F2

Seq. No.	279504
Contig ID	96317_1.R1011
5'-most EST	xsy700211565.h1
Method	BLASTX
NCBI GI	g3341695
BLAST score	373
E value	1.0e-35
Match length	128
% identity	55
NCBI Description	(AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	279505
Contig ID	96324_1.R1011
5'-most EST	uwc700153248.h1

Method	BLASTX
NCBI GI	g3850588
BLAST score	305
E value	1.0e-29
Match length	155
% identity	50
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]

Seq. No.	279506
Contig ID	96335_1.R1011
5'-most EST	LIB3137-035-Q1-K1-A1
Method	BLASTX
NCBI GI	g4538903
BLAST score	1128
E value	1.0e-123
Match length	424
% identity	54
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	279507
Contig ID	96343_1.R1011
5'-most EST	uC-zmflb73242b04a1
Method	BLASTX
NCBI GI	g1352468
BLAST score	635
E value	2.0e-66
Match length	143
% identity	89
NCBI Description	BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) >gi_1122439 (U16123) invertase [Zea mays]

Seq. No.	279508
Contig ID	96393_1.R1011
5'-most EST	LIB3137-035-Q1-K1-G5

Seq. No.	279509
Contig ID	96412_1.R1011
5'-most EST	uC-zmrob73033e05b1
Method	BLASTX
NCBI GI	g2911058
BLAST score	311
E value	3.0e-28
Match length	122
% identity	47
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	279510
Contig ID	96419_1.R1011
5'-most EST	xmt700264441.h1

Seq. No.	279511
Contig ID	96449_1.R1011
5'-most EST	LIB3137-036-Q1-K1-F1

Method	BLASTX
NCBI GI	g1354510
BLAST score	564
E value	8.0e-58
Match length	138
% identity	76
NCBI Description	(U55205) HAL2-like protein [Arabidopsis thaliana]

Seq. No.	279512
Contig ID	96471_1.R1011
5'-most EST	uC-zmflmo17122a04b1

Seq. No.	279513
Contig ID	96472_1.R1011
5'-most EST	LIB3137-038-Q1-K1-A12
Method	BLASTN
NCBI GI	g2738749
BLAST score	169
E value	4.0e-90
Match length	295
% identity	94
NCBI Description	Zea mays ATP sulfurylase mRNA, complete cds

Seq. No.	279514
Contig ID	96476_1.R1011
5'-most EST	ceu700434616.h1

Seq. No.	279515
Contig ID	96478_1.R1011
5'-most EST	LIB3137-038-Q1-K1-A8
Method	BLASTN
NCBI GI	g1906603
BLAST score	113
E value	1.0e-56
Match length	298
% identity	85
NCBI Description	Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence

Seq. No.	279516
Contig ID	96491_1.R1011
5'-most EST	pmx700089378.h1
Method	BLASTX
NCBI GI	g2129855
BLAST score	834
E value	1.0e-128
Match length	258
% identity	83
NCBI Description	mitogen-activated protein kinase MMK2 (EC 2.7.1.-) - alfalfa

Seq. No.	279517
Contig ID	96499_1.R1011
5'-most EST	LIB3137-038-Q1-K1-D1
Method	BLASTX
NCBI GI	g2244979

BLAST score	263
E value	5.0e-23
Match length	108
% identity	53
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	279518
Contig ID	96501_1.R1011
5'-most EST	LIB3137-038-Q1-K1-D12

Seq. No.	279519
Contig ID	96505_1.R1011
5'-most EST	uC-zmflb73214h08b1
Method	BLASTX
NCBI GI	g2780365
BLAST score	247
E value	1.0e-20
Match length	92
% identity	53
NCBI Description	(AB007693) Elongin C [Drosophila melanogaster]

Seq. No.	279520
Contig ID	96525_1.R1011
5'-most EST	cat700017962.r1
Method	BLASTX
NCBI GI	g4377315
BLAST score	168
E value	1.0e-11
Match length	90
% identity	39
NCBI Description	(AE001679) YtgB-like predicted rRNA methylase [Chlamydia pneumoniae]

Seq. No.	279521
Contig ID	96539_1.R1011
5'-most EST	uC-zmroteosinte004b05b1

Seq. No.	279522
Contig ID	96574_1.R1011
5'-most EST	xmt700258356.h1
Method	BLASTX
NCBI GI	g3413699
BLAST score	233
E value	4.0e-23
Match length	77
% identity	71
NCBI Description	(AC004747) putative heat shock protein [Arabidopsis thaliana]

Seq. No.	279523
Contig ID	96596_1.R1011
5'-most EST	uC-zmromo17080b10a1

Seq. No.	279524
Contig ID	96600_1.R1011
5'-most EST	LIB3137-039-Q1-K1-E2

Seq. No.	279525
Contig ID	96605_1.R1011
5'-most EST	uwc700155715.h1
Method	BLASTX
NCBI GI	g2833379
BLAST score	178
E value	5.0e-13
Match length	82
% identity	55
NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi_1076397_pir__S51270 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) - Arabidopsis thaliana >gi_633140_emb_CAA58717_ (X83764) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana] >gi_3608149 (AC005314) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana]

Seq. No.	279526
Contig ID	96612_1.R1011
5'-most EST	LIB3137-039-Q1-K1-F3

Seq. No.	279527
Contig ID	96622_1.R1011
5'-most EST	wen700334786.h1

Seq. No.	279528
Contig ID	96635_1.R1011
5'-most EST	uC-zmflmo17027c06a1

Seq. No.	279529
Contig ID	96698_1.R1011
5'-most EST	uC-zmflb73048b11b1

Seq. No.	279530
Contig ID	96713_1.R1011
5'-most EST	LIB3137-040-Q1-K1-H9
Method	BLASTX
NCBI GI	g4097880
BLAST score	624
E value	4.0e-65
Match length	160
% identity	77
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	279531
Contig ID	96716_1.R1011
5'-most EST	uC-zmflb73177h07b1
Method	BLASTX
NCBI GI	g3913464
BLAST score	586
E value	6.0e-61
Match length	138
% identity	86
NCBI Description	BETAINE-ALDEHYDE DEHYDROGENASE (BADH) >gi_2244604_dbj_BAA21098_ (AB001348) betaine aldehyde dehydrogenase [Oryza sativa]

Seq. No.	279532
Contig ID	96718_1.R1011
5'-most EST	dyk700104405.h1
Seq. No.	279533
Contig ID	96721_1.R1011
5'-most EST	uC-zmflb73276g06b1
Seq. No.	279534
Contig ID	96722_1.R1011
5'-most EST	hvj700622686.h1
Method	BLASTX
NCBI GI	g4467159
BLAST score	264
E value	3.0e-23
Match length	75
% identity	60
NCBI Description	(AL035540) hypothetical protein [Arabidopsis thaliana]
Seq. No.	279535
Contig ID	96727_1.R1011
5'-most EST	LIB3137-041-Q1-K1-B5
Method	BLASTX
NCBI GI	g1857256
BLAST score	308
E value	2.0e-28
Match length	90
% identity	58
NCBI Description	(U75360) MURAZC [Zea mays]
Seq. No.	279536
Contig ID	96736_1.R1011
5'-most EST	uC-zmflmo17136h11b1
Seq. No.	279537
Contig ID	96742_2.R1011
5'-most EST	hvj700621539.h1
Seq. No.	279538
Contig ID	96745_1.R1011
5'-most EST	uC-zmflb73344c11a2
Seq. No.	279539
Contig ID	96758_1.R1011
5'-most EST	LIB3137-041-Q1-K1-F11
Seq. No.	279540
Contig ID	96796_1.R1011
5'-most EST	LIB3137-043-Q1-K1-A4
Seq. No.	279541
Contig ID	96798_1.R1011
5'-most EST	uC-zmflmo17044c10b1
Seq. No.	279542
Contig ID	96823_1.R1011

5'-most EST	uC-zmroteosinte009g04b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279543
Contig ID	96837_1.R1011
5'-most EST	uC-zmflB73022g09b1

Seq. No.	279544
Contig ID	96837_2.R1011
5'-most EST	wyr700242543.h1

Seq. No.	279545
Contig ID	96847_1.R1011
5'-most EST	cyk700050345.f1
Method	BLASTX
NCBI GI	g3249088
BLAST score	160
E value	1.0e-10
Match length	68
% identity	46
NCBI Description	(AC004473) Contains similarity to goliath protein gb_M97204 from D. melanogster. [Arabidopsis thaliana]

Seq. No.	279546
Contig ID	96855_1.R1011
5'-most EST	LIB3137-045-Q1-K1-B6
Method	BLASTX
NCBI GI	g1113941
BLAST score	242
E value	2.0e-20
Match length	85
% identity	58
NCBI Description	(U40713) Pv42p [Phaseolus vulgaris]

Seq. No.	279547
Contig ID	96863_1.R1011
5'-most EST	LIB3137-044-Q1-K1-A9

Seq. No.	279548
Contig ID	96870_1.R1011
5'-most EST	wyr700235295.h1
Method	BLASTN
NCBI GI	g1399389
BLAST score	524
E value	0.0e+00
Match length	621
% identity	96
NCBI Description	Zea mays beta-D-glucosidase (glu1) gene, complete cds

Seq. No.	279549
Contig ID	96870_3.R1011

5'-most EST	xsy700208416.h1
Method	BLASTN
NCBI GI	g1518674
BLAST score	105
E value	8.0e-52
Match length	152
% identity	93
NCBI Description	Zea mays beta-D-glucosidase (glu1) gene, intron 10 transposon 2, complete sequence

Seq. No.	279550
Contig ID	96895_1.R1011
5'-most EST	tzu700201761.h1
Method	BLASTX
NCBI GI	g2495714
BLAST score	269
E value	3.0e-23
Match length	228
% identity	32
NCBI Description	HYPOTHETICAL PROTEIN KIAA0188 >gi_1136436_dbj_BAA11505_ (D80010) KIAA0188 [Homo sapiens]

Seq. No.	279551
Contig ID	96897_1.R1011
5'-most EST	nbm700471756.h1

Seq. No.	279552
Contig ID	96940_1.R1011
5'-most EST	uC-zmflb73171h11b1

Seq. No.	279553
Contig ID	96986_1.R1011
5'-most EST	LIB3137-047-Q1-K1-E4
Method	BLASTX
NCBI GI	g2245007
BLAST score	186
E value	7.0e-14
Match length	111
% identity	45
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279554
Contig ID	96996_1.R1011
5'-most EST	yyf700349418.h1
Method	BLASTN
NCBI GI	g829147
BLAST score	237
E value	1.0e-131
Match length	277
% identity	97
NCBI Description	Z.mays gene for cyclophilin

Seq. No.	279555
Contig ID	97011_1.R1011
5'-most EST	fwa700098979.h1
Method	BLASTX
NCBI GI	g3202024

BLAST score	960
E value	1.0e-107
Match length	236
% identity	79
NCBI Description	(AF069315) thylakoid-bound L-ascorbate peroxidase precursor [Mesembryanthemum crystallinum]

Seq. No.	279556
Contig ID	97017_1.R1011
5'-most EST	LIB3137-049-Q1-K1-C11
Method	BLASTX
NCBI GI	g4490706
BLAST score	338
E value	8.0e-32
Match length	116
% identity	54
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	279557
Contig ID	97023_1.R1011
5'-most EST	xsy700212785.h1
Method	BLASTX
NCBI GI	g626598
BLAST score	323
E value	7.0e-30
Match length	160
% identity	42
NCBI Description	hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) >gi_500710 (U10400) Ysc84p [Saccharomyces cerevisiae]

Seq. No.	279558
Contig ID	97042_1.R1011
5'-most EST	uC-zmflb73070d11b1
Method	BLASTX
NCBI GI	g1168654
BLAST score	326
E value	4.0e-53
Match length	170
% identity	59
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) - garden asparagus >gi_452712_emb_CAA54525_ (X77319) beta-galactosidase [Asparagus officinalis]

Seq. No.	279559
Contig ID	97045_1.R1011
5'-most EST	xjt700096975.h1
Method	BLASTX
NCBI GI	g4539346
BLAST score	542
E value	2.0e-58
Match length	234
% identity	58
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	279560

Contig ID	97058_1.R1011
5'-most EST	uC-zmflmo17126c12b1
Method	BLASTX
NCBI GI	g2459435
BLAST score	746
E value	1.0e-146
Match length	355
% identity	69
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	279561
Contig ID	97075_1.R1011
5'-most EST	LIB3137-050-Q1-K1-C1

Seq. No.	279562
Contig ID	97078_1.R1011
5'-most EST	LIB3137-050-Q1-K1-C8
Method	BLASTX
NCBI GI	g4490304
BLAST score	840
E value	2.0e-90
Match length	183
% identity	89
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	279563
Contig ID	97092_1.R1011
5'-most EST	wyr700238946.h1
Method	BLASTX
NCBI GI	g3522946
BLAST score	151
E value	8.0e-10
Match length	66
% identity	44
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	279564
Contig ID	97104_1.R1011
5'-most EST	LIB3137-050-Q1-K1-G12

Seq. No.	279565
Contig ID	97120_1.R1011
5'-most EST	LIB3137-056-Q1-K1-B10

Seq. No.	279566
Contig ID	97128_1.R1011
5'-most EST	LIB3137-056-Q1-K1-G10

Seq. No.	279567
Contig ID	97155_1.R1011
5'-most EST	pmx700086891.h1

Seq. No.	279568
Contig ID	97165_1.R1011
5'-most EST	LIB3137-057-Q1-K1-D9

Seq. No.	279569
Contig ID	97172_1.R1011
5'-most EST	LIB3137-057-Q1-K1-F2

Seq. No.	279570
Contig ID	97192_1.R1011
5'-most EST	LIB83-013-Q1-E1-H2

Seq. No.	279571
Contig ID	97202_1.R1011
5'-most EST	LIB3137-058-Q1-K1-A7
Method	BLASTX
NCBI GI	g4406759
BLAST score	358
E value	8.0e-34
Match length	114
% identity	62
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279572
Contig ID	97210_1.R1011
5'-most EST	wyr700242232.h1
Method	BLASTX
NCBI GI	g3089611
BLAST score	211
E value	8.0e-17
Match length	63
% identity	67
NCBI Description	(AF086791) enolase [Zymomonas mobilis]

Seq. No.	279573
Contig ID	97251_1.R1011
5'-most EST	uC-zmflB73042d01b1

Seq. No.	279574
Contig ID	97286_1.R1011
5'-most EST	uwc700151145.h1
Method	BLASTX
NCBI GI	g2281105
BLAST score	169
E value	9.0e-12
Match length	87
% identity	47
NCBI Description	(AC002333) unknown protein [Arabidopsis thaliana]

Seq. No.	279575
Contig ID	97291_1.R1011
5'-most EST	LIB3137-059-Q1-K1-B7

Seq. No.	279576
Contig ID	97324_1.R1011
5'-most EST	LIB3137-059-Q1-K1-F8

Seq. No.	279577
Contig ID	97325_1.R1011
5'-most EST	LIB3137-059-Q1-K1-F9

Seq. No.	279578
Contig ID	97335_1.R1011
5'-most EST	LIB3137-059-Q1-K1-H1
Method	BLASTX
NCBI GI	g1127575
BLAST score	280
E value	6.0e-25
Match length	53
% identity	83
NCBI Description	(U33817) dhurrinase [Sorghum bicolor]

Seq. No.	279579
Contig ID	97357_1.R1011
5'-most EST	xjt700095627.h1
Method	BLASTX
NCBI GI	g2191152
BLAST score	453
E value	1.0e-44
Match length	224
% identity	45
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	279580
Contig ID	97359_1.R1011
5'-most EST	tzu700201186.h1
Method	BLASTX
NCBI GI	g3386619
BLAST score	230
E value	1.0e-18
Match length	277
% identity	29
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279581
Contig ID	97365_1.R1011
5'-most EST	uC-zmf1b73199g03b1
Method	BLASTX
NCBI GI	g4206210
BLAST score	753
E value	5.0e-80
Match length	245
% identity	57
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	279582
Contig ID	97415_2.R1011
5'-most EST	pmx700086789.h1
Method	BLASTX
NCBI GI	g3377813
BLAST score	187
E value	9.0e-14
Match length	60
% identity	53
NCBI Description	(AF076275) No definition line found [Arabidopsis thaliana]

Seq. No.	279583
Contig ID	97419_1.R1011
5'-most EST	LIB3137-061-Q1-K1-C6
Seq. No.	279584
Contig ID	97424_1.R1011
5'-most EST	xmt700266661.h1
Seq. No.	279585
Contig ID	97427_1.R1011
5'-most EST	uC-zmflmo17179f05b1
Seq. No.	279586
Contig ID	97442_1.R1011
5'-most EST	uC-zmflmo17015f08b1
Method	BLASTX
NCBI GI	g4544389
BLAST score	402
E value	5.0e-39
Match length	194
% identity	46
NCBI Description	(AC007047) putative homeodomain protein [Arabidopsis thaliana]
Seq. No.	279587
Contig ID	97446_1.R1011
5'-most EST	ntr700072078.h1
Seq. No.	279588
Contig ID	97549_1.R1011
5'-most EST	uC-zmflmo17122f06b1
Seq. No.	279589
Contig ID	97552_1.R1011
5'-most EST	uC-zmflb73344b12a2
Seq. No.	279590
Contig ID	97552_2.R1011
5'-most EST	wty700168141.h1
Seq. No.	279591
Contig ID	97552_3.R1011
5'-most EST	xmt700263745.h1
Method	BLASTX
NCBI GI	g3785983
BLAST score	184
E value	9.0e-14
Match length	58
% identity	57
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]
Seq. No.	279592
Contig ID	97554_1.R1011
5'-most EST	LIB3153-004-Q1-K1-C1
Seq. No.	279593

Contig ID	97567_1.R1011
5'-most EST	uC-zmroteosinte034b01b1
Method	BLASTX
NCBI GI	g2497492
BLAST score	528
E value	2.0e-53
Match length	241
% identity	48
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_1653646_dbj_BAA18558_ (D90915) uridine monophosphate kinase [Synechocystis sp.]

Seq. No.	279594
Contig ID	97581_1.R1011
5'-most EST	gct701168471.h1
Method	BLASTX
NCBI GI	g1899175
BLAST score	265
E value	4.0e-72
Match length	206
% identity	78
NCBI Description	(U90262) calcium-dependent calmodulin-independent protein kinase CDPK [Cucurbita pepo]

Seq. No.	279595
Contig ID	97588_1.R1011
5'-most EST	LIB3153-004-Q1-K1-G9
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279596
Contig ID	97590_1.R1011
5'-most EST	xtd700282210.h2

Seq. No.	279597
Contig ID	97595_1.R1011
5'-most EST	gct701173746.h1

Seq. No.	279598
Contig ID	97607_1.R1011
5'-most EST	LIB3153-005-Q1-K1-C7
Method	BLASTX
NCBI GI	g1136434
BLAST score	320
E value	1.0e-29
Match length	122
% identity	55
NCBI Description	(D80009) KIAA0187 [Homo sapiens]

Seq. No.	279599
Contig ID	97647_1.R1011
5'-most EST	uC-zmflmo17070d09b1

Method	BLASTX
NCBI GI	g4033467
BLAST score	525
E value	2.0e-53
Match length	143
% identity	66
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP31 >gi_1707366_emb_CAA67798_ (X99435) splicing factor [Arabidopsis thaliana]

Seq. No.	279600
Contig ID	97651_1.R1011
5'-most EST	ymt700222511.h1
Method	BLASTX
NCBI GI	g2911079
BLAST score	364
E value	2.0e-34
Match length	115
% identity	61
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	279601
Contig ID	97665_1.R1011
5'-most EST	fC-zmst700335261a1
Method	BLASTX
NCBI GI	g2746784
BLAST score	196
E value	7.0e-15
Match length	87
% identity	46
NCBI Description	(AF040642) Similar to amino acid permease [Caenorhabditis elegans]

Seq. No.	279602
Contig ID	97689_1.R1011
5'-most EST	xdb700339806.h1
Method	BLASTX
NCBI GI	g4455293
BLAST score	183
E value	7.0e-14
Match length	59
% identity	61
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	279603
Contig ID	97745_1.R1011
5'-most EST	LIB3153-009-Q1-K1-E5

Seq. No.	279604
Contig ID	97756_1.R1011
5'-most EST	qmh700028072.f1

Seq. No.	279605
Contig ID	97798_1.R1011
5'-most EST	uC-zmflmo17068b05b2

Seq. No.	279606

Contig ID	97798_2.R1011
5'-most EST	yyf700348687.h1

Seq. No.	279607
Contig ID	97800_1.R1011
5'-most EST	tzu700205179.h1
Method	BLASTX
NCBI GI	g2143629
BLAST score	266
E value	7.0e-23
Match length	164
% identity	38
NCBI Description	Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - rat >gi_986941 (L42810) 'Ca2+/calmodulin-dependent protein kinase kinase' [Rattus norvegicus] >gi_1583255_prf__2120334A Ca/calmodulin-dependent protein kinase kinase [Rattus norvegicus]

Seq. No.	279608
Contig ID	97808_1.R1011
5'-most EST	pmx700085954.h1

Seq. No.	279609
Contig ID	97808_2.R1011
5'-most EST	cyk700050488.f1
Method	BLASTX
NCBI GI	g4204263
BLAST score	146
E value	2.0e-09
Match length	42
% identity	55
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	279610
Contig ID	97831_1.R1011
5'-most EST	pmx700082448.h1

Seq. No.	279611
Contig ID	97838_1.R1011
5'-most EST	LIB3153-011-Q1-K1-E11

Seq. No.	279612
Contig ID	97852_1.R1011
5'-most EST	xsy700207524.h1
Method	BLASTX
NCBI GI	g4538974
BLAST score	250
E value	2.0e-21
Match length	79
% identity	61
NCBI Description	(AL049487) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279613
Contig ID	97871_1.R1011
5'-most EST	cyk700050701.f1
Method	BLASTX
NCBI GI	g1403671

BLAST score	176
E value	1.0e-12
Match length	74
% identity	59
NCBI Description	(U34757) phosphoribosylanthranilate isomerase [Arabidopsis thaliana]

Seq. No.	279614
Contig ID	97888_1.R1011
5'-most EST	uC-zmflb73239b07a1

Seq. No.	279615
Contig ID	97903_1.R1011
5'-most EST	cyk700050092.f1
Method	BLASTX
NCBI GI	g4539383
BLAST score	224
E value	6.0e-18
Match length	106
% identity	50
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	279616
Contig ID	97918_1.R1011
5'-most EST	LIB3153-013-Q1-K1-C9

Seq. No.	279617
Contig ID	97926_1.R1011
5'-most EST	uC-zmflb73151e06a2

Seq. No.	279618
Contig ID	97931_2.R1011
5'-most EST	uC-zmflb73078a07b2
Method	BLASTX
NCBI GI	g3402675
BLAST score	200
E value	5.0e-15
Match length	118
% identity	36
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279619
Contig ID	97934_1.R1011
5'-most EST	hbs701183808.h1

Seq. No.	279620
Contig ID	97934_2.R1011
5'-most EST	fdz701164270.h1

Seq. No.	279621
Contig ID	97934_3.R1011
5'-most EST	LIB36-001-Q1-E1-A4

Seq. No.	279622
Contig ID	97942_1.R1011
5'-most EST	fdz701161403.h1

Seq. No.	279623
Contig ID	97943_1.R1011
5'-most EST	rvt700550263.h1

Seq. No.	279624
Contig ID	97944_1.R1011
5'-most EST	uC-zmflb73001h06b1

Seq. No.	279625
Contig ID	97952_1.R1011
5'-most EST	uC-zmroteosinte119b10b1

Seq. No.	279626
Contig ID	97953_1.R1011
5'-most EST	LIB36-001-Q1-E1-C2

Seq. No.	279627
Contig ID	97965_1.R1011
5'-most EST	LIB36-001-Q1-E1-D5
Method	BLASTN
NCBI GI	g5091496
BLAST score	45
E value	5.0e-16
Match length	124
% identity	93
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	279628
Contig ID	97967_1.R1011
5'-most EST	LIB36-001-Q1-E1-D7
Method	BLASTX
NCBI GI	g4056456
BLAST score	550
E value	2.0e-56
Match length	151
% identity	72
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	279629
Contig ID	97978_1.R1011
5'-most EST	uC-zmflmo17091a08a1

Seq. No.	279630
Contig ID	97980_1.R1011
5'-most EST	uC-zmflmo17040e07a1

Seq. No.	279631
Contig ID	97981_1.R1011
5'-most EST	uC-zmflmo17319a02a1

Seq. No.	279632
Contig ID	98005_1.R1011

5'-most EST	LIB36-001-Q1-E1-H4
Seq. No.	279633
Contig ID	98005_2.R1011
5'-most EST	ceu700421604.h1
Seq. No.	279634
Contig ID	98017_1.R1011
5'-most EST	qmh700026265.f1
Seq. No.	279635
Contig ID	98051_1.R1011
5'-most EST	ceu700432527.h1
Seq. No.	279636
Contig ID	98065_1.R1011
5'-most EST	uC-zmflB73043a03b1
Seq. No.	279637
Contig ID	98097_1.R1011
5'-most EST	uC-zmflMo17062g03b1
Method	BLASTX
NCBI GI	g466044
BLAST score	324
E value	1.0e-29
Match length	143
% identity	44
NCBI Description	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi_630780_pir__S44909 ZK686.4 protein - Caenorhabditis elegans >gi_304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]
Seq. No.	279638
Contig ID	98097_2.R1011
5'-most EST	LIB36-003-Q1-E1-A7
Method	BLASTX
NCBI GI	g466044
BLAST score	254
E value	8.0e-22
Match length	88
% identity	50
NCBI Description	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi_630780_pir__S44909 ZK686.4 protein - Caenorhabditis elegans >gi_304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]
Seq. No.	279639
Contig ID	98108_1.R1011
5'-most EST	LIB36-003-Q1-E1-B6
Method	BLASTX
NCBI GI	g2935416
BLAST score	240
E value	3.0e-20
Match length	100
% identity	60

NCBI Description	(AF047896) isoflavone reductase homolog [Betula pendula]
Seq. No.	279640
Contig ID	98108_2.R1011
5'-most EST	clt700041791.f1
Seq. No.	279641
Contig ID	98109_1.R1011
5'-most EST	LIB36-003-Q1-E1-B7
Method	BLASTX
NCBI GI	g2289002
BLAST score	338
E value	3.0e-31
Match length	130
% identity	50
NCBI Description	(AC002335) unknown protein [Arabidopsis thaliana]
Seq. No.	279642
Contig ID	98118_1.R1011
5'-most EST	LIB36-003-Q1-E1-C4
Seq. No.	279643
Contig ID	98127_1.R1011
5'-most EST	LIB84-021-Q1-E1-D8
Seq. No.	279644
Contig ID	98131_1.R1011
5'-most EST	LIB36-003-Q1-E1-D5
Method	BLASTX
NCBI GI	g1711355
BLAST score	204
E value	2.0e-18
Match length	114
% identity	48
NCBI Description	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE >gi_421786_pir__S34678 short-chain alcohol dehydrogenase - Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain alcohol dehydrogenase [Picea abies]
Seq. No.	279645
Contig ID	98137_1.R1011
5'-most EST	LIB36-003-Q1-E1-E10
Method	BLASTX
NCBI GI	g4512683
BLAST score	188
E value	3.0e-14
Match length	54
% identity	65
NCBI Description	(AC006931) putative lipase [Arabidopsis thaliana] >gi_4559323_gb_AAD22985.1_AC007087_4 (AC007087) putative lipase [Arabidopsis thaliana]
Seq. No.	279646
Contig ID	98140_1.R1011
5'-most EST	LIB36-003-Q1-E1-E2
Seq. No.	279647

Contig ID	98156_1.R1011
5'-most EST	LIB36-003-Q1-E1-F8
Method	BLASTX
NCBI GI	g3805956
BLAST score	359
E value	3.0e-34
Match length	117
% identity	55
NCBI Description	(Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	279648
Contig ID	98159_1.R1011
5'-most EST	LIB36-003-Q1-E1-G10

Seq. No.	279649
Contig ID	98194_1.R1011
5'-most EST	LIB36-004-Q1-E1-B12
Method	BLASTX
NCBI GI	g4512678
BLAST score	212
E value	3.0e-36
Match length	136
% identity	65
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	279650
Contig ID	98196_1.R1011
5'-most EST	LIB36-004-Q1-E1-B3
Method	BLASTX
NCBI GI	g461812
BLAST score	413
E value	2.0e-40
Match length	137
% identity	62
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	279651
Contig ID	98199_1.R1011
5'-most EST	uC-zmflb73135a07b2

Seq. No.	279652
Contig ID	98208_1.R1011
5'-most EST	LIB36-004-Q1-E1-C4

Seq. No.	279653
Contig ID	98209_1.R1011
5'-most EST	hbs70i182161.h1

Seq. No.	279654
Contig ID	98219_1.R1011
5'-most EST	LIB83-013-Q1-E1-A11

Seq. No. 279655

Contig ID	98234_1.R1011
5'-most EST	LIB36-004-Q1-E1-F1
Method	BLASTX
NCBI GI	g320622
BLAST score	888
E value	8.0e-96
Match length	173
% identity	98
NCBI Description	probable protein kinase - maize (fragment) >gi_168618 (M62985) protein kinase [Zea mays]

Seq. No.	279656
Contig ID	98243_1.R1011
5'-most EST	mwy700439088.h1
Method	BLASTX
NCBI GI	g2982991
BLAST score	152
E value	1.0e-09
Match length	109
% identity	32
NCBI Description	(AE000682) hypothetical protein [Aquifex aeolicus]

Seq. No.	279657
Contig ID	98254_1.R1011
5'-most EST	LIB36-004-Q1-E1-G9

Seq. No.	279658
Contig ID	98267_1.R1011
5'-most EST	LIB36-005-Q1-E1-A2
Method	BLASTX
NCBI GI	g1652104
BLAST score	226
E value	1.0e-18
Match length	67
% identity	64
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	279659
Contig ID	98271_1.R1011
5'-most EST	LIB36-005-Q1-E1-A6

Seq. No.	279660
Contig ID	98296_1.R1011
5'-most EST	clt700042341.f1
Method	BLASTX
NCBI GI	g4335757
BLAST score	151
E value	1.0e-09
Match length	65
% identity	48
NCBI Description	(AC006284) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279661
Contig ID	98307_1.R1011
5'-most EST	LIB36-005-Q1-E1-D9
Method	BLASTX
NCBI GI	g100347

BLAST score	330
E value	1.0e-30
Match length	78
% identity	79
NCBI Description	monosaccharide transport protein MST1 - common tobacco >gi_19885_emb_CAA47324_ (X66856) monosaccharid transporter [Nicotiana tabacum]

Seq. No.	279662
Contig ID	98320_1.R1011
5'-most EST	LIB36-005-Q1-E1-F1

Seq. No.	279663
Contig ID	98329_1.R1011
5'-most EST	LIB36-005-Q1-E1-F8
Method	BLASTX
NCBI GI	g3298562
BLAST score	199
E value	9.0e-18
Match length	145
% identity	45
NCBI Description	(U91543) zinc-finger helicase [Homo sapiens]

Seq. No.	279664
Contig ID	98370_1.R1011
5'-most EST	LIB36-006-Q1-E1-C1

Seq. No.	279665
Contig ID	98375_1.R1011
5'-most EST	LIB36-006-Q1-E1-C4
Method	BLASTX
NCBI GI	g3927836
BLAST score	250
E value	3.0e-21
Match length	54
% identity	81
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	279666
Contig ID	98381_1.R1011
5'-most EST	uC-zmf1b73242d11b2
Method	BLASTX
NCBI GI	g2589164
BLAST score	586
E value	3.0e-66
Match length	182
% identity	71
NCBI Description	(D88452) aldehyde oxidase-2 [Zea mays]

Seq. No.	279667
Contig ID	98393_1.R1011
5'-most EST	LIB36-006-Q1-E1-E1
Method	BLASTX
NCBI GI	g2773154
BLAST score	283
E value	2.0e-25
Match length	76

% identity	75
NCBI Description	(AF039573) abscisic acid- and stress-inducible protein [Oryza sativa]

Seq. No.	279668
Contig ID	98399_1.R1011
5'-most EST	LIB36-006-Q1-E1-E6

Seq. No.	279669
Contig ID	98413_1.R1011
5'-most EST	LIB36-006-Q1-E1-G11

Seq. No.	279670
Contig ID	98414_1.R1011
5'-most EST	LIB84-008-Q1-E1-G10
Method	BLASTX
NCBI GI	g3776572
BLAST score	783
E value	1.0e-83
Match length	183
% identity	83
NCBI Description	(AC005388) ESTs gb_R65052, gb_AA712146, gb_H76533, gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383, gb_Z29721 and gb_Z29722 come from this gene. [Arabidopsis thaliana]

Seq. No.	279671
Contig ID	98444_1.R1011
5'-most EST	LIB36-007-Q1-E1-B4

Seq. No.	279672
Contig ID	98446_1.R1011
5'-most EST	qmh700028060.f1

Seq. No.	279673
Contig ID	98447_1.R1011
5'-most EST	LIB36-007-Q1-E1-B7
Method	BLASTX
NCBI GI	g4539676
BLAST score	398
E value	9.0e-39
Match length	84
% identity	92
NCBI Description	(AF061282) patatin-like protein [Sorghum bicolor]

Seq. No.	279674
Contig ID	98462_1.R1011
5'-most EST	LIB36-007-Q1-E1-D11

Seq. No.	279675
Contig ID	98491_1.R1011
5'-most EST	fC-zmle700441811f7

Seq. No.	279676
Contig ID	98497_1.R1011
5'-most EST	LIB36-007-Q1-E1-H1
Method	BLASTX

NCBI GI	g82080
BLAST score	265
E value	4.0e-23
Match length	74
% identity	65
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	279677
Contig ID	98502_1.R1011
5'-most EST	fC-zmfl700610775a1

Seq. No.	279678
Contig ID	98503_1.R1011
5'-most EST	uC-zmflb73034e01b2

Seq. No.	279679
Contig ID	98503_2.R1011
5'-most EST	LIB36-007-Q1-E1-H9

Seq. No.	279680
Contig ID	98511_1.R1011
5'-most EST	uC-zmflb73415a03a1

Seq. No.	279681
Contig ID	98544_1.R1011
5'-most EST	LIB36-008-Q1-E1-E4

Seq. No.	279682
Contig ID	98598_1.R1011
5'-most EST	LIB36-009-Q1-E1-D6

Seq. No.	279683
Contig ID	98613_1.R1011
5'-most EST	pmx700083604.h1
Method	BLASTX
NCBI GI	g99486
BLAST score	148
E value	3.0e-09
Match length	41
% identity	66
NCBI Description	chlorophyll a/b-binding protein (clone pINEab 31) - Scotch pine >gi_20792_emb_CAA41406_ (X58516) Type II chlorophyll a /b-binding protein [Pinus sylvestris]

Seq. No.	279684
Contig ID	98635_1.R1011
5'-most EST	LIB84-026-Q1-E1-B10

Seq. No.	279685
Contig ID	98637_1.R1011
5'-most EST	clt700044650.f1
Method	BLASTX
NCBI GI	g4115379
BLAST score	243
E value	3.0e-20

Match length	115
% identity	44
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	279686
Contig ID	98671_1.R1011
5'-most EST	uC-zmflb73063g08b1

Seq. No.	279687
Contig ID	98729_1.R1011
5'-most EST	LIB36-011-Q2-E2-A3
Method	BLASTX
NCBI GI	g3790207
BLAST score	216
E value	3.0e-17
Match length	91
% identity	43
NCBI Description	(AJ222980) delta6-acyl-lipid desaturase [Physcomitrella patens] >gi_3790209_emb_CAA11033_ (AJ222981) delta6-acyl-lipid desaturase [Physcomitrella patens]

Seq. No.	279688
Contig ID	98730_1.R1011
5'-most EST	LIB36-011-Q2-E2-F6

Seq. No.	279689
Contig ID	98757_1.R1011
5'-most EST	LIB36-011-Q2-E2-D10

Seq. No.	279690
Contig ID	98761_1.R1011
5'-most EST	LIB36-011-Q2-E2-D3
Method	BLASTX
NCBI GI	g1170922
BLAST score	509
E value	2.0e-51
Match length	240
% identity	44
NCBI Description	AMMONIUM TRANSPORTER MEP2 >gi_1084510_pir__S51089 ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae) >gi_619514_emb_CAA58587_ (X83608) ammonium transporter [Saccharomyces cerevisiae] >gi_854496_emb_CAA86884_ (Z46843) NH3 permease [Saccharomyces cerevisiae] >gi_1302091_emb_CAA96025_ (Z71418) ORF YNL142w [Saccharomyces cerevisiae]

Seq. No.	279691
Contig ID	98791_1.R1011
5'-most EST	LIB36-011-Q2-E2-H11
Method	BLASTN
NCBI GI	g2618602
BLAST score	283
E value	1.0e-158
Match length	433
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	279692
Contig ID	98835_1.R1011
5'-most EST	LIB36-012-Q1-E1-B9
Method	BLASTX
NCBI GI	g2618699
BLAST score	481
E value	3.0e-48
Match length	163
% identity	55
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	279693
Contig ID	98847_1.R1011
5'-most EST	ymt700218953.h1

Seq. No.	279694
Contig ID	98854_1.R1011
5'-most EST	clt700045308.f1
Method	BLASTX
NCBI GI	g114009
BLAST score	205
E value	1.0e-15
Match length	82
% identity	46
NCBI Description	APAG PROTEIN >gi_72927_pir__BVECAG apaG protein - Escherichia coli >gi_40918_emb_CAA28418_ (X04711) URF (apaG) (AA 1-375) [Escherichia coli] >gi_216475_dbj_BAA01326_ (D10483) apaG protein [Escherichia coli] >gi_1786235 (AE000115) orf, hypothetical protein [Escherichia coli]

Seq. No.	279695
Contig ID	98879_1.R1011
5'-most EST	LIB36-012-Q1-E1-G4
Method	BLASTX
NCBI GI	g3668080
BLAST score	283
E value	5.0e-25
Match length	62
% identity	77
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	279696
Contig ID	98891_1.R1011
5'-most EST	uC-zmflb73160c07b2

Seq. No.	279697
Contig ID	98909_1.R1011
5'-most EST	uC-zmflmo17190h01b1
Method	BLASTX
NCBI GI	g4337177
BLAST score	1514
E value	1.0e-169
Match length	353
% identity	80

NCBI Description	(AC006416) Identical to gb_Y10557 g5bf gene from Arabidopsis thaliana. ESTs gb_R30578, gb_R90475, gb_T22384, gb_T22425, gb_N64934 and gb_T46767 come from this gene. [Arabidopsis thaliana]

Seq. No.	279698
Contig ID	98913_1.R1011
5'-most EST	LIB36-013-Q1-E1-B8
Method	BLASTX
NCBI GI	g4589960
BLAST score	152
E value	7.0e-10
Match length	45
% identity	73
NCBI Description	(AC007169) unknown protein [Arabidopsis thaliana]

Seq. No.	279699
Contig ID	98923_1.R1011
5'-most EST	LIB84-024-Q1-E1-E7

Seq. No.	279700
Contig ID	98926_1.R1011
5'-most EST	LIB36-013-Q1-E1-D1

Seq. No.	279701
Contig ID	98937_1.R1011
5'-most EST	LIB36-013-Q1-E1-D9
Method	BLASTX
NCBI GI	g4539302
BLAST score	149
E value	3.0e-09
Match length	90
% identity	39
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	279702
Contig ID	98989_1.R1011
5'-most EST	cyk70O048496.f1

Seq. No.	279703
Contig ID	98989_2.R1011
5'-most EST	uC-zmflb73073c07b3

Seq. No.	279704
Contig ID	99040_1.R1011
5'-most EST	qmh70O029145.f1
Method	BLASTX
NCBI GI	g2342730
BLAST score	591
E value	4.0e-61
Match length	148
% identity	78
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279705
Contig ID	99046_1.R1011
5'-most EST	ceu70O434582.h1

Seq. No.	279706
Contig ID	99054_1.R1011
5'-most EST	uC-zmflmo17128g05b1
Method	BLASTX
NCBI GI	g3548802
BLAST score	385
E value	6.0e-37
Match length	179
% identity	47
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	279707
Contig ID	99077_1.R1011
5'-most EST	LIB36-015-Q1-E1-D10

Seq. No.	279708
Contig ID	99078_1.R1011
5'-most EST	LIB36-015-Q1-E1-D12
Method	BLASTX
NCBI GI	g1351303
BLAST score	573
E value	3.0e-59
Match length	135
% identity	79
NCBI Description	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS) >gi_619732 (U18770) indole-3-glycerol phosphate synthase [Arabidopsis thaliana]

Seq. No.	279709
Contig ID	99128_1.R1011
5'-most EST	uC-zmflmo17185c03b1

Seq. No.	279710
Contig ID	99129_1.R1011
5'-most EST	xsy700208013.h1

Seq. No.	279711
Contig ID	99131_1.R1011
5'-most EST	LIB36-015-Q1-E1-H8

Seq. No.	279712
Contig ID	99144_1.R1011
5'-most EST	LIB36-016-Q2-E2-A4
Method	BLASTX
NCBI GI	g3080369
BLAST score	271
E value	7.0e-24
Match length	123
% identity	54
NCBI Description	(AL022580) putative protein [Arabidopsis thaliana]

Seq. No.	279713
Contig ID	99145_1.R1011
5'-most EST	LIB36-016-Q2-E2-A5

Method	BLASTX
NCBI GI	g2668505
BLAST score	180
E value	7.0e-13
Match length	89
% identity	40
NCBI Description	(U61837) putative cyclin G1 interacting protein [Homo sapiens]

Seq. No.	279714
Contig ID	99173_1.R1011
5'-most EST	uC-zmroteosinte106h08b2
Method	BLASTX
NCBI GI	g2062169
BLAST score	231
E value	3.0e-35
Match length	165
% identity	49
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	279715
Contig ID	99185_1.R1011
5'-most EST	uC-zmflmo17045a04b1

Seq. No.	279716
Contig ID	99193_1.R1011
5'-most EST	LIB36-016-Q2-E2-F10

Seq. No.	279717
Contig ID	99199_1.R1011
5'-most EST	uC-zmflmo17134e01b1

Seq. No.	279718
Contig ID	99199_2.R1011
5'-most EST	LIB36-016-Q2-E2-F8
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279719
Contig ID	99212_1.R1011
5'-most EST	uC-zmflmo17282h08b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	34
E value	3.0e-09
Match length	34
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279720
Contig ID	99227_1.R1011

5'-most EST	wty700169133.h1
Seq. No.	279721
Contig ID	99229_1.R1011
5'-most EST	hbs701182072.h1
Method	BLASTX
NCBI GI	g2281090
BLAST score	505
E value	3.0e-51
Match length	155
% identity	68
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.	279722
Contig ID	99256_1.R1011
5'-most EST	LIB36-017-Q1-E1-D12
Seq. No.	279723
Contig ID	99266_1.R1011
5'-most EST	LIB36-017-Q1-E1-E10
Seq. No.	279724
Contig ID	99276_1.R1011
5'-most EST	LIB36-017-Q1-E1-F1
Seq. No.	279725
Contig ID	99296_1.R1011
5'-most EST	LIB36-017-Q1-E1-G7
Method	BLASTX
NCBI GI	g2244765
BLAST score	187
E value	5.0e-14
Match length	81
% identity	44
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.	279726
Contig ID	99299_1.R1011
5'-most EST	LIB36-017-Q1-E1-H11
Method	BLASTX
NCBI GI	g1652264
BLAST score	153
E value	8.0e-10
Match length	128
% identity	31
NCBI Description	(D90904) hypothetical protein [Synechocystis sp.]
Seq. No.	279727
Contig ID	99318_1.R1011
5'-most EST	uC-zmroteosinte010c07b1
Method	BLASTX
NCBI GI	g2392772
BLAST score	265
E value	6.0e-23
Match length	87
% identity	57
NCBI Description	(AC002534) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No.	279728
Contig ID	99320_1.R1011
5'-most EST	clt70̄044561.f1
Method	BLASTX
NCBI GI	g3402675
BLAST score	163
E value	5.0e-11
Match length	74
% identity	46
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279729
Contig ID	99376_1.R1011
5'-most EST	ceu70̄427934.h1

Seq. No.	279730
Contig ID	99417_1.R1011
5'-most EST	LIB36-019-Q1-E1-D1
Method	BLASTX
NCBI GI	g464367
BLAST score	184
E value	1.0e-13
Match length	93
% identity	42
NCBI Description	POLYGALACTURONASE INHIBITOR PRECURSOR (POLYGALACTURONASE-INHIBITING PROTEIN) >gi_543660_pir__JQ2262 Polygalacturonase inhibitor precursor - Pyrus communis >gi_169684 (L09264) polygalacturonase inhibitor [Pyrus communis]

Seq. No.	279731
Contig ID	99443_1.R1011
5'-most EST	LIB36-019-Q1-E1-F6

Seq. No.	279732
Contig ID	99460_1.R1011
5'-most EST	clt70̄045841.f1

Seq. No.	279733
Contig ID	99461_1.R1011
5'-most EST	wyr70̄243408.h1

Seq. No.	279734
Contig ID	99464_1.R1011
5'-most EST	LIB36-019-Q1-E1-H8

Seq. No.	279735
Contig ID	99479_1.R1011
5'-most EST	hbs70̄185722.h1
Method	BLASTX
NCBI GI	g3646451
BLAST score	198
E value	6.0e-15
Match length	136
% identity	36

NCBI Description	(AL031603) mRNA cap methyltransferase [Schizosaccharomyces pombe]

Seq. No.	279736
Contig ID	99484_1.R1011
5'-most EST	LIB36-020-Q1-E1-B6
Method	BLASTX
NCBI GI	g400890
BLAST score	263
E value	6.0e-23
Match length	113
% identity	41
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	279737
Contig ID	99490_1.R1011
5'-most EST	wyr700236232.h1

Seq. No.	279738
Contig ID	99500_1.R1011
5'-most EST	LIB36-020-Q1-E1-D10
Method	BLASTX
NCBI GI	g3522946
BLAST score	604
E value	2.0e-62
Match length	299
% identity	45
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	279739
Contig ID	99502_1.R1011
5'-most EST	uC-zmflmo17133h12b1

Seq. No.	279740
Contig ID	99504_1.R1011
5'-most EST	LIB36-020-Q1-E1-D4
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279741
Contig ID	99505_1.R1011
5'-most EST	ceu700423866.h1

Seq. No.	279742
Contig ID	99515_1.R1011
5'-most EST	LIB36-020-Q1-E1-E5

Seq. No.	279743
Contig ID	99516_1.R1011
5'-most EST	mwy700441662.h1
Method	BLASTX
NCBI GI	g1001794
BLAST score	433
E value	2.0e-42
Match length	148
% identity	52
NCBI Description	(D64005) hypothetical protein [Synechocystis sp.]

Seq. No.	279744
Contig ID	99523_1.R1011
5'-most EST	LIB36-020-Q1-E1-F2

Seq. No.	279745
Contig ID	99525_1.R1011
5'-most EST	yyf700351294.h1
Method	BLASTX
NCBI GI	g3834303
BLAST score	383
E value	8.0e-37
Match length	123
% identity	66
NCBI Description	(AC005679) F9K20.3 [Arabidopsis thaliana]

Seq. No.	279746
Contig ID	99529_1.R1011
5'-most EST	LIB84-028-Q1-E1-C7
Method	BLASTX
NCBI GI	g4512678
BLAST score	233
E value	6.0e-19
Match length	168
% identity	38
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	279747
Contig ID	99536_1.R1011
5'-most EST	LIB36-020-Q1-E1-G4

Seq. No.	279748
Contig ID	99543_1.R1011
5'-most EST	LIB36-020-Q1-E1-H10

Seq. No.	279749
Contig ID	99548_1.R1011
5'-most EST	uC-zmflmo17310e12b1
Method	BLASTX
NCBI GI	g4204278
BLAST score	387
E value	5.0e-37
Match length	158
% identity	47
NCBI Description	(AC004146) putative Cytochrome P450 protein [Arabidopsis thaliana]

Seq. No.	279750
Contig ID	99551_1.R1011
5'-most EST	mwy700440344.h1
Seq. No.	279751
Contig ID	99558_1.R1011
5'-most EST	LIB84-022-Q1-E1-E6
Seq. No.	279752
Contig ID	99581_1.R1011
5'-most EST	wty700169404.h1
Seq. No.	279753
Contig ID	99586_1.R1011
5'-most EST	LIB36-021-Q1-E1-D5
Method	BLASTX
NCBI GI	g730138
BLAST score	582
E value	4.0e-60
Match length	130
% identity	82
NCBI Description	NITRATE REDUCTASE (NR)
Seq. No.	279754
Contig ID	99587_1.R1011
5'-most EST	uC-zmflmo17262b03b1
Seq. No.	279755
Contig ID	99598_1.R1011
5'-most EST	dyk700106757.h1
Method	BLASTX
NCBI GI	g1070358
BLAST score	523
E value	3.0e-53
Match length	124
% identity	84
NCBI Description	(X93171) oxalate oxidase-like protein or germin-like protein [Hordeum vulgare]
Seq. No.	279756
Contig ID	99615_1.R1011
5'-most EST	uC-zmflmo17393a02a1
Seq. No.	279757
Contig ID	99675_1.R1011
5'-most EST	xsy700213462.h1
Method	BLASTX
NCBI GI	g1655536
BLAST score	512
E value	6.0e-52
Match length	193
% identity	51
NCBI Description	(Y09095) chloride channel [Arabidopsis thaliana] >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel protein [Arabidopsis thaliana]
Seq. No.	279758

Contig ID	99676_1.R1011
5'-most EST	LIB36-022-Q1-E1-E10
Method	BLASTX
NCBI GI	g3386604
BLAST score	373
E value	1.0e-35
Match length	161
% identity	49
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	279759
Contig ID	99701_1.R1011
5'-most EST	LIB36-022-Q1-E1-G4

Seq. No.	279760
Contig ID	99705_1.R1011
5'-most EST	uC-zmflMo17003d03b1

Seq. No.	279761
Contig ID	99706_1.R1011
5'-most EST	tzu700205038.h1
Method	BLASTX
NCBI GI	g3249064
BLAST score	288
E value	1.0e-25
Match length	108
% identity	56
NCBI Description	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4 contig gb_Z97344. [Arabidopsis thaliana]

Seq. No.	279762
Contig ID	99724_1.R1011
5'-most EST	LIB83-001-Q1-E1-A6

Seq. No.	279763
Contig ID	99727_1.R1011
5'-most EST	xsy700213754.h1
Method	BLASTX
NCBI GI	g731834
BLAST score	148
E value	3.0e-09
Match length	77
% identity	49
NCBI Description	HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION >gi_1077790_pir__S49797 hypothetical protein YIL083c - yeast (Saccharomyces cerevisiae) >gi_577131_emb_CAA86711.1_ (Z46728) YI9910.13c, unknown orf, len: 365, CAI: 0.17 [Saccharomyces cerevisiae]

Seq. No.	279764
Contig ID	99732_1.R1011
5'-most EST	LIB83-001-Q1-E1-B2

Seq. No.	279765
Contig ID	99742_1.R1011
5'-most EST	rvl700457960.h1

Method	BLASTX
NCBI GI	g3201969
BLAST score	558
E value	3.0e-57
Match length	159
% identity	61
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No.	279766
Contig ID	99746_1.R1011
5'-most EST	uC-zmrob73051c01a1
Method	BLASTX
NCBI GI	g3668087
BLAST score	786
E value	8.0e-84
Match length	200
% identity	46
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279767
Contig ID	99747_1.R1011
5'-most EST	LIB83-001-Q1-E1-C7
Method	BLASTX
NCBI GI	g3122818
BLAST score	221
E value	8.0e-18
Match length	101
% identity	40
NCBI Description	30S RIBOSOMAL PROTEIN S6 >gi_2196757 (AF003196) ribosomal protein S6 [Neisseria gonorrhoeae]

Seq. No.	279768
Contig ID	99766_1.R1011
5'-most EST	uC-zmflmo17159c11b1

Seq. No.	279769
Contig ID	99766_2.R1011
5'-most EST	LIB83-001-Q1-E1-E8

Seq. No.	279770
Contig ID	99772_1.R1011
5'-most EST	uC-zmflb73401f09a1

Seq. No.	279771
Contig ID	99794_1.R1011
5'-most EST	LIB83-001-Q1-E1-H3

Seq. No.	279772
Contig ID	99797_1.R1011
5'-most EST	gct701176804.h1

Seq. No.	279773
Contig ID	99800_1.R1011
5'-most EST	LIB83-002-Q1-E1-A10
Method	BLASTX
NCBI GI	g3135274
BLAST score	538

E value	4.0e-55
Match length	138
% identity	72
NCBI Description	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	279774
Contig ID	99882_1.R1011
5'-most EST	ceu700425893.h1

Seq. No.	279775
Contig ID	99890_1.R1011
5'-most EST	uer700582915.h1
Method	BLASTX
NCBI GI	g3426035
BLAST score	327
E value	1.0e-31
Match length	106
% identity	64
NCBI Description	(AC005168) putative ripening-associated protein [Arabidopsis thaliana]

Seq. No.	279776
Contig ID	99898_1.R1011
5'-most EST	LIB83-003-Q1-E1-B10

Seq. No.	279777
Contig ID	99899_1.R1011
5'-most EST	LIB83-003-Q1-E1-B11

Seq. No.	279778
Contig ID	99904_1.R1011
5'-most EST	LIB83-003-Q1-E1-B5

Seq. No.	279779
Contig ID	99915_1.R1011
5'-most EST	fdz701162862.h1

Seq. No.	279780
Contig ID	99916_1.R1011
5'-most EST	LIB83-003-Q1-E1-C6

Seq. No.	279781
Contig ID	99928_1.R1011
5'-most EST	uer700579569.h1

Seq. No.	279782
Contig ID	99935_1.R1011
5'-most EST	LIB83-003-Q1-E1-E6
Method	BLASTX
NCBI GI	g1931640
BLAST score	531
E value	4.0e-54
Match length	160
% identity	59
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	279783
Contig ID	99937_1.R1011
5'-most EST	LIB83-003-Q1-E1-E8

Seq. No.	279784
Contig ID	99938_1.R1011
5'-most EST	uC-zmroteosinte046b07b1
Method	BLASTX
NCBI GI	g3877656
BLAST score	444
E value	7.0e-44
Match length	228
% identity	25
NCBI Description	(Z72511) similar to nucleotide translocator [Caenorhabditis elegans]

Seq. No.	279785
Contig ID	99941_1.R1011
5'-most EST	LIB84-015-Q1-E1-E4

Seq. No.	279786
Contig ID	99949_1.R1011
5'-most EST	LIB84-008-Q1-E1-A10
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279787
Contig ID	99955_1.R1011
5'-most EST	uC-zmflb73170h07a1

Seq. No.	279788
Contig ID	99959_1.R1011
5'-most EST	uC-zmflmo17294d11b1

Seq. No.	279789
Contig ID	99959_3.R1011
5'-most EST	uC-zmflb73242b09b1
Method	BLASTX
NCBI GI	g2739387
BLAST score	184
E value	1.0e-13
Match length	70
% identity	49
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279790
Contig ID	99965_1.R1011
5'-most EST	uC-zmflmo17235h08b1
Method	BLASTX
NCBI GI	g2134385
BLAST score	765

E value	3.0e-81
Match length	238
% identity	63
NCBI Description	protein kinase - chicken >gi_571460 (U16656) protein kinase [Gallus gallus]

Seq. No.	279791
Contig ID	99969_1.R1011
5'-most EST	uC-zmflb73172c12b2

Seq. No.	279792
Contig ID	99977_1.R1011
5'-most EST	LIB83-004-Q1-E1-C10

Seq. No.	279793
Contig ID	99984_1.R1011
5'-most EST	LIB83-004-Q1-E2-D9

Seq. No.	279794
Contig ID	99984_2.R1011
5'-most EST	hbs701181027.h1

Seq. No.	279795
Contig ID	99986_1.R1011
5'-most EST	LIB83-004-Q1-E2-E9

Seq. No.	279796
Contig ID	99987_1.R1011
5'-most EST	uC-zmflmo17139e09b1
Method	BLASTX
NCBI GI	g3881189
BLAST score	449
E value	2.0e-44
Match length	112
% identity	72
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No.	279797
Contig ID	99988_1.R1011
5'-most EST	LIB83-004-Q1-E1-F9

Seq. No.	279798
Contig ID	99994_1.R1011
5'-most EST	ceu700429335.h1

Seq. No.	279799
Contig ID	99994_2.R1011
5'-most EST	ceu700428791.h1

Seq. No.	279800
Contig ID	100000_1.R1011
5'-most EST	LIB83-004-Q1-E2-A4
Method	BLASTX
NCBI GI	g4587610

BLAST score	635
E value	2.0e-66
Match length	175
% identity	67
NCBI Description	(AC006951) putative indole-3-glycerol phosphate synthase precursor [Arabidopsis thaliana]

Seq. No.	279801
Contig ID	100003_1.R1011
5'-most EST	wyr700238769.h1
Method	BLASTX
NCBI GI	g4455338
BLAST score	1071
E value	1.0e-117
Match length	361
% identity	61
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	279802
Contig ID	100013_1.R1011
5'-most EST	wen700335069.h1
Method	BLASTX
NCBI GI	g3759177
BLAST score	308
E value	5.0e-28
Match length	83
% identity	72
NCBI Description	(AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807.1_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No.	279803
Contig ID	100019_1.R1011
5'-most EST	pmx700091728.h1
Method	BLASTX
NCBI GI	g3413706
BLAST score	432
E value	2.0e-42
Match length	134
% identity	57
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279804
Contig ID	100020_1.R1011
5'-most EST	LIB83-004-Q1-E2-C4
Method	BLASTX
NCBI GI	g4588002
BLAST score	562
E value	1.0e-57
Match length	164
% identity	59
NCBI Description	(AF085279) hypothetical ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	279805
Contig ID	100023_1.R1011
5'-most EST	uC-zmroteosinte016f09b1

Seq. No. 279806
Contig ID 100031_1.R1011
5'-most EST uC-zmrob73053f05a1

Seq. No. 279807
Contig ID 100033_1.R1011
5'-most EST LIB83-004-Q1-E2-D5

Seq. No. 279808
Contig ID 100035_1.R1011
5'-most EST ceu700428236.h1

Seq. No. 279809
Contig ID 100062_1.R1011
5'-most EST LIB83-009-Q1-E1-E2

Seq. No. 279810
Contig ID 100065_1.R1011
5'-most EST bdu700382307.h1
Method BLASTX
NCBI GI g3738297
BLAST score 822
E value 1.0e-87
Match length 305
% identity 34
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 279811
Contig ID 100066_1.R1011
5'-most EST LIB83-004-Q1-E2-G6

Seq. No. 279812
Contig ID 100070_1.R1011
5'-most EST LIB83-004-Q1-E2-H1

Seq. No. 279813
Contig ID 100073_1.R1011
5'-most EST uC-zmflmo17245h08b1

Seq. No. 279814
Contig ID 100078_1.R1011
5'-most EST pwr700452145.h1
Method BLASTX
NCBI GI g4455326
BLAST score 387
E value 9.0e-46
Match length 145
% identity 63
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 279815
Contig ID 100079_1.R1011
5'-most EST LIB83-004-Q1-E2-H8
Method BLASTX
NCBI GI g3135257
BLAST score 257

E value 3.0e-22
Match length 68
% identity 74
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 279816
Contig ID 100079_2.R1011
5'-most EST uC-zmflb73405e03a2

Seq. No. 279817
Contig ID 100082_1.R1011
5'-most EST dyk700106666.h1

Seq. No. 279818
Contig ID 100098_1.R1011
5'-most EST LIB83-005-Q1-E1-B4

Seq. No. 279819
Contig ID 100101_1.R1011
5'-most EST mwy700441209.h1

Seq. No. 279820
Contig ID 100121_1.R1011
5'-most EST LIB83-005-Q1-E1-D3

Seq. No. 279821
Contig ID 100122_1.R1011
5'-most EST LIB83-005-Q1-E1-D4

Seq. No. 279822
Contig ID 100131_1.R1011
5'-most EST LIB83-005-Q1-E1-E12

Seq. No. 279823
Contig ID 100144_1.R1011
5'-most EST pmx700086978.h1

Seq. No. 279824
Contig ID 100145_1.R1011
5'-most EST zuv700354263.h1
Method BLASTX
NCBI GI g2460251
BLAST score 840
E value 2.0e-90
Match length 186
% identity 88
NCBI Description (AF020791) ferrochelatase [Hordeum vulgare]

Seq. No. 279825
Contig ID 100146_1.R1011
5'-most EST LIB83-005-Q1-E1-F5
Method BLASTX
NCBI GI g2149640
BLAST score 248
E value 6.0e-21
Match length 166
% identity 34

NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	279826
Contig ID	100155_1.R1011
5'-most EST	wyr700244120.h1
Method	BLASTX
NCBI GI	g3023946
BLAST score	350
E value	2.0e-32
Match length	304
% identity	32
NCBI Description	HIRA PROTEIN (TUP1 LIKE ENHANCER OF SPLIT PROTEIN 1) >gi_2352031 (U94324) Tuple1/HirA [Fugu rubripes] >gi_2352036 (U94325) Tuple1/HirA [Fugu rubripes]

Seq. No.	279827
Contig ID	100159_1.R1011
5'-most EST	LIB83-005-Q1-E1-G6
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	279828
Contig ID	100160_1.R1011
5'-most EST	LIB83-005-Q1-E1-G7
Method	BLASTX
NCBI GI	g961450
BLAST score	258
E value	3.0e-22
Match length	140
% identity	39
NCBI Description	(D63879) KIAA0156 gene product is related to Xenopus nucleolin. [Homo sapiens]

Seq. No.	279829
Contig ID	100163_1.R1011
5'-most EST	uC-zmflmo17074g04b1
Method	BLASTX
NCBI GI	g4490310
BLAST score	382
E value	7.0e-55
Match length	211
% identity	55
NCBI Description	(AL035678) somatic embryogenesis receptor-like kinase-like protein [Arabidopsis thaliana]

Seq. No.	279830
Contig ID	100167_1.R1011
5'-most EST	LIB83-005-Q1-E1-H2
Method	BLASTX
NCBI GI	g4263704
BLAST score	268
E value	2.0e-23

Match length	101
% identity	50
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	279831
Contig ID	100168_1.R1011
5'-most EST	LIB83-005-Q1-E1-H3

Seq. No.	279832
Contig ID	100172_1.R1011
5'-most EST	uC-zmflb73256f01a1
Method	BLASTX
NCBI GI	g118023
BLAST score	162
E value	3.0e-11
Match length	32
% identity	97
NCBI Description	CYTOCHROME C >gi_65506_pir__CCPO cytochrome c - potato (tentative sequence)

Seq. No.	279833
Contig ID	100180_1.R1011
5'-most EST	LIB83-006-Q1-E1-A4
Method	BLASTX
NCBI GI	g1364059
BLAST score	397
E value	2.0e-38
Match length	150
% identity	49
NCBI Description	dioscorin class A precursor - Dioscorea cayenensis >gi_433463_emb_CAA53781_ (X76187) storage protein [Dioscorea cayenensis]

Seq. No.	279834
Contig ID	100182_1.R1011
5'-most EST	uC-zmflmo17292e05a1

Seq. No.	279835
Contig ID	100190_1.R1011
5'-most EST	uC-zmflmo17154a05b1
Method	BLASTX
NCBI GI	g4220515
BLAST score	265
E value	4.0e-23
Match length	77
% identity	61
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	279836
Contig ID	100208_1.R1011
5'-most EST	uC-zmflmo17310d05b1

Seq. No.	279837
Contig ID	100211_1.R1011
5'-most EST	LIB83-010-Q1-E1-H5

Seq. No.	279838
Contig ID	100212_1.R1011
5'-most EST	pwr700452860.h1
Method	BLASTX
NCBI GI	g2245081
BLAST score	530
E value	5.0e-54
Match length	199
% identity	54
NCBI Description	(Z97343) myosin II heavy chain homolog [Arabidopsis thaliana]

Seq. No.	279839
Contig ID	100225_1.R1011
5'-most EST	uC-zmflb73079c02b2
Method	BLASTX
NCBI GI	g3377509
BLAST score	562
E value	9.0e-58
Match length	113
% identity	95
NCBI Description	(AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No.	279840
Contig ID	100238_1.R1011
5'-most EST	LIB83-006-Q1-E1-F5

Seq. No.	279841
Contig ID	100254_1.R1011
5'-most EST	LIB83-006-Q1-E1-H1
Method	BLASTX
NCBI GI	g3548809
BLAST score	447
E value	2.0e-44
Match length	154
% identity	53
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	279842
Contig ID	100263_1.R1011
5'-most EST	LIB83-006-Q1-E1-H7

Seq. No.	279843
Contig ID	100268_1.R1011
5'-most EST	uC-zmflmo17040c11b1
Method	BLASTX
NCBI GI	g3150404
BLAST score	156
E value	2.0e-10
Match length	77
% identity	49
NCBI Description	(AC004165) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	279844
Contig ID	100271_1.R1011
5'-most EST	LIB83-007-Q1-E1-A4

Method	BLASTX
NCBI GI	g4455301
BLAST score	747
E value	2.0e-79
Match length	188
% identity	78
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	279845
Contig ID	100274_1.R1011
5'-most EST	uC-zmroteosinte082c02b2
Method	BLASTX
NCBI GI	g2262113
BLAST score	234
E value	3.0e-19
Match length	250
% identity	38
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	279846
Contig ID	100283_1.R1011
5'-most EST	uC-zmflmo17198a07b1

Seq. No.	279847
Contig ID	100289_1.R1011
5'-most EST	wty700173085.h1
Method	BLASTX
NCBI GI	g2286155
BLAST score	520
E value	8.0e-71
Match length	149
% identity	92
NCBI Description	(AF007582) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase [Zea mays]

Seq. No.	279848
Contig ID	100292_1.R1011
5'-most EST	wyr700237839.h1
Method	BLASTX
NCBI GI	g560610
BLAST score	187
E value	5.0e-14
Match length	40
% identity	65
NCBI Description	trypsin inhibitor, WTI [Triticum aestivum=wheat, variety San Pastore, endosperm, Peptide, 71 aa]

Seq. No.	279849
Contig ID	100293_1.R1011
5'-most EST	LIB83-007-Q1-E1-C4
Method	BLASTX
NCBI GI	g4539394
BLAST score	517
E value	1.0e-52
Match length	169
% identity	56

NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

Seq. No. 279850
Contig ID 100301_1.R1011
5'-most EST uC-zmflb73144e07b1

Seq. No. 279851
Contig ID 100310_1.R1011
5'-most EST hvj700622846.h1

Seq. No. 279852
Contig ID 100311_1.R1011
5'-most EST LIB83-007-Q1-E1-E11
Method BLASTX
NCBI GI g4544445
BLAST score 489
E value 5.0e-61
Match length 160
% identity 68
NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]

Seq. No. 279853
Contig ID 100317_1.R1011
5'-most EST LIB83-007-Q1-E1-E6

Seq. No. 279854
Contig ID 100330_1.R1011
5'-most EST qmh700029246.f1

Seq. No. 279855
Contig ID 100339_1.R1011
5'-most EST uer700580914.h1
Method BLASTX
NCBI GI g4567225
BLAST score 169
E value 1.0e-11
Match length 88
% identity 42
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 279856
Contig ID 100353_1.R1011
5'-most EST uC-zmflm017211b11b1
Method BLASTX
NCBI GI g2576255
BLAST score 559
E value 5.0e-57
Match length 187
% identity 63
NCBI Description (AJ001729) TH65 protein [Arabidopsis thaliana]

Seq. No. 279857
Contig ID 100353_2.R1011
5'-most EST fwa700099620.h1
Method BLASTX
NCBI GI g2576255

BLAST score	190
E value	1.0e-14
Match length	86
% identity	49
NCBI Description	(AJ001729) TH65 protein [Arabidopsis thaliana]

Seq. No.	279858
Contig ID	100362_1.R1011
5'-most EST	cat700016610.r1

Seq. No.	279859
Contig ID	100373_1.R1011
5'-most EST	nbm700474494.h1
Method	BLASTN
NCBI GI	g3450841
BLAST score	60
E value	6.0e-25
Match length	159
% identity	91
NCBI Description	Oryza sativa mitogen activated protein kinase kinase (MEK1) mRNA, complete cds

Seq. No.	279860
Contig ID	100375_1.R1011
5'-most EST	xyt700346396.h1

Seq. No.	279861
Contig ID	100376_1.R1011
5'-most EST	LIB83-008-Q1-E1-C5

Seq. No.	279862
Contig ID	100391_1.R1011
5'-most EST	LIB83-008-Q1-E1-D9
Method	BLASTX
NCBI GI	g2827552
BLAST score	225
E value	2.0e-18
Match length	98
% identity	45
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	279863
Contig ID	100401_1.R1011
5'-most EST	xjt700092113.h1

Seq. No.	279864
Contig ID	100405_1.R1011
5'-most EST	LIB83-008-Q1-E1-F3

Seq. No.	279865
Contig ID	100413_1.R1011
5'-most EST	uC-zmrob73005g12b1
Method	BLASTX
NCBI GI	g3928095
BLAST score	454
E value	4.0e-45
Match length	146

% identity	61
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No.	279866
Contig ID	100437_1.R1011
5'-most EST	uC-zmflmo17313f06b1
Method	BLASTX
NCBI GI	g2244926
BLAST score	310
E value	3.0e-28
Match length	104
% identity	59
NCBI Description	(Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No.	279867
Contig ID	100437_2.R1011
5'-most EST	LIB83-009-Q1-E1-A5
Method	BLASTX
NCBI GI	g2244926
BLAST score	284
E value	3.0e-25
Match length	99
% identity	56
NCBI Description	(Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No.	279868
Contig ID	100443_1.R1011
5'-most EST	xmt700257849.h1

Seq. No.	279869
Contig ID	100449_1.R1011
5'-most EST	LIB83-009-Q1-E1-B9

Seq. No.	279870
Contig ID	100464_1.R1011
5'-most EST	LIB83-009-Q1-E1-D2
Method	BLASTX
NCBI GI	g4417266
BLAST score	499
E value	5.0e-61
Match length	190
% identity	64
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279871
Contig ID	100465_1.R1011
5'-most EST	cyk700050865.f1

Seq. No.	279872
Contig ID	100466_1.R1011
5'-most EST	uC-zmflb73064d10b1
Method	BLASTX
NCBI GI	g4115949
BLAST score	655
E value	2.0e-68
Match length	264
% identity	55

NCBI Description	(AF118223) contains similarity to adenosine deaminases [Arabidopsis thaliana]

Seq. No.	279873
Contig ID	100471_1.R1011
5'-most EST	xyt700344720.h1
Method	BLASTX
NCBI GI	g4049353
BLAST score	518
E value	1.0e-52
Match length	185
% identity	57
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	279874
Contig ID	100472_2.R1011
5'-most EST	mwy700442827.h1
Method	BLASTX
NCBI GI	g1769898
BLAST score	175
E value	5.0e-13
Match length	69
% identity	51
NCBI Description	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq. No.	279875
Contig ID	100487_1.R1011
5'-most EST	LIB83-009-Q1-E1-G1

Seq. No.	279876
Contig ID	100493_1.R1011
5'-most EST	xjt700094315.h1

Seq. No.	279877
Contig ID	100496_1.R1011
5'-most EST	uC-zmflb73144e02b1
Method	BLASTX
NCBI GI	g4336610
BLAST score	752
E value	4.0e-80
Match length	188
% identity	80
NCBI Description	(AF099112) sigma factor; Sig3 [Zea mays]

Seq. No.	279878
Contig ID	100496_2.R1011
5'-most EST	xjt700093427.h1
Method	BLASTN
NCBI GI	g4336609
BLAST score	408
E value	0.0e+00
Match length	852
% identity	99
NCBI Description	Zea mays sigma factor (sig3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	279879

Contig ID	100498_1.R1011
5'-most EST	uC-zmflmo17061f03b1
Method	BLASTX
NCBI GI	g4467123
BLAST score	170
E value	7.0e-12
Match length	102
% identity	34
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279880
Contig ID	100516_1.R1011
5'-most EST	LIB83-010-Q1-E1-B12

Seq. No.	279881
Contig ID	100521_1.R1011
5'-most EST	hbs701181916.h1

Seq. No.	279882
Contig ID	100525_1.R1011
5'-most EST	uC-zmflmo17215c03b1

Seq. No.	279883
Contig ID	100526_1.R1011
5'-most EST	LIB83-010-Q1-E1-C3

Seq. No.	279884
Contig ID	100527_1.R1011
5'-most EST	LIB83-010-Q1-E1-C4
Method	BLASTX
NCBI GI	g3122918
BLAST score	151
E value	7.0e-10
Match length	78
% identity	38
NCBI Description	TAS PROTEIN >gi_882727 (U29581) ORF_o346 [Escherichia coli] >gi_1789199 (AE000367) orf, hypothetical protein [Escherichia coli] >gi_2342573_emb_CAA74961_ (Y14609) tas [Escherichia coli]

Seq. No.	279885
Contig ID	100544_1.R1011
5'-most EST	uC-zmflmo17001c05b1

Seq. No.	279886
Contig ID	100561_1.R1011
5'-most EST	dyk700103741.h1
Method	BLASTX
NCBI GI	g3738302
BLAST score	206
E value	7.0e-16
Match length	88
% identity	49
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	279887
Contig ID	100571_1.R1011
5'-most EST	uC-zmflb73149a07b1
Method	BLASTX
NCBI GI	g2244904
BLAST score	176
E value	2.0e-12
Match length	184
% identity	35
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No.	279888
Contig ID	100572_1.R1011
5'-most EST	uC-zmflmo17310g05b1
Method	BLASTX
NCBI GI	g4539400
BLAST score	153
E value	1.0e-09
Match length	77
% identity	47
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	279889
Contig ID	100584_1.R1011
5'-most EST	uC-zmroteosinte091g09b2

Seq. No.	279890
Contig ID	100593_1.R1011
5'-most EST	fwa700099373.h1
Method	BLASTX
NCBI GI	g4587513
BLAST score	458
E value	1.0e-45
Match length	160
% identity	56
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	279891
Contig ID	100597_1.R1011
5'-most EST	LIB83-011-Q1-E1-B9

Seq. No.	279892
Contig ID	100618_1.R1011
5'-most EST	LIB83-011-Q1-E1-D8

Seq. No.	279893
Contig ID	100625_1.R1011
5'-most EST	dyk700102772.h1
Method	BLASTX
NCBI GI	g2462826
BLAST score	327
E value	5.0e-34
Match length	214
% identity	43
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	279894
Contig ID	100631_1.R1011
5'-most EST	uC-zmflmo17199e09b1
Method	BLASTX
NCBI GI	g4510375
BLAST score	268
E value	7.0e-28
Match length	130
% identity	57
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]

Seq. No.	279895
Contig ID	100641_1.R1011
5'-most EST	xsy700208309.h1
Method	BLASTX
NCBI GI	g2244865
BLAST score	526
E value	2.0e-53
Match length	264
% identity	49
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279896
Contig ID	100643_1.R1011
5'-most EST	xjt700095748.h1

Seq. No.	279897
Contig ID	100657_1.R1011
5'-most EST	gwl700616768.h1
Method	BLASTX
NCBI GI	g4056507
BLAST score	226
E value	2.0e-18
Match length	71
% identity	65
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	279898
Contig ID	100661_1.R1011
5'-most EST	dyk700104005.h1
Method	BLASTX
NCBI GI	g1353193
BLAST score	617
E value	5.0e-64
Match length	194
% identity	59
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	279899
Contig ID	100662_1.R1011
5'-most EST	uC-zmflb73347h03a1

Seq. No. 279900
Contig ID 100680_1.R1011
5'-most EST uC-zmflmo17215h08b1

Seq. No. 279901
Contig ID 100701_1.R1011
5'-most EST uC-zmflb73285a11b1
Method BLASTX
NCBI GI g3193292
BLAST score 827
E value 2.0e-88
Match length 194
% identity 81
NCBI Description (AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No. 279902
Contig ID 100713_1.R1011
5'-most EST vux700161576.h1

Seq. No. 279903
Contig ID 100716_1.R1011
5'-most EST wty700171388.h1

Seq. No. 279904
Contig ID 100716_2.R1011
5'-most EST ypc700803564.h1

Seq. No. 279905
Contig ID 100732_1.R1011
5'-most EST LIB83-012-Q1-E1-H11

Seq. No. 279906
Contig ID 100747_1.R1011
5'-most EST LIB83-013-Q1-E1-A9

Seq. No. 279907
Contig ID 100752_1.R1011
5'-most EST LIB83-013-Q1-E1-B4

Seq. No. 279908
Contig ID 100775_1.R1011
5'-most EST LIB83-013-Q1-E1-D8
Method BLASTX
NCBI GI g4490753
BLAST score 179
E value 5.0e-13
Match length 147
% identity 31
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 279909
Contig ID 100786_1.R1011
5'-most EST rvl700454611.h1
Method BLASTX
NCBI GI g4185136

BLAST score	163
E value	2.0e-22
Match length	112
% identity	54
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	279910
Contig ID	100800_1.R1011
5'-most EST	wty700170943.h1
Method	BLASTX
NCBI GI	g3913366
BLAST score	769
E value	5.0e-82
Match length	194
% identity	83
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >gi_1597723 (U67422) CRINKLY4 precursor [Zea mays]

Seq. No.	279911
Contig ID	100816_1.R1011
5'-most EST	yyf700351208.h1
Method	BLASTX
NCBI GI	g132521
BLAST score	410
E value	7.0e-40
Match length	96
% identity	88
NCBI Description	RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN RGP1) >gi_100684_pir__S16554 GTP-binding protein rgp1 - rice >gi_20356_emb_CAA41966_ (X59276) GTP-binding protein [Oryza sativa] >gi_228209_prf__1718315A GTP-binding protein [Oryza sativa]

Seq. No.	279912
Contig ID	100822_1.R1011
5'-most EST	LIB83-014-Q1-E1-B10

Seq. No.	279913
Contig ID	100830_1.R1011
5'-most EST	LIB83-014-Q1-E1-B7
Method	BLASTX
NCBI GI	g1305531
BLAST score	464
E value	2.0e-46
Match length	104
% identity	77
NCBI Description	(U55219) defective chloroplasts and leaves; required for chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi_1323698 (U55278) DCL [Solanum lycopersicum]

Seq. No.	279914
Contig ID	100839_1.R1011
5'-most EST	clt700041516.f1
Method	BLASTX
NCBI GI	g2160175

BLAST score 215
E value 5.0e-17
Match length 47
% identity 66
NCBI Description (AC000132) Strong similarity to Dianthus cysteine proteinase (gb_U17135). [Arabidopsis thaliana]

Seq. No. 279915
Contig ID 100841_1.R1011
5'-most EST ymt700221615.h1
Method BLASTX
NCBI GI g2342860
BLAST score 167
E value 2.0e-11
Match length 146
% identity 32
NCBI Description (U67168) E4/E8 binding protein-1 [Lycopersicon esculentum]

Seq. No. 279916
Contig ID 100845_1.R1011
5'-most EST LIB83-014-Q1-E1-D1

Seq. No. 279917
Contig ID 100848_1.R1011
5'-most EST uC-zmflb73305b07a1

Seq. No. 279918
Contig ID 100848_2.R1011
5'-most EST hbs701183331.h1
Method BLASTX
NCBI GI g4559292
BLAST score 414
E value 5.0e-44
Match length 131
% identity 68
NCBI Description (AF124148) trehalase 1 GMTRE1 [Glycine max]

Seq. No. 279919
Contig ID 100855_1.R1011
5'-most EST LIB83-014-Q1-E1-D9
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 47
% identity 66
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 279920
Contig ID 100856_1.R1011
5'-most EST uer700581855.h1
Method BLASTX
NCBI GI g3004555
BLAST score 182
E value 3.0e-13
Match length 184
% identity 30

NCBI Description	(AC003673) similar to salt inducible protein [Arabidopsis thaliana]

Seq. No.	279921
Contig ID	100866_1.R1011
5'-most EST	ymt700218665.h1

Seq. No.	279922
Contig ID	100883_1.R1011
5'-most EST	uC-zmflMo17006f05b1

Seq. No.	279923
Contig ID	100891_1.R1011
5'-most EST	xjt700095880.h1
Method	BLASTX
NCBI GI	g2498291
BLAST score	335
E value	4.0e-31
Match length	150
% identity	45
NCBI Description	DIHYDRODIPICOLINATE REDUCTASE >gi_1651716_dbj_BAA16644_ (D90899) dihydrodipicolinate reductase [Synechocystis sp.]

Seq. No.	279924
Contig ID	100892_2.R1011
5'-most EST	ceu700422940.h1

Seq. No.	279925
Contig ID	100901_1.R1011
5'-most EST	LIB83-015-Q1-E1-A4
Method	BLASTX
NCBI GI	g3386609
BLAST score	286
E value	2.0e-25
Match length	210
% identity	36
NCBI Description	(AC004665) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	279926
Contig ID	100910_1.R1011
5'-most EST	LIB83-015-Q1-E1-B2
Method	BLASTX
NCBI GI	g3128203
BLAST score	504
E value	5.0e-51
Match length	154
% identity	62
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	279927
Contig ID	100940_1.R1011
5'-most EST	dyk700106577.h1

Seq. No.	279928
Contig ID	100955_1.R1011
5'-most EST	hbs701183195.h1

Seq. No. 279929
Contig ID 100959_1.R1011
5'-most EST LIB83-015-Q1-E1-F4

Seq. No. 279930
Contig ID 100965_1.R1011
5'-most EST rvt700552080.h1
Method BLASTX
NCBI GI g4579746
BLAST score 245
E value 1.0e-20
Match length 114
% identity 41
NCBI Description (AB017105) DNA helicase Q1 [Mus musculus]

Seq. No. 279931
Contig ID 100973_1.R1011
5'-most EST LIB84-015-Q1-E1-E7
Method BLASTX
NCBI GI g1652582
BLAST score 149
E value 2.0e-09
Match length 99
% identity 36
NCBI Description (D90906) hypothetical protein [Synechocystis sp.]

Seq. No. 279932
Contig ID 100976_1.R1011
5'-most EST LIB83-015-Q1-E1-H10

Seq. No. 279933
Contig ID 101000_1.R1011
5'-most EST yyf700349518.h1

Seq. No. 279934
Contig ID 101002_1.R1011
5'-most EST LIB83-016-Q1-E1-B2

Seq. No. 279935
Contig ID 101024_1.R1011
5'-most EST LIB83-016-Q1-E1-D2
Method BLASTX
NCBI GI g4589931
BLAST score 162
E value 8.0e-11
Match length 122
% identity 30
NCBI Description (AB024705) fls485 [Homo sapiens]

Seq. No. 279936
Contig ID 101029_1.R1011
5'-most EST uC-zmflmo17158h02b1
Method BLASTX
NCBI GI g2731443
BLAST score 233
E value 4.0e-19

Match length	145
% identity	37
NCBI Description	(U96923) [prot= cDNA of the glycoamidase gene [Aspergillus niger]

Seq. No.	279937
Contig ID	101034_1.R1011
5'-most EST	LIB83-016-Q1-E1-E12
Method	BLASTX
NCBI GI	g4490937
BLAST score	164
E value	2.0e-11
Match length	101
% identity	38
NCBI Description	(AJ132261) hypothetical helicase K12H4.8-like protein [Homo sapiens]

Seq. No.	279938
Contig ID	101038_1.R1011
5'-most EST	LIB83-016-Q1-E1-E5
Method	BLASTX
NCBI GI	g4589961
BLAST score	204
E value	8.0e-16
Match length	185
% identity	8
NCBI Description	(AC007169) unknown protein [Arabidopsis thaliana]

Seq. No.	279939
Contig ID	101059_1.R1011
5'-most EST	LIB83-016-Q1-E1-G3

Seq. No.	279940
Contig ID	101100_1.R1011
5'-most EST	nwy700447570.h1
Method	BLASTX
NCBI GI	g4204267
BLAST score	549
E value	2.0e-66
Match length	184
% identity	69
NCBI Description	(AC005223) 55585 [Arabidopsis thaliana]

Seq. No.	279941
Contig ID	101110_1.R1011
5'-most EST	LIB84-001-Q1-E1-D9

Seq. No.	279942
Contig ID	101121_1.R1011
5'-most EST	LIB84-001-Q1-E1-F4

Seq. No.	279943
Contig ID	101125_1.R1011
5'-most EST	uC-zmflb73274c10a1
Method	BLASTX
NCBI GI	g3021281
BLAST score	155

E value	3.0e-10
Match length	76
% identity	51
NCBI Description	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	279944
Contig ID	101125_2.R1011
5'-most EST	uC-zmflmo17321d01a1

Seq. No.	279945
Contig ID	101139_1.R1011
5'-most EST	uC-zmflmo17238d10a1

Seq. No.	279946
Contig ID	101145_1.R1011
5'-most EST	LIB84-002-Q1-E1-A5

Seq. No.	279947
Contig ID	101152_1.R1011
5'-most EST	LIB84-002-Q1-E1-B5

Seq. No.	279948
Contig ID	101159_1.R1011
5'-most EST	LIB84-002-Q1-E1-C11

Seq. No.	279949
Contig ID	101160_1.R1011
5'-most EST	nbm700473130.h1

Seq. No.	279950
Contig ID	101185_1.R1011
5'-most EST	uC-zmflmo17240h02b1
Method	BLASTX
NCBI GI	g2245082
BLAST score	597
E value	8.0e-62
Match length	203
% identity	57
NCBI Description	(Z97343) SCARECROW homolog [Arabidopsis thaliana]

Seq. No.	279951
Contig ID	101187_1.R1011
5'-most EST	fdz701158331.h1
Method	BLASTX
NCBI GI	g1620986
BLAST score	242
E value	2.0e-20
Match length	55
% identity	85
NCBI Description	(Y08858) 40S ribosomal protein S17 [Nicotiana plumbaginifolia]

Seq. No.	279952
Contig ID	101190_1.R1011
5'-most EST	LIB84-002-Q1-E1-G2

Seq. No.	279953
Contig ID	101208_1.R1011
5'-most EST	LIB84-003-Q1-E1-A4
Method	BLASTX
NCBI GI	g418596
BLAST score	285
E value	2.0e-25
Match length	93
% identity	55
NCBI Description	PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W >gi_485540_pir__S33911 hypothetical protein YHR148w - yeast (Saccharomyces cerevisiae) >gi_4014_emb_CAA49237_ (X69480) uORF1 [Saccharomyces cerevisiae] >gi_500654 (U10397) Yhr148wp [Saccharomyces cerevisiae]

Seq. No.	279954
Contig ID	101212_1.R1011
5'-most EST	LIB84-003-Q1-E1-A8
Method	BLASTX
NCBI GI	g3608143
BLAST score	266
E value	3.0e-23
Match length	65
% identity	77
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	279955
Contig ID	101228_1.R1011
5'-most EST	LIB84-003-Q1-E1-C6
Method	BLASTX
NCBI GI	g4468980
BLAST score	540
E value	3.0e-55
Match length	153
% identity	65
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	279956
Contig ID	101229_1.R1011
5'-most EST	LIB84-003-Q1-E1-C7
Method	BLASTX
NCBI GI	g121065
BLAST score	199
E value	2.0e-15
Match length	101
% identity	46
NCBI Description	TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCN3) (GCD COMPLEX SUBUNIT GCN3) (TRANSCRIPTIONAL ACTIVATOR GCN3) >gi_83571_pir__A31562 translation activator GCN3 - yeast (Saccharomyces cerevisiae) >gi_171580 (M23356) transcriptional activator protein GCN3 [Saccharomyces cerevisiae] >gi_486453_emb_CAA82098_ (Z28251) ORF YKR026c [Saccharomyces cerevisiae]

Seq. No. 279957

Contig ID	101259_1.R1011
5'-most EST	wyr700237916.h1
Seq. No.	279958
Contig ID	101263_1.R1011
5'-most EST	bdu700383181.h1
Seq. No.	279959
Contig ID	101264_1.R1011
5'-most EST	xsy700217769.h1
Method	BLASTX
NCBI GI	g3176684
BLAST score	199
E value	2.0e-15
Match length	78
% identity	50
NCBI Description	(AC003671) Contains similarity to equilibratiave nucleoside transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317, gb_T20785, gb_AA586285 and gb_AA712578 come from this gene. [Arabidopsis thaliana]
Seq. No.	279960
Contig ID	101266_1.R1011
5'-most EST	uC-zmflmo17209b09a1
Seq. No.	279961
Contig ID	101286_1.R1011
5'-most EST	uwc700155468.h1
Seq. No.	279962
Contig ID	101296_1.R1011
5'-most EST	uC-zmflmo17139c11a1
Seq. No.	279963
Contig ID	101307_1.R1011
5'-most EST	LIB84-004-Q1-E1-C11
Method	BLASTX
NCBI GI	g3249065
BLAST score	709
E value	5.0e-75
Match length	185
% identity	72
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]
Seq. No.	279964
Contig ID	101312_1.R1011
5'-most EST	LIB84-004-Q1-E1-C6
Seq. No.	279965
Contig ID	101320_1.R1011
5'-most EST	pmx700090550.h1
Seq. No.	279966
Contig ID	101324_1.R1011
5'-most EST	LIB84-004-Q1-E1-D7

Method	BLASTX
NCBI GI	g2244771
BLAST score	376
E value	4.0e-36
Match length	100
% identity	68
NCBI Description	(Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No.	279967
Contig ID	101325_1.R1011
5'-most EST	wen700335343.h1

Seq. No.	279968
Contig ID	101333_1.R1011
5'-most EST	ceu700429607.h1

Seq. No.	279969
Contig ID	101348_1.R1011
5'-most EST	LIB84-004-Q1-E1-G11

Seq. No.	279970
Contig ID	101363_1.R1011
5'-most EST	xjt700094009.h1

Seq. No.	279971
Contig ID	101375_1.R1011
5'-most EST	LIB84-005-Q1-E1-A9

Seq. No.	279972
Contig ID	101397_1.R1011
5'-most EST	LIB84-005-Q1-E1-D5

Seq. No.	279973
Contig ID	101398_1.R1011
5'-most EST	tzu700204438.h1
Method	BLASTX
NCBI GI	g3242789
BLAST score	773
E value	2.0e-82
Match length	206
% identity	70
NCBI Description	(AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No.	279974
Contig ID	101404_1.R1011
5'-most EST	LIB84-005-Q1-E1-E3

Seq. No.	279975
Contig ID	101404_2.R1011
5'-most EST	nbm700474793.h1
Method	BLASTX
NCBI GI	g4505121
BLAST score	218
E value	6.0e-18
Match length	95
% identity	43

NCBI Description	UNKNOWN >gi_3800809 (AF072250) methyl-CpG binding protein MBD4 [Homo sapiens] >gi_4539759_gb_AAD22195.1_AF114784_1 (AF114784) methyl-CpG binding endonuclease [Homo sapiens]

Seq. No.	279976
Contig ID	101425_1.R1011
5'-most EST	uC-zmflb73262a01b3
Method	BLASTX
NCBI GI	g2981475
BLAST score	208
E value	2.0e-16
Match length	119
% identity	42
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]

Seq. No.	279977
Contig ID	101428_1.R1011
5'-most EST	wyr700236511.h1
Method	BLASTX
NCBI GI	g4581111
BLAST score	172
E value	4.0e-12
Match length	165
% identity	28
NCBI Description	(AC005825) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	279978
Contig ID	101429_1.R1011
5'-most EST	LIB84-006-Q1-E1-A12

Seq. No.	279979
Contig ID	101436_1.R1011
5'-most EST	uC-zmflb73072f10a1

Seq. No.	279980
Contig ID	101457_1.R1011
5'-most EST	LIB84-006-Q1-E1-D3
Method	BLASTX
NCBI GI	g2245138
BLAST score	246
E value	5.0e-21
Match length	86
% identity	53
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	279981
Contig ID	101460_1.R1011
5'-most EST	LIB84-006-Q1-E1-D6

Seq. No.	279982
Contig ID	101473_1.R1011
5'-most EST	uC-zmflB73021g01b1
Method	BLASTX
NCBI GI	g1729868
BLAST score	171

E value	9.0e-12
Match length	43
% identity	84
NCBI Description	PROBABLE T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_1177337_emb_CAA93213_ (Z69239) unknown [Schizosaccharomyces pombe]

Seq. No.	279983
Contig ID	101481_1.R1011
5'-most EST	uC-zmflb73274f06b1
Method	BLASTX
NCBI GI	g3914239
BLAST score	760
E value	8.0e-81
Match length	241
% identity	63
NCBI Description	PROTEIN PHOSPHATASE 2C ABI2 (PP2C) >gi_1945140_emb_CAA70163_ (Y08966) ABI2 protein phosphatase 2C [Arabidopsis thaliana] >gi_1945142_emb_CAA70162_ (Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana] >gi_2564213_emb_CAA72538_ (Y11840) ABI2 [Arabidopsis thaliana]

Seq. No.	279984
Contig ID	101490_1.R1011
5'-most EST	ceu700431308.h1
Method	BLASTX
NCBI GI	g2832622
BLAST score	225
E value	2.0e-18
Match length	97
% identity	42
NCBI Description	(AL021711) cyclic phosphodiesterase - like protein [Arabidopsis thaliana]

Seq. No.	279985
Contig ID	101512_1.R1011
5'-most EST	ceu700434310.h1

Seq. No.	279986
Contig ID	101528_1.R1011
5'-most EST	LIB84-008-Q1-E1-B1
Method	BLASTX
NCBI GI	g2621249
BLAST score	226
E value	2.0e-18
Match length	146
% identity	42
NCBI Description	(AE000807) conserved protein [Methanobacterium thermoautotrophicum]

Seq. No.	279987
Contig ID	101532_1.R1011
5'-most EST	ceu700432822.h1
Method	BLASTX
NCBI GI	g4455232
BLAST score	259

E value	1.0e-33
Match length	110
% identity	54
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	279988
Contig ID	101560_1.R1011
5'-most EST	LIB84-008-Q1-E1-D7
Method	BLASTX
NCBI GI	g1568480
BLAST score	642
E value	2.0e-67
Match length	142
% identity	85
NCBI Description	(Z71703) cdc2-like protein kinase [Beta vulgaris]

Seq. No.	279989
Contig ID	101562_1.R1011
5'-most EST	LIB84-008-Q1-E1-E10

Seq. No.	279990
Contig ID	101570_1.R1011
5'-most EST	LIB84-008-Q1-E1-E7

Seq. No.	279991
Contig ID	101570_2.R1011
5'-most EST	xsy700208225.h1
Method	BLASTX
NCBI GI	g3063444
BLAST score	654
E value	2.0e-68
Match length	157
% identity	76
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana]

Seq. No.	279992
Contig ID	101571_1.R1011
5'-most EST	mwy700440882.h1

Seq. No.	279993
Contig ID	101579_1.R1011
5'-most EST	uC-zmflmo17079f09b1
Method	BLASTX
NCBI GI	g3935141
BLAST score	179
E value	7.0e-21
Match length	135
% identity	39
NCBI Description	(AC005106) T25N20.5 [Arabidopsis thaliana]

Seq. No.	279994
Contig ID	101581_1.R1011
5'-most EST	fdz701165848.h1
Method	BLASTX
NCBI GI	g2388571
BLAST score	175
E value	2.0e-12

Match length	78
% identity	49
NCBI Description	(AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb_X98321). [Arabidopsis thaliana] >gi_2738254 (U97684) peroxidase precursor [Arabidopsis thaliana]

Seq. No.	279995
Contig ID	101586_2.R1011
5'-most EST	uC-zmflb73349b12a2
Method	BLASTX
NCBI GI	g4185141
BLAST score	574
E value	4.0e-59
Match length	190
% identity	69
NCBI Description	(AC005724) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	279996
Contig ID	101599_1.R1011
5'-most EST	kem700612014.h1
Method	BLASTX
NCBI GI	g4049342
BLAST score	370
E value	4.0e-35
Match length	227
% identity	19
NCBI Description	(AL034567) adenylate translocator (brittle-1)-like protein [Arabidopsis thaliana]

Seq. No.	279997
Contig ID	101602_1.R1011
5'-most EST	LIB84-008-Q1-E1-H6
Method	BLASTX
NCBI GI	g2133315
BLAST score	321
E value	1.0e-29
Match length	135
% identity	46
NCBI Description	met-10+ protein - Neurospora crassa >gi_773387 (L40806) Restriction enzyme inactivation of met-10 complementation in this region. Sequence similarity to S. cerevisiae chromosome VIII cosmid 9205, accession no. U10556 CDS residues 22627-24126 [Neurospora crassa] >gi_1583208_prf__2120297B met-10 gene [Neurospora crassa]

Seq. No.	279998
Contig ID	101607_1.R1011
5'-most EST	uC-zmroB73030g09b1
Method	BLASTX
NCBI GI	g2582381
BLAST score	1488
E value	1.0e-166
Match length	307
% identity	87
NCBI Description	(AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No.	279999
Contig ID	101608_1.R1011
5'-most EST	pmx700091626.h1
Seq. No.	280000
Contig ID	101612_1.R1011
5'-most EST	LIB84-026-Q1-E1-E3
Seq. No.	280001
Contig ID	101616_1.R1011
5'-most EST	uC-zmflmo17297g05b1
Method	BLASTX
NCBI GI	g2980798
BLAST score	176
E value	3.0e-12
Match length	53
% identity	55
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]
Seq. No.	280002
Contig ID	101617_1.R1011
5'-most EST	clt700045512.f1
Method	BLASTX
NCBI GI	g2827704
BLAST score	148
E value	2.0e-09
Match length	81
% identity	68
NCBI Description	(AL021684) LRR-like protein [Arabidopsis thaliana]
Seq. No.	280003
Contig ID	101620_1.R1011
5'-most EST	vux700159644.h2
Seq. No.	280004
Contig ID	101621_1.R1011
5'-most EST	uC-zmflmo17015c03b1
Seq. No.	280005
Contig ID	101622_1.R1011
5'-most EST	rvt700548408.h1
Seq. No.	280006
Contig ID	101628_1.R1011
5'-most EST	uC-zmflb73048e04b1
Method	BLASTX
NCBI GI	g3249105
BLAST score	933
E value	1.0e-101
Match length	282
% identity	62
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.	280007
Contig ID	101636_1.R1011

5'-most EST	wty700166750.h1
Seq. No.	280008
Contig ID	101641_1.R1011
5'-most EST	xsy700208471.h1
Method	BLASTX
NCBI GI	g2832623
BLAST score	398
E value	2.0e-38
Match length	145
% identity	51
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]
Seq. No.	280009
Contig ID	101644_1.R1011
5'-most EST	LIB84-010-Q1-E1-E4
Seq. No.	280010
Contig ID	101645_1.R1011
5'-most EST	fwa700101313.h1
Seq. No.	280011
Contig ID	101646_1.R1011
5'-most EST	tzu700201310.h1
Method	BLASTX
NCBI GI	g1703089
BLAST score	222
E value	7.0e-18
Match length	112
% identity	38
NCBI Description	ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE) (APH) (ACYLAMINOACYL-PEPTIDASE) (DNF15S2 PROTEIN) >gi_2118063_pir__JC4655 acylaminoacyl-peptidase (EC 3.4.19.1) - human >gi_556514_dbj_BAA07476_ (D38441) acylamino acid-releasing enzyme [Homo sapiens]
Seq. No.	280012
Contig ID	101652_1.R1011
5'-most EST	ceu700427063.h1
Method	BLASTX
NCBI GI	g3335348
BLAST score	154
E value	4.0e-10
Match length	63
% identity	49
NCBI Description	(AC004512) T8F5.20 [Arabidopsis thaliana]
Seq. No.	280013
Contig ID	101652_2.R1011
5'-most EST	LIB84-010-Q1-E1-F8
Seq. No.	280014
Contig ID	101660_1.R1011
5'-most EST	LIB84-011-Q1-E1-C3
Seq. No.	280015

Contig ID	101674_1.R1011
5'-most EST	tfd700573910.h1
Method	BLASTX
NCBI GI	g2739382
BLAST score	270
E value	2.0e-23
Match length	180
% identity	37
NCBI Description	(AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	280016
Contig ID	101687_1.R1011
5'-most EST	LIB84-012-Q1-E12-C4

Seq. No.	280017
Contig ID	101688_1.R1011
5'-most EST	LIB84-012-Q1-E12-C5

Seq. No.	280018
Contig ID	101697_1.R1011
5'-most EST	LIB84-012-Q1-E12-E5
Method	BLASTX
NCBI GI	g4503609
BLAST score	438
E value	2.0e-43
Match length	154
% identity	58
NCBI Description	electron-transfer-flavoprotein, beta polypeptide >gi_585110_sp_P38117_ETFB_HUMAN ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) >gi_479194_pir__S32482 electron transfer flavoprotein beta chain - human >gi_2781203_pdb_1EFV_B Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution >gi_297902_emb_CAA50441_ (X71129) electron transfer flavoprotein beta subunit [Homo sapiens]

Seq. No.	280019
Contig ID	101712_1.R1011
5'-most EST	uC-zmflMo17019e08b1

Seq. No.	280020
Contig ID	101721_1.R1011
5'-most EST	LIB84-013-Q1-E1-A7

Seq. No.	280021
Contig ID	101737_1.R1011
5'-most EST	uC-zmromo17067d01a1
Method	BLASTX
NCBI GI	g1717850
BLAST score	228
E value	7.0e-19
Match length	72
% identity	60
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_1072386_emb_CAA63352_ (X92664) ubiquitin-conjugating

enzyme UbcM2 [Mus musculus]

Seq. No.	280022
Contig ID	101739_1.R1011
5'-most EST	rvl700458511.h1

Seq. No.	280023
Contig ID	101757_1.R1011
5'-most EST	fwa700101202.h1

Seq. No.	280024
Contig ID	101766_1.R1011
5'-most EST	LIB84-013-Q1-E1-F8
Method	BLASTX
NCBI GI	g1899050
BLAST score	921
E value	1.0e-99
Match length	237
% identity	70
NCBI Description	(U62773) ripening-associated protein [Lycopersicon esculentum]

Seq. No.	280025
Contig ID	101771_1.R1011
5'-most EST	LIB84-013-Q1-E1-G2

Seq. No.	280026
Contig ID	101782_1.R1011
5'-most EST	vux700161478.h1
Method	BLASTX
NCBI GI	g4503719
BLAST score	358
E value	9.0e-34
Match length	152
% identity	47
NCBI Description	fragile histidine triad gene >gi_1706794_sp_P49789_FHIT_HUMAN BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE) (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE) (FRAGILE HISTIDINE TRIAD PROTEIN) >gi_3114520_pdb_4FIT_ Fhit-Apo >gi_3114524_pdb_6FIT_ Fhit-Transition State Analog >gi_3318895_pdb_1FHI_ Substrate Analog (Ib2) Complex With The Fragile Histidine Triad Protein, Fhit >gi_1203836 (U46922) member of the histidine triad (HIT) gene family; similar to the S. pombe diadenosine 5',5'''-P1,P4-tetraphosphate asymmetrical hydrolase [Homo sapiens] >gi_1945066 (U76272) diadenosine triphosphate (Ap3A) hydrolase [Homo sapiens]

Seq. No.	280027
Contig ID	101801_1.R1011
5'-most EST	ymt700219193.h1

Seq. No.	280028
Contig ID	101804_1.R1011
5'-most EST	LIB84-014-Q1-E1-B5

Seq. No.	280029
Contig ID	101858_1.R1011
5'-most EST	pmx700082996.h1
Method	BLASTX
NCBI GI	g282994
BLAST score	756
E value	2.0e-80
Match length	237
% identity	59
NCBI Description	Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No.	280030
Contig ID	101873_1.R1011
5'-most EST	mwy700442156.h1

Seq. No.	280031
Contig ID	101893_1.R1011
5'-most EST	uC-zmroteosinte019h07b1

Seq. No.	280032
Contig ID	101895_1.R1011
5'-most EST	uC-zmflmo17308f08b1

Seq. No.	280033
Contig ID	101895_2.R1011
5'-most EST	uC-zmflmo17184f12b1

Seq. No.	280034
Contig ID	101913_1.R1011
5'-most EST	ceu700430320.h1

Seq. No.	280035
Contig ID	101913_3.R1011
5'-most EST	uC-zmflb73136c09b1

Seq. No.	280036
Contig ID	101929_1.R1011
5'-most EST	xjt700093565.h1
Method	BLASTX
NCBI GI	g4502327
BLAST score	148
E value	7.0e-11
Match length	97
% identity	44
NCBI Description	AU RNA-binding protein/enoyl-Coenzyme A hydratase >gi_2135070_pir__I37195 enoyl-CoA hydratase (EC 4.2.1.17) / AU-specific RNA-binding protein - human >gi_780241_emb_CAA56260_ (X79888) AU-binding protein/Enoyl-CoA hydratase [Homo sapiens]

Seq. No.	280037
Contig ID	101929_2.R1011
5'-most EST	uC-zmflmo17022b07b1
Method	BLASTX
NCBI GI	g2245034

BLAST score	284
E value	3.0e-25
Match length	112
% identity	55
NCBI Description	(Z97342) enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	280038
Contig ID	101953_1.R1011
5'-most EST	uC-zmflmo17051g01b1
Method	BLASTX
NCBI GI	g3249105
BLAST score	477
E value	1.0e-47
Match length	149
% identity	61
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	280039
Contig ID	101955_1.R1011
5'-most EST	LIB84-016-Q1-E1-F6
Method	BLASTX
NCBI GI	g2244898
BLAST score	650
E value	3.0e-68
Match length	138
% identity	87
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	280040
Contig ID	101966_1.R1011
5'-most EST	pmx700089530.h1
Method	BLASTX
NCBI GI	g4510428
BLAST score	258
E value	5.0e-42
Match length	167
% identity	53
NCBI Description	(AC006929) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	280041
Contig ID	101974_1.R1011
5'-most EST	uC-zmflb73302h11a1

Seq. No.	280042
Contig ID	101993_1.R1011
5'-most EST	LIB84-017-Q1-E1-B9
Method	BLASTX
NCBI GI	g4006867
BLAST score	358
E value	4.0e-41
Match length	168
% identity	56
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	280043
Contig ID	102022_1.R1011
5'-most EST	uC-zmroteosinte016a03b1
Method	BLASTX
NCBI GI	g4322346
BLAST score	204
E value	9.0e-16
Match length	93
% identity	42
NCBI Description	(AF081825) sodium-dependent high-affinity dicarboxylate transporter [Rattus norvegicus]

Seq. No.	280044
Contig ID	102099_1.R1011
5'-most EST	ceu700428275.h1
Method	BLASTX
NCBI GI	g1173347
BLAST score	442
E value	9.0e-44
Match length	128
% identity	70
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	280045
Contig ID	102106_1.R1011
5'-most EST	wty700172359.h1
Method	BLASTX
NCBI GI	g322598
BLAST score	205
E value	6.0e-16
Match length	149
% identity	34
NCBI Description	St12p protein - Arabidopsis thaliana

Seq. No.	280046
Contig ID	102109_1.R1011
5'-most EST	wty700167278.h1
Method	BLASTX
NCBI GI	g2459447
BLAST score	149
E value	3.0e-09
Match length	36
% identity	78
NCBI Description	(AC002332) putative Mlo protein [Arabidopsis thaliana]

Seq. No.	280047
Contig ID	102113_1.R1011
5'-most EST	wty700168920.h1
Method	BLASTX
NCBI GI	g2739044
BLAST score	202
E value	8.0e-16

Match length	87
% identity	48
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No.	280048
Contig ID	102119_1.R1011
5'-most EST	uC-zmrob73044f11a1
Method	BLASTX
NCBI GI	g1076816
BLAST score	1280
E value	1.0e-142
Match length	261
% identity	94
NCBI Description	nitrate reductase (NADH) (EC 1.6.6.1) (clone Zmnr1S) - maize (fragment) >gi_168517 (M77792) nitrate reductase [Zea mays]

Seq. No.	280049
Contig ID	102123_1.R1011
5'-most EST	mwy700438561.h1

Seq. No.	280050
Contig ID	102124_1.R1011
5'-most EST	fC-zmfl700351896g1
Method	BLASTX
NCBI GI	g4107003
BLAST score	761
E value	3.0e-81
Match length	152
% identity	95
NCBI Description	(D82036) OSK5 [Oryza sativa] >gi_4107007_dbj_BAA36297_ (D82038) OSK3 [Oryza sativa]

Seq. No.	280051
Contig ID	102140_1.R1011
5'-most EST	uC-zmroteosinte001a04b1
Method	BLASTX
NCBI GI	g1076509
BLAST score	192
E value	1.0e-14
Match length	94
% identity	40
NCBI Description	chloroplast RNA binding protein - kidney bean >gi_558629_emb_CAA57551_ (X82030) chloroplast RNA binding protein [Phaseolus vulgaris]

Seq. No.	280052
Contig ID	102158_1.R1011
5'-most EST	uwc700151119.h1

Seq. No.	280053
Contig ID	102171_1.R1011
5'-most EST	qmh700028526.f1
Method	BLASTX
NCBI GI	g1903034
BLAST score	352

E value	3.0e-33
Match length	108
% identity	60
NCBI Description	(X94625) amp-binding protein [Brassica napus]

Seq. No.	280054
Contig ID	102179_1.R1011
5'-most EST	uC-zmroteosinte043b08b2
Method	BLASTX
NCBI GI	g4432832
BLAST score	280
E value	1.0e-24
Match length	91
% identity	62
NCBI Description	(AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No.	280055
Contig ID	102181_1.R1011
5'-most EST	LIB84-023-Q1-E1-G2

Seq. No.	280056
Contig ID	102191_1.R1011
5'-most EST	fwa700097865.h1
Method	BLASTX
NCBI GI	g2494034
BLAST score	342
E value	4.0e-32
Match length	92
% identity	70
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	280057
Contig ID	102193_1.R1011
5'-most EST	vux700156851.h1

Seq. No.	280058
Contig ID	102204_1.R1011
5'-most EST	LIB84-024-Q1-E1-B12
Method	BLASTX
NCBI GI	g3777602
BLAST score	227
E value	8.0e-19
Match length	79
% identity	63
NCBI Description	(AF095709) 50S ribosomal protein L10 [Oryza sativa]

Seq. No.	280059
Contig ID	102232_1.R1011
5'-most EST	LIB84-024-Q1-E1-E8
Method	BLASTX
NCBI GI	g710465
BLAST score	268
E value	2.0e-23
Match length	128

% identity	42
NCBI Description	OEP86=outer envelope protein [Peas, Peptide Chloroplast, 878 aa]

Seq. No.	280060
Contig ID	102244_1.R1011
5'-most EST	fdz701165791.h1
Method	BLASTX
NCBI GI	g2496192
BLAST score	171
E value	6.0e-12
Match length	165
% identity	28
NCBI Description	HYPOTHETICAL PROTEIN MJ1612 >gi_2129191_pir__C64501 phosphonopyruvate decarboxylase BcpC homolog - Methanococcus jannaschii >gi_1592213 (U67601) phosphonopyruvate decarboxylase (bcpC) [Methanococcus jannaschii]

Seq. No.	280061
Contig ID	102257_1.R1011
5'-most EST	LIB84-024-Q1-E1-H9
Method	BLASTX
NCBI GI	g4263714
BLAST score	683
E value	7.0e-72
Match length	173
% identity	80
NCBI Description	(AC006223) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	280062
Contig ID	102278_1.R1011
5'-most EST	LIB84-025-Q1-E1-D10
Method	BLASTX
NCBI GI	g2618699
BLAST score	271
E value	1.0e-23
Match length	141
% identity	38
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	280063
Contig ID	102280_1.R1011
5'-most EST	uC-zmflmo17190h04b1

Seq. No.	280064
Contig ID	102280_2.R1011
5'-most EST	dyk700103561.h1

Seq. No.	280065
Contig ID	102287_1.R1011
5'-most EST	LIB84-025-Q1-E1-G12
Method	BLASTX
NCBI GI	g4056493
BLAST score	193
E value	2.0e-14

Match length	100
% identity	36
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	280066
Contig ID	102290_1.R1011
5'-most EST	hvj700624238.h1
Method	BLASTX
NCBI GI	g465602
BLAST score	206
E value	2.0e-16
Match length	83
% identity	52
NCBI Description	HYPOTHETICAL 32.9 KD PROTEIN IN NFO-FRUA INTERGENIC REGION >gi_405885 (U00007) yeiN [Escherichia coli] >gi_1788490 (AE000306) orf, hypothetical protein [Escherichia coli] >gi_744200_prf__2014253BL yeiN gene [Escherichia coli]

Seq. No.	280067
Contig ID	102298_1.R1011
5'-most EST	ceu700422088.h1

Seq. No.	280068
Contig ID	102321_1.R1011
5'-most EST	LIB84-026-Q1-E1-C12
Method	BLASTX
NCBI GI	g4454017
BLAST score	419
E value	4.0e-41
Match length	147
% identity	54
NCBI Description	(AL035396) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280069
Contig ID	102334_1.R1011
5'-most EST	uC-zmflb73349a08a2

Seq. No.	280070
Contig ID	102340_1.R1011
5'-most EST	LIB84-026-Q1-E1-E11
Method	BLASTX
NCBI GI	g4455199
BLAST score	372
E value	1.0e-35
Match length	154
% identity	54
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	280071
Contig ID	102353_1.R1011
5'-most EST	pmx700088511.h1
Method	BLASTX
NCBI GI	g1293835
BLAST score	501
E value	4.0e-50
Match length	304
% identity	38

NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]

Seq. No. 280072
Contig ID 102378_1.R1011
5'-most EST hbs701181576.h1
Method BLASTX
NCBI GI g3004565
BLAST score 552
E value 1.0e-72
Match length 202
% identity 32
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 280073
Contig ID 102381_1.R1011
5'-most EST LIB84-027-Q1-E1-B1
Method BLASTX
NCBI GI g4336436
BLAST score 195
E value 5.0e-15
Match length 82
% identity 61
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No. 280074
Contig ID 102384_1.R1011
5'-most EST dyk700102052.h1
Method BLASTX
NCBI GI g4140326
BLAST score 198
E value 3.0e-15
Match length 108
% identity 44
NCBI Description (AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)bacterial, worm and yeast hypothetical proteins) [Homo sapiens]

Seq. No. 280075
Contig ID 102393_1.R1011
5'-most EST uC-zmflmo17045c06a1

Seq. No. 280076
Contig ID 102402_1.R1011
5'-most EST LIB84-027-Q1-E1-D1

Seq. No. 280077
Contig ID 102406_1.R1011
5'-most EST LIB84-027-Q1-E1-D2
Method BLASTX
NCBI GI g1399181
BLAST score 520
E value 4.0e-53
Match length 127
% identity 76
NCBI Description (U50738) lycopene epsilon cyclase [Arabidopsis thaliana]

Seq. No. 280078

Contig ID	102411_2.R1011
5'-most EST	tzu700201132.h1
Method	BLASTN
NCBI GI	g602605
BLAST score	41
E value	1.0e-13
Match length	88
% identity	88
NCBI Description	Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No.	280079
Contig ID	102438_1.R1011
5'-most EST	LIB84-027-Q1-E1-G4
Method	BLASTN
NCBI GI	g2062705
BLAST score	37
E value	5.0e-11
Match length	37
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	280080
Contig ID	102438_2.R1011
5'-most EST	nbm700465154.h1

Seq. No.	280081
Contig ID	102443_1.R1011
5'-most EST	LIB84-027-Q1-E1-G9
Method	BLASTX
NCBI GI	g4336747
BLAST score	416
E value	6.0e-41
Match length	126
% identity	62
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No.	280082
Contig ID	102448_1.R1011
5'-most EST	gct701167363.h1

Seq. No.	280083
Contig ID	102456_1.R1011
5'-most EST	LIB84-028-Q1-E1-A12

Seq. No.	280084
Contig ID	102457_1.R1011
5'-most EST	xsy700214480.h1
Method	BLASTX
NCBI GI	g4239887
BLAST score	790
E value	2.0e-84
Match length	164
% identity	92
NCBI Description	(AB016801) MAP kinase 4 [Zea mays]

Seq. No.	280085
Contig ID	102458_1.R1011

5'-most EST	uC-zmflmo17126a08b1
Method	BLASTX
NCBI GI	g3329368
BLAST score	389
E value	1.0e-37
Match length	169
% identity	50
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	280086
Contig ID	102466_1.R1011
5'-most EST	LIB84-028-Q1-E1-B10

Seq. No.	280087
Contig ID	102471_1.R1011
5'-most EST	LIB84-028-Q1-E1-B9

Seq. No.	280088
Contig ID	102475_1.R1011
5'-most EST	uC-zmflmo17013e08b1
Method	BLASTX
NCBI GI	g3193327
BLAST score	261
E value	3.0e-22
Match length	66
% identity	74
NCBI Description	(AF069299) No definition line found [Arabidopsis thaliana]

Seq. No.	280089
Contig ID	102478_1.R1011
5'-most EST	uC-zmroteosinte047d03b1
Method	BLASTX
NCBI GI	g1305531
BLAST score	234
E value	3.0e-19
Match length	98
% identity	43
NCBI Description	(U55219) defective chloroplasts and leaves; required for chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi_1323698 (U55278) DCL [Solanum lycopersicum]

Seq. No.	280090
Contig ID	102478_2.R1011
5'-most EST	afb700381328.h1
Method	BLASTX
NCBI GI	g1305531
BLAST score	166
E value	1.0e-11
Match length	71
% identity	42
NCBI Description	(U55219) defective chloroplasts and leaves; required for chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi_1323698 (U55278) DCL [Solanum lycopersicum]

Seq. No.	280091

Contig ID	102482_1.R1011
5'-most EST	uC-zmflmo17061b10b1
Method	BLASTN
NCBI GI	g3329456
BLAST score	38
E value	6.0e-12
Match length	38
% identity	100
NCBI Description	Mus musculus TRAAK K+ channel subunit mRNA, complete cds

Seq. No.	280092
Contig ID	102483_1.R1011
5'-most EST	LIB84-028-Q1-E1-D1

Seq. No.	280093
Contig ID	102484_1.R1011
5'-most EST	LIB84-028-Q1-E1-D10

Seq. No.	280094
Contig ID	102503_1.R1011
5'-most EST	LIB84-028-Q1-E1-E8
Method	BLASTX
NCBI GI	g2500139
BLAST score	466
E value	7.0e-47
Match length	108
% identity	83
NCBI Description	PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1) >gi_1653916_dbj_BAA18826_ (D90917) peptide chain release factor [Synechocystis sp.]

Seq. No.	280095
Contig ID	102507_1.R1011
5'-most EST	LIB84-028-Q1-E1-F11

Seq. No.	280096
Contig ID	102512_1.R1011
5'-most EST	uC-zmroteosinte086f06b1
Method	BLASTX
NCBI GI	g2213588
BLAST score	357
E value	8.0e-34
Match length	150
% identity	49
NCBI Description	(AC000348) T7N9.8 [Arabidopsis thaliana]

Seq. No.	280097
Contig ID	102514_1.R1011
5'-most EST	LIB84-028-Q1-E1-F8

Seq. No.	280098
Contig ID	102530_1.R1011
5'-most EST	uC-zmflb73278b02b1
Method	BLASTX
NCBI GI	g3522947
BLAST score	422
E value	3.0e-41

Match length	153
% identity	55
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280099
Contig ID	102558_1.R1011
5'-most EST	LIB84-029-Q1-E1-C1

Seq. No.	280100
Contig ID	102578_1.R1011
5'-most EST	LIB84-029-Q1-E1-E10
Method	BLASTX
NCBI GI	g1617272
BLAST score	386
E value	3.0e-37
Match length	122
% identity	62
NCBI Description	(Z72151) AMP-binding protein [Brassica napus]

Seq. No.	280101
Contig ID	102600_1.R1011
5'-most EST	pmx700088538.h1

Seq. No.	280102
Contig ID	102603_1.R1011
5'-most EST	LIB84-029-Q1-E1-G9

Seq. No.	280103
Contig ID	102622_1.R1011
5'-most EST	LIB84-030-Q1-E1-A8
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	2.0e-11
Match length	37
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	280104
Contig ID	102626_1.R1011
5'-most EST	fwa700099575.h1

Seq. No.	280105
Contig ID	102627_1.R1011
5'-most EST	gct701179787.h1

Seq. No.	280106
Contig ID	102636_1.R1011
5'-most EST	LIB84-030-Q1-E1-C1
Method	BLASTX
NCBI GI	g1016270
BLAST score	300
E value	4.0e-27
Match length	103
% identity	60
NCBI Description	(U35123) p-glycoprotein [Urechis caupo]

Seq. No.	280107
Contig ID	102643_1.R1011
5'-most EST	xmt700267637.h1

Seq. No.	280108
Contig ID	102653_1.R1011
5'-most EST	LIB84-030-Q1-E1-D5

Seq. No.	280109
Contig ID	102654_1.R1011
5'-most EST	LIB84-030-Q1-E1-D6
Method	BLASTX
NCBI GI	g2130080
BLAST score	170
E value	5.0e-12
Match length	63
% identity	44
NCBI Description	Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]

Seq. No.	280110
Contig ID	102668_1.R1011
5'-most EST	gct701180062.h1
Method	BLASTX
NCBI GI	g3176659
BLAST score	150
E value	2.0e-09
Match length	81
% identity	40
NCBI Description	(AC004393) Strong similarity to receptor kinase gb_M80238 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	280111
Contig ID	102684_1.R1011
5'-most EST	mwy700438604.h1

Seq. No.	280112
Contig ID	102695_1.R1011
5'-most EST	vux700162437.h1

Seq. No.	280113
Contig ID	102702_1.R1011
5'-most EST	uC-zmroteosinte093c10b2
Method	BLASTX
NCBI GI	g3775987
BLAST score	656
E value	1.0e-68
Match length	220
% identity	59
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.	280114
Contig ID	102702_2.R1011
5'-most EST	uC-zmflm017214f01b1

Method	BLASTX
NCBI GI	g4079811
BLAST score	172
E value	9.0e-24
Match length	339
% identity	7
NCBI Description	(AF071173) Herc2 [Mus musculus]

Seq. No.	280115
Contig ID	102708_1.R1011
5'-most EST	uC-zmflB73002a07b1

Seq. No.	280116
Contig ID	102712_1.R1011
5'-most EST	ymt700223285.h1
Method	BLASTX
NCBI GI	g1871185
BLAST score	432
E value	2.0e-42
Match length	124
% identity	64
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	280117
Contig ID	102730_1.R1011
5'-most EST	uC-zmflb73119b03b1

Seq. No.	280118
Contig ID	102734_1.R1011
5'-most EST	clt700044565.f1

Seq. No.	280119
Contig ID	102734_2.R1011
5'-most EST	wty700164858.h1

Seq. No.	280120
Contig ID	102744_1.R1011
5'-most EST	uC-zmflmo17156f10b1
Method	BLASTX
NCBI GI	g3367534
BLAST score	524
E value	5.0e-90
Match length	213
% identity	76
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	280121
Contig ID	102751_1.R1011
5'-most EST	uC-zmflMo17064g08b1
Method	BLASTX
NCBI GI	g3128186
BLAST score	155
E value	4.0e-10
Match length	44
% identity	64

NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280122
Contig ID	102780_1.R1011
5'-most EST	uC-zmflB73002h07b1
Method	BLASTX
NCBI GI	g2501572
BLAST score	271
E value	7.0e-34
Match length	124
% identity	65
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No.	280123
Contig ID	102786_1.R1011
5'-most EST	uC-zmflb73003a01b1

Seq. No.	280124
Contig ID	102799_1.R1011
5'-most EST	uC-zmflb73003d09b1
Method	BLASTX
NCBI GI	g3258314
BLAST score	180
E value	4.0e-13
Match length	147
% identity	33
NCBI Description	(AP000007) 432aa long hypothetical protein [Pyrococcus horikoshii]

Seq. No.	280125
Contig ID	102802_1.R1011
5'-most EST	uC-zmflb73003e10b1
Method	BLASTX
NCBI GI	g1345643
BLAST score	252
E value	2.0e-21
Match length	100
% identity	54
NCBI Description	FLAVONOID 3',5'-HYDROXYLASE 2 (F3'5'H) (CYTOCHROME P450 75A3) (CYPLXXVA3) >gi_629709_pir__S38984 flavonoid 3',5'-hydroxylase Hf2 - garden petunia >gi_311654_emb_CAA80265_ (Z22544) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_738771_prf__2001426A flavonoid 3',5'-hydroxylase [Petunia x hybrida]

Seq. No.	280126
Contig ID	102807_1.R1011
5'-most EST	uC-zmflb73003f06b1

Seq. No.	280127
Contig ID	102809_1.R1011
5'-most EST	uC-zmflb73003f09b1
Method	BLASTX
NCBI GI	g1430907
BLAST score	208

E value	5.0e-25
Match length	156
% identity	41
NCBI Description	(Z49144) multidrug resistance-associated protein 2 [Oryctolagus cuniculus]

Seq. No.	280128
Contig ID	102810_1.R1011
5'-most EST	uC-zmflb73003f12b1

Seq. No.	280129
Contig ID	102812_1.R1011
5'-most EST	uC-zmflB73003g04b1
Method	BLASTX
NCBI GI	g3779218
BLAST score	433
E value	5.0e-43
Match length	104
% identity	82
NCBI Description	(AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No.	280130
Contig ID	102813_1.R1011
5'-most EST	nbm700473214.h1
Method	BLASTX
NCBI GI	g1805460
BLAST score	210
E value	5.0e-17
Match length	96
% identity	45
NCBI Description	(D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis] >gi_2632692_emb_CAB12199_ (Z99106) similar to succinate-semialdehyde dehydrogenase [Bacillus subtilis]

Seq. No.	280131
Contig ID	102814_1.R1011
5'-most EST	xmt700260467.h1

Seq. No.	280132
Contig ID	102816_1.R1011
5'-most EST	uC-zmflb73003g09b1

Seq. No.	280133
Contig ID	102819_1.R1011
5'-most EST	uC-zmroteosinte070d09b1
Method	BLASTX
NCBI GI	g135460
BLAST score	625
E value	3.0e-65
Match length	146
% identity	84
NCBI Description	TUBULIN BETA-2 CHAIN >gi_100933_pir__S14702 tubulin beta-2 chain - maize >gi_22184_emb_CAA37061_ (X52879) beta 2 tubulin (AA 1-444) [Zea mays]

Seq. No.	280134

Contig ID	102829_1.R1011
5'-most EST	clt700045827.f1
Seq. No.	280135
Contig ID	102832_1.R1011
5'-most EST	uwc700154504.h1
Method	BLASTX
NCBI GI	g1653242
BLAST score	468
E value	2.0e-46
Match length	290
% identity	37
NCBI Description	(D90912) hypothetical protein [Synechocystis sp.]
Seq. No.	280136
Contig ID	102836_1.R1011
5'-most EST	uC-zmflB73004b06b1
Seq. No.	280137
Contig ID	102843_1.R1011
5'-most EST	nbm700470447.h1
Seq. No.	280138
Contig ID	102845_1.R1011
5'-most EST	uC-zmflB73004c05b1
Seq. No.	280139
Contig ID	102863_1.R1011
5'-most EST	uC-zmflB73004e04b1
Method	BLASTX
NCBI GI	g4455169
BLAST score	232
E value	3.0e-19
Match length	118
% identity	42
NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]
Seq. No.	280140
Contig ID	102865_1.R1011
5'-most EST	pwr700452427.h1
Seq. No.	280141
Contig ID	102869_1.R1011
5'-most EST	uC-zmflB73004e11b1
Seq. No.	280142
Contig ID	102870_1.R1011
5'-most EST	uC-zmflB73004e12b1
Method	BLASTX
NCBI GI	g2827699
BLAST score	333
E value	4.0e-31
Match length	86
% identity	69
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	280143
Contig ID	102870_2.R1011
5'-most EST	uC-zmflb73086e08b2
Method	BLASTX
NCBI GI	g2827699
BLAST score	179
E value	1.0e-12
Match length	47
% identity	66
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	280144
Contig ID	102870_3.R1011
5'-most EST	ntr700073505.h1

Seq. No.	280145
Contig ID	102880_1.R1011
5'-most EST	uC-zmflb73164a06b2

Seq. No.	280146
Contig ID	102882_1.R1011
5'-most EST	uC-zmflB73004g06b1
Method	BLASTX
NCBI GI	g1707640
BLAST score	190
E value	3.0e-14
Match length	59
% identity	68
NCBI Description	(X98355) transcription factor GAMyb [Oryza sativa]

Seq. No.	280147
Contig ID	102884_1.R1011
5'-most EST	uC-zmflB73004g08b1

Seq. No.	280148
Contig ID	102903_1.R1011
5'-most EST	uC-zmflB73005a06b1

Seq. No.	280149
Contig ID	102915_1.R1011
5'-most EST	uC-zmflmo17159h11b1

Seq. No.	280150
Contig ID	102919_1.R1011
5'-most EST	uC-zmflB73005c05b1
Method	BLASTX
NCBI GI	g3341747
BLAST score	617
E value	5.0e-64
Match length	200
% identity	62
NCBI Description	(AF077130) receptor-like protein kinase [Oryza sativa]

Seq. No.	280151
Contig ID	102926_1.R1011
5'-most EST	uC-zmflb73005d08a1

Seq. No.	280152
Contig ID	102932_1.R1011
5'-most EST	uC-zmflb73265d08b4
Method	BLASTX
NCBI GI	g3269290
BLAST score	169
E value	9.0e-12
Match length	63
% identity	57
NCBI Description	(AL030978) putative receptor like kinase [Arabidopsis thaliana]

Seq. No.	280153
Contig ID	102943_1.R1011
5'-most EST	wyr700239260.h1
Method	BLASTX
NCBI GI	g2582351
BLAST score	242
E value	4.0e-20
Match length	114
% identity	44
NCBI Description	(AF018639) unknown [Dictyostelium discoideum]

Seq. No.	280154
Contig ID	102946_1.R1011
5'-most EST	uC-zmflb73005g07a1

Seq. No.	280155
Contig ID	102948_1.R1011
5'-most EST	uC-zmflB73005g03b1

Seq. No.	280156
Contig ID	102973_1.R1011
5'-most EST	pmx700090517.h1

Seq. No.	280157
Contig ID	102974_1.R1011
5'-most EST	wty700165708.h1

Seq. No.	280158
Contig ID	102975_1.R1011
5'-most EST	uC-zmflB73006b04b1

Seq. No.	280159
Contig ID	102984_1.R1011
5'-most EST	fwa700101424.h1

Seq. No.	280160
Contig ID	102987_1.R1011
5'-most EST	uC-zmflB73006c06b1

Seq. No.	280161
Contig ID	102987_2.R1011
5'-most EST	cjh700195181.h1
Method	BLASTX
NCBI GI	g1091678
BLAST score	313

E value	2.0e-28
Match length	90
% identity	64
NCBI Description	activator-like transposable element [Pennisetum glaucum]

Seq. No.	280162
Contig ID	102988_1.R1011
5'-most EST	mwy700442545.h1

Seq. No.	280163
Contig ID	102989_1.R1011
5'-most EST	rvt700551895.h1

Seq. No.	280164
Contig ID	102991_1.R1011
5'-most EST	uC-zmflB73006c10b1

Seq. No.	280165
Contig ID	102993_1.R1011
5'-most EST	uC-zmflmo17300f05b1
Method	BLASTN
NCBI GI	g3550435
BLAST score	53
E value	2.0e-20
Match length	132
% identity	86
NCBI Description	Hordeum vulgare Hotr1 gene

Seq. No.	280166
Contig ID	103011_1.R1011
5'-most EST	uC-zmflB73006e09b1

Seq. No.	280167
Contig ID	103016_1.R1011
5'-most EST	uC-zmflb73412h11a1

Seq. No.	280168
Contig ID	103023_1.R1011
5'-most EST	uC-zmflmo17270h03b1
Method	BLASTX
NCBI GI	g2262113
BLAST score	751
E value	6.0e-80
Match length	203
% identity	70
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	280169
Contig ID	103026_1.R1011
5'-most EST	pmx700091046.h1

Seq. No.	280170
Contig ID	103028_1.R1011
5'-most EST	uC-zmflm017209c02b1
Method	BLASTX
NCBI GI	g4008008
BLAST score	203

E value	9.0e-16
Match length	61
% identity	67
NCBI Description	(AF084035) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	280171
Contig ID	103028_2.R1011
5'-most EST	uC-zmflb73362d11a2
Method	BLASTX
NCBI GI	g4008008
BLAST score	147
E value	3.0e-09
Match length	52
% identity	62
NCBI Description	(AF084035) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	280172
Contig ID	103037_1.R1011
5'-most EST	uC-zmflmo17131f09b1

Seq. No.	280173
Contig ID	103043_1.R1011
5'-most EST	uC-zmflB73006h10b1
Method	BLASTX
NCBI GI	g1931647
BLAST score	601
E value	2.0e-62
Match length	156
% identity	73
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	280174
Contig ID	103063_1.R1011
5'-most EST	uC-zmflB73007c02b1

Seq. No.	280175
Contig ID	103093_1.R1011
5'-most EST	uC-zmflb73014b03b1
Method	BLASTX
NCBI GI	g3193306
BLAST score	706
E value	2.0e-74
Match length	204
% identity	69
NCBI Description	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]

Seq. No.	280176
Contig ID	103106_1.R1011
5'-most EST	uC-zmflB73007g06b1

Seq. No.	280177
Contig ID	103113_1.R1011

5'-most EST	xyt700346627.h1
Method	BLASTX
NCBI GI	g3695388
BLAST score	178
E value	8.0e-13
Match length	54
% identity	50
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	280178
Contig ID	103116_1.R1011
5'-most EST	uC-zmflB73007h06b1
Method	BLASTX
NCBI GI	g3805854
BLAST score	391
E value	9.0e-40
Match length	207
% identity	45
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	280179
Contig ID	103123_1.R1011
5'-most EST	uC-zmflB73008a04b1
Method	BLASTX
NCBI GI	g3914365
BLAST score	717
E value	6.0e-76
Match length	169
% identity	79
NCBI Description	PHOSPHOLIPASE D 2 PRECURSOR (PLD 2) (CHOLINE PHOSPHATASE 2) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 2) >gi_1902901_dbj_BAA19466_ (AB001919) phospholipase D [Oryza sativa]

Seq. No.	280180
Contig ID	103133_1.R1011
5'-most EST	cat700016563.r1
Method	BLASTX
NCBI GI	g2108252
BLAST score	609
E value	4.0e-63
Match length	152
% identity	39
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	280181
Contig ID	103135_1.R1011
5'-most EST	uC-zmflB73008b06b1

Seq. No.	280182
Contig ID	103136_1.R1011
5'-most EST	uC-zmflB73010g08b1
Method	BLASTX
NCBI GI	g347855

BLAST score	494
E value	1.0e-49
Match length	115
% identity	84
NCBI Description	(L21753) glucose transporter [Saccharum hybrid cultivar H65-7052]

Seq. No.	280183
Contig ID	103140_1.R1011
5'-most EST	uC-zmflb73008c01b1

Seq. No.	280184
Contig ID	103149_1.R1011
5'-most EST	yyf700351136.h1
Method	BLASTX
NCBI GI	g1346107
BLAST score	1563
E value	1.0e-175
Match length	312
% identity	95
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi_557696 (U12233) GTP binding protein beta subunit [Zea mays]

Seq. No.	280185
Contig ID	103161_1.R1011
5'-most EST	uC-zmflb73008e05b1
Method	BLASTX
NCBI GI	g2464901
BLAST score	390
E value	1.0e-37
Match length	100
% identity	77
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	280186
Contig ID	103162_1.R1011
5'-most EST	uC-zmflb73118g01b1
Method	BLASTX
NCBI GI	g3355486
BLAST score	416
E value	1.0e-40
Match length	137
% identity	60
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	280187
Contig ID	103166_1.R1011
5'-most EST	uC-zmflb73008e11b1
Method	BLASTX
NCBI GI	g1706082
BLAST score	394
E value	2.0e-38
Match length	133
% identity	70
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536

CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa]
>gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	280188
Contig ID	103193_1.R1011
5'-most EST	uC-zmflB73008h03b1

Seq. No.	280189
Contig ID	103194_1.R1011
5'-most EST	uC-zmflb73051c12b1

Seq. No.	280190
Contig ID	103197_1.R1011
5'-most EST	uC-zmflb73008h07b1
Method	BLASTX
NCBI GI	g4008006
BLAST score	306
E value	8.0e-28
Match length	136
% identity	49
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	280191
Contig ID	103206_1.R1011
5'-most EST	uC-zmflB73009a05b1
Method	BLASTX
NCBI GI	g4185131
BLAST score	281
E value	1.0e-24
Match length	154
% identity	44
NCBI Description	(AC005724) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	280192
Contig ID	103216_1.R1011
5'-most EST	uC-zmflB73009b07b1

Seq. No.	280193
Contig ID	103220_1.R1011
5'-most EST	wen700336725.h1

Seq. No.	280194
Contig ID	103225_1.R1011
5'-most EST	ymt700223363.h1
Method	BLASTX
NCBI GI	g2104683
BLAST score	195
E value	8.0e-15
Match length	112
% identity	31
NCBI Description	(X97908) transcription factor [Vicia faba]

Seq. No.	280195

Contig ID	103249_1.R1011
5'-most EST	wuj700282015.h1
Method	BLASTX
NCBI GI	g3915309
BLAST score	381
E value	2.0e-36
Match length	195
% identity	41
NCBI Description	D-XYLOSE-PROTON SYMPORT (D-XYLOSE TRANSPORTER) >gi_2895856 (AF045552) D-xylose proton-symporter [Lactobacillus brevis]

Seq. No.	280196
Contig ID	103260_1.R1011
5'-most EST	uC-zmflmo17059h07b1
Method	BLASTX
NCBI GI	g3540179
BLAST score	455
E value	3.0e-45
Match length	153
% identity	58
NCBI Description	(AC004122) putative amino acid permease [Arabidopsis thaliana]

Seq. No.	280197
Contig ID	103260_2.R1011
5'-most EST	uC-zmflb73151a04b1
Method	BLASTX
NCBI GI	g1076290
BLAST score	164
E value	1.0e-23
Match length	100
% identity	61
NCBI Description	amino acid transporter AAP4 - Arabidopsis thaliana >gi_608671_emb_CAA54631_ (X77500) amino acid transporter [Arabidopsis thaliana]

Seq. No.	280198
Contig ID	103271_1.R1011
5'-most EST	uC-zmflb73183h07b1

Seq. No.	280199
Contig ID	103271_2.R1011
5'-most EST	uC-zmflmo17221f04a1

Seq. No.	280200
Contig ID	103274_1.R1011
5'-most EST	uC-zmflB73009g09b1

Seq. No.	280201
Contig ID	103275_1.R1011
5'-most EST	uC-zmflB73009g11b1
Method	BLASTX
NCBI GI	g3885339
BLAST score	581
E value	6.0e-60
Match length	221
% identity	55

NCBI Description	(AC005623) putative bzip protein [Arabidopsis thaliana]
Seq. No.	280202
Contig ID	103281_1.R1011
5'-most EST	uC-zmf1B73009h05b1
Method	BLASTX
NCBI GI	g629688
BLAST score	144
E value	8.0e-09
Match length	74
% identity	39
NCBI Description	dehydroquinase shikimate dehydrogenase - Common tobacco >gi_535771 (L32794) dehydroquinate dehydratase/shikimate dehydrogenase [Nicotiana tabacum]
Seq. No.	280203
Contig ID	103284_1.R1011
5'-most EST	uC-zmf1mo17001e04b1
Seq. No.	280204
Contig ID	103299_1.R1011
5'-most EST	uC-zmf1b73092a11b2
Method	BLASTN
NCBI GI	g22435
BLAST score	38
E value	8.0e-12
Match length	42
% identity	98
NCBI Description	Z.mays PK1 gene for receptor-like protein kinase
Seq. No.	280205
Contig ID	103305_1.R1011
5'-most EST	uC-zmf1B73010b08b1
Seq. No.	280206
Contig ID	103314_1.R1011
5'-most EST	fwa700100787.h1
Seq. No.	280207
Contig ID	103335_1.R1011
5'-most EST	fxb700397456.h1
Seq. No.	280208
Contig ID	103344_1.R1011
5'-most EST	uC-zmf1B73010f05b1
Seq. No.	280209
Contig ID	103352_1.R1011
5'-most EST	fdz701162958.h1
Seq. No.	280210
Contig ID	103360_1.R1011
5'-most EST	ceu700433794.h1
Method	BLASTX
NCBI GI	g1800217
BLAST score	592
E value	6.0e-65

Match length	140
% identity	94
NCBI Description	(U56730) Phytochrome B [Sorghum bicolor]

Seq. No.	280211
Contig ID	103364_1.R1011
5'-most EST	uC-zmflB73010h03b1
Method	BLASTX
NCBI GI	g2134102
BLAST score	411
E value	4.0e-40
Match length	144
% identity	62
NCBI Description	kinesin-like protein 1 - African clawed frog >gi_562793_emb_CAA57539_ (X82012) kinesin-like protein 1 [Xenopus laevis]

Seq. No.	280212
Contig ID	103372_1.R1011
5'-most EST	uC-zmflB73010h12b1
Method	BLASTX
NCBI GI	g2791896
BLAST score	893
E value	2.0e-96
Match length	230
% identity	74
NCBI Description	(Y08997) 146kDa nuclear protein [Xenopus laevis]

Seq. No.	280213
Contig ID	103374_1.R1011
5'-most EST	uC-zmflB73021a02b1

Seq. No.	280214
Contig ID	103374_2.R1011
5'-most EST	uC-zmflmo17300c09a1
Method	BLASTX
NCBI GI	g2288988
BLAST score	233
E value	1.0e-18
Match length	131
% identity	37
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280215
Contig ID	103398_1.R1011
5'-most EST	uC-zmflb73169a09b2
Method	BLASTX
NCBI GI	g2980764
BLAST score	151
E value	6.0e-10
Match length	55
% identity	60
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	280216
Contig ID	103418_1.R1011
5'-most EST	uC-zmflB73021e08b1

Seq. No. 280217
Contig ID 103436_1.R1011
5'-most EST uC-zmflB73021g06b1

Seq. No. 280218
Contig ID 103443_1.R1011
5'-most EST uC-zmflB73021h06b1
Method BLASTX
NCBI GI g3461815
BLAST score 206
E value 3.0e-21
Match length 122
% identity 51
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 280219
Contig ID 103455_1.R1011
5'-most EST ymt700220824.h1

Seq. No. 280220
Contig ID 103464_1.R1011
5'-most EST uC-zmflb73022b09b1
Method BLASTX
NCBI GI g1203832
BLAST score 226
E value 2.0e-18
Match length 65
% identity 63
NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No. 280221
Contig ID 103476_1.R1011
5'-most EST uC-zmflb73022c10b1
Method BLASTX
NCBI GI g2827039
BLAST score 592
E value 2.0e-61
Match length 155
% identity 75
NCBI Description (AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No. 280222
Contig ID 103482_1.R1011
5'-most EST uC-zmflb73022d04b1
Method BLASTX
NCBI GI g4539404
BLAST score 532
E value 8.0e-81
Match length 182
% identity 77
NCBI Description (AL049524) putative protein [Arabidopsis thaliana]

Seq. No. 280223

Contig ID	103484_1.R1011
5'-most EST	uC-zmflB73022d06b1
Method	BLASTX
NCBI GI	g2130038
BLAST score	250
E value	3.0e-21
Match length	68
% identity	65
NCBI Description	high affinity nitrate transporter homolog BCH1 - barley >gi_1680655 (U34198) BCH1 [Hordeum vulgare]

Seq. No.	280224
Contig ID	103494_1.R1011
5'-most EST	uC-zmflb73022e05b1

Seq. No.	280225
Contig ID	103503_1.R1011
5'-most EST	uC-zmflb73068b03b1
Method	BLASTX
NCBI GI	g3367537
BLAST score	373
E value	1.0e-35
Match length	165
% identity	45
NCBI Description	(AC004392) Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375. [Arabid

Seq. No.	280226
Contig ID	103514_1.R1011
5'-most EST	uC-zmflB73022g01b1

Seq. No.	280227
Contig ID	103518_1.R1011
5'-most EST	uC-zmflb73022g06b1

Seq. No.	280228
Contig ID	103529_1.R1011
5'-most EST	uC-zmflB73022h07b1
Method	BLASTX
NCBI GI	g1076390
BLAST score	158
E value	2.0e-10
Match length	38
% identity	84
NCBI Description	protein phosphatase 2A pDF2 - Arabidopsis thaliana >gi_683504_emb_CAA57529_ (X82003) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	280229
Contig ID	103530_1.R1011
5'-most EST	dyk700104572.h1

Seq. No.	280230
Contig ID	103533_1.R1011

5'-most EST	uC-zmflb73022h12b1
Method	BLASTX
NCBI GI	g1931652
BLAST score	522
E value	5.0e-53
Match length	158
% identity	56
NCBI Description	(U95973) phosphatidylinositol-4-phosphate 5-kinase isolog [Arabidopsis thaliana]

Seq. No.	280231
Contig ID	103551_1.R1011
5'-most EST	uC-zmflb73066c12a1

Seq. No.	280232
Contig ID	103557_1.R1011
5'-most EST	ymt700220802.h1
Method	BLASTX
NCBI GI	g2501296
BLAST score	531
E value	5.0e-54
Match length	236
% identity	46
NCBI Description	DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA gyrase B subunit [Synechocystis sp.]

Seq. No.	280233
Contig ID	103567_1.R1011
5'-most EST	uC-zmflB73106f07b1
Method	BLASTX
NCBI GI	g3236259
BLAST score	201
E value	3.0e-44
Match length	158
% identity	70
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	280234
Contig ID	103580_1.R1011
5'-most EST	uC-zmflb73217g10b2
Method	BLASTX
NCBI GI	g2865175
BLAST score	331
E value	8.0e-31
Match length	74
% identity	78
NCBI Description	(AB010945) AtRer1A [Arabidopsis thaliana]

Seq. No.	280235
Contig ID	103593_1.R1011
5'-most EST	uC-zmflB73025g05b2
Method	BLASTX
NCBI GI	g3540219
BLAST score	534
E value	2.0e-54
Match length	176

% identity	61
NCBI Description	(D87686) KIAA0017 protein [Homo sapiens]

Seq. No.	280236
Contig ID	103595_1.R1011
5'-most EST	uC-zmflb73029b06b1
Method	BLASTX
NCBI GI	g4567301
BLAST score	205
E value	3.0e-16
Match length	114
% identity	39
NCBI Description	(AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No.	280237
Contig ID	103596_1.R1011
5'-most EST	uC-zmflmo17302f04a1
Method	BLASTX
NCBI GI	g2245136
BLAST score	989
E value	1.0e-107
Match length	276
% identity	72
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	280238
Contig ID	103598_1.R1011
5'-most EST	uC-zmflB73025g10b2

Seq. No.	280239
Contig ID	103603_1.R1011
5'-most EST	uC-zmflB73025h03b2
Method	BLASTX
NCBI GI	g3096922
BLAST score	346
E value	1.0e-32
Match length	136
% identity	57
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	280240
Contig ID	103604_1.R1011
5'-most EST	uC-zmflB73025h04b2
Method	BLASTX
NCBI GI	g3600048
BLAST score	793
E value	8.0e-85
Match length	197
% identity	69
NCBI Description	(AF080120) similar to hypothetical proteins in Schizosaccharomyces pombe (GB:Z98533) and C. elegans (GB:Z48334 and Z78419) [Arabidopsis thaliana]

Seq. No.	280241
Contig ID	103624_1.R1011
5'-most EST	uC-zmflB73042b04b1

Seq. No.	280242
Contig ID	103625_1.R1011
5'-most EST	xjt700095257.h1
Method	BLASTX
NCBI GI	g4539404
BLAST score	703
E value	2.0e-74
Match length	162
% identity	77
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	280243
Contig ID	103627_1.R1011
5'-most EST	wty700168408.h1

Seq. No.	280244
Contig ID	103627_2.R1011
5'-most EST	uC-zmflmo17015e07b1

Seq. No.	280245
Contig ID	103628_1.R1011
5'-most EST	uC-zmflb73232f01b1

Seq. No.	280246
Contig ID	103642_1.R1011
5'-most EST	uC-zmflB73042c11b1

Seq. No.	280247
Contig ID	103655_1.R1011
5'-most EST	uC-zmflB73042e02b1

Seq. No.	280248
Contig ID	103660_1.R1011
5'-most EST	uC-zmflm017025f10b1
Method	BLASTX
NCBI GI	g4454042
BLAST score	176
E value	1.0e-12
Match length	65
% identity	51
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	280249
Contig ID	103711_1.R1011
5'-most EST	uC-zmflB73043b09b1

Seq. No.	280250
Contig ID	103712_1.R1011
5'-most EST	uC-zmflB73043b10b1

Seq. No.	280251
Contig ID	103727_1.R1011
5'-most EST	uC-zmflB73043d01b1
Method	BLASTX
NCBI GI	g4467134
BLAST score	146

E value 4.0e-09
Match length 32
% identity 91
NCBI Description (AL035540) protein kinase like protein [Arabidopsis thaliana]

Seq. No. 280252
Contig ID 103743_1.R1011
5'-most EST uC-zmflB73043e05b1
Method BLASTX
NCBI GI g4115538
BLAST score 432
E value 1.0e-42
Match length 160
% identity 54
NCBI Description (AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No. 280253
Contig ID 103747_1.R1011
5'-most EST uC-zmflB73043e09b1
Method BLASTN
NCBI GI g3452287
BLAST score 135
E value 9.0e-70
Match length 242
% identity 93
NCBI Description Zea mays retrotransposon Fourf 3' LTR, partial sequence

Seq. No. 280254
Contig ID 103755_1.R1011
5'-most EST uC-zmflB73043f05b1

Seq. No. 280255
Contig ID 103757_1.R1011
5'-most EST uC-zmflb73043f07b1
Method BLASTX
NCBI GI g2655098
BLAST score 618
E value 2.0e-64
Match length 164
% identity 73
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 280256
Contig ID 103762_1.R1011
5'-most EST uC-zmflB73043g03b1
Method BLASTX
NCBI GI g2244792
BLAST score 220
E value 1.0e-17
Match length 74
% identity 57
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 280257
Contig ID 103763_1.R1011

5'-most EST	uC-zmflb73020e01b1
Method	BLASTX
NCBI GI	g3600039
BLAST score	559
E value	2.0e-57
Match length	175
% identity	59
NCBI Description	(AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No.	280258
Contig ID	103775_1.R1011
5'-most EST	uC-zmflB73043h04b1

Seq. No.	280259
Contig ID	103777_1.R1011
5'-most EST	uC-zmflB73043h06b1

Seq. No.	280260
Contig ID	103778_1.R1011
5'-most EST	uC-zmflB73043h09b1

Seq. No.	280261
Contig ID	103780_1.R1011
5'-most EST	uC-zmflB73043h11b1

Seq. No.	280262
Contig ID	103781_1.R1011
5'-most EST	uC-zmflB73043h12b1

Seq. No.	280263
Contig ID	103837_1.R1011
5'-most EST	uC-zmflB73044f12b1

Seq. No.	280264
Contig ID	103849_1.R1011
5'-most EST	ymt700221139.h1
Method	BLASTX
NCBI GI	g2135057
BLAST score	403
E value	1.0e-38
Match length	236
% identity	40
NCBI Description	EB1 - human >gi_998357 (U24166) EB1 [Homo sapiens]

Seq. No.	280265
Contig ID	103856_1.R1011
5'-most EST	uC-zmflB73044h11b1
Method	BLASTX
NCBI GI	g3360291
BLAST score	822
E value	1.0e-92
Match length	183
% identity	93
NCBI Description	(AF023165) leucine-rich repeat transmembrane protein kinase 2 [Zea mays]

Seq. No.	280266
Contig ID	103860_1.R1011
5'-most EST	uC-zmflmo17022a11b1

Seq. No.	280267
Contig ID	103863_1.R1011
5'-most EST	ymt700221360.h1
Method	BLASTX
NCBI GI	g4263791
BLAST score	336
E value	1.0e-44
Match length	284
% identity	42
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	280268
Contig ID	103883_1.R1011
5'-most EST	uC-zmflB73045c05b1
Method	BLASTX
NCBI GI	g1946355
BLAST score	311
E value	1.0e-37
Match length	189
% identity	44
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	280269
Contig ID	103889_1.R1011
5'-most EST	uC-zmflB73045c11b1

Seq. No.	280270
Contig ID	103892_1.R1011
5'-most EST	ypc700803733.h1
Method	BLASTX
NCBI GI	g3176714
BLAST score	1267
E value	1.0e-140
Match length	339
% identity	73
NCBI Description	(AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana]

Seq. No.	280271
Contig ID	103894_1.R1011
5'-most EST	uC-zmflB73045d04b1
Method	BLASTX
NCBI GI	g4467126
BLAST score	350
E value	1.0e-45
Match length	179
% identity	56
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	280272
Contig ID	103895_1.R1011
5'-most EST	rvt700550861.h1
Method	BLASTX
NCBI GI	g4544390
BLAST score	928
E value	1.0e-100
Match length	324
% identity	57
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280273
Contig ID	103904_1.R1011
5'-most EST	uC-zmflb73080e11b2

Seq. No.	280274
Contig ID	103906_1.R1011
5'-most EST	uC-zmflB73045e06b1

Seq. No.	280275
Contig ID	103946_1.R1011
5'-most EST	uC-zmflB73046a02b1

Seq. No.	280276
Contig ID	103948_1.R1011
5'-most EST	xyt700344049.h1

Seq. No.	280277
Contig ID	103954_2.R1011
5'-most EST	xyt700347203.h1
Method	BLASTX
NCBI GI	g2499226
BLAST score	193
E value	9.0e-15
Match length	123
% identity	33
NCBI Description	CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) >gi_2134920_pir__JC5023 CMP-sialic acid transporter - human >gi_1669558_dbj_BAA13522_ (D87969) CMP-sialic acid transporter [Homo sapiens]

Seq. No.	280278
Contig ID	103955_1.R1011
5'-most EST	uC-zmflb73263h07b1

Seq. No.	280279
Contig ID	103956_1.R1011
5'-most EST	uC-zmflB73046b01b1

Seq. No.	280280
Contig ID	103957_1.R1011
5'-most EST	uC-zmflb73046b02b1

Seq. No.	280281
Contig ID	103961_1.R1011
5'-most EST	xmt700263895.h1
Method	BLASTX

09604076 - 040400

NCBI GI	g4455179
BLAST score	275
E value	6.0e-24
Match length	212
% identity	38
NCBI Description	(AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280282
Contig ID	103962_1.R1011
5'-most EST	uC-zmflmo17021h03b1

Seq. No.	280283
Contig ID	103967_1.R1011
5'-most EST	uC-zmflB73046c01b1

Seq. No.	280284
Contig ID	103968_1.R1011
5'-most EST	uC-zmflb73046c02b1

Seq. No.	280285
Contig ID	103969_1.R1011
5'-most EST	uC-zmflB73046c03b1

Seq. No.	280286
Contig ID	103974_1.R1011
5'-most EST	uC-zmflB73046c08b1

Seq. No.	280287
Contig ID	103975_1.R1011
5'-most EST	xmt700260730.h1

Seq. No.	280288
Contig ID	103991_1.R1011
5'-most EST	uC-zmflb73046e02b1
Method	BLASTX
NCBI GI	g2244792
BLAST score	442
E value	1.0e-43
Match length	129
% identity	66
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	280289
Contig ID	103995_1.R1011
5'-most EST	uC-zmflb73181d03b2

Seq. No.	280290
Contig ID	104001_1.R1011
5'-most EST	uC-zmflb73046f01b1

Seq. No.	280291
Contig ID	104002_1.R1011
5'-most EST	nbm700473457.h1

Seq. No.	280292
Contig ID	104014_1.R1011
5'-most EST	uC-zmflB73046g04b1

Seq. No.	280293
Contig ID	104020_1.R1011
5'-most EST	uC-zmflb73165b10b2

Seq. No.	280294
Contig ID	104025_1.R1011
5'-most EST	uC-zmflb73028g11b1
Method	BLASTX
NCBI GI	g2462659
BLAST score	282
E value	7.0e-25
Match length	213
% identity	33
NCBI Description	(X93208) NRD2 convertase [Rattus sp.]

Seq. No.	280295
Contig ID	104031_1.R1011
5'-most EST	uC-zmflB73046h12b1

Seq. No.	280296
Contig ID	104032_1.R1011
5'-most EST	uC-zmflb73174g09b1
Method	BLASTX
NCBI GI	g3327868
BLAST score	352
E value	3.0e-33
Match length	108
% identity	64
NCBI Description	(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana]

Seq. No.	280297
Contig ID	104049_1.R1011
5'-most EST	uC-zmflb73047b06b1

Seq. No.	280298
Contig ID	104051_1.R1011
5'-most EST	uC-zmflB73047b08b1

Seq. No.	280299
Contig ID	104053_1.R1011
5'-most EST	uC-zmflmo17129c08b1
Method	BLASTX
NCBI GI	g1652704
BLAST score	389
E value	3.0e-37
Match length	288
% identity	33
NCBI Description	(D90907) hypothetical protein [Synechocystis sp.]

Seq. No.	280300
Contig ID	104059_1.R1011
5'-most EST	uC-zmflB73047c05b1
Method	BLASTX
NCBI GI	g4038056
BLAST score	239

E value	4.0e-20
Match length	122
% identity	41
NCBI Description	(AC005897) putative transposon [Arabidopsis thaliana]

Seq. No.	280301
Contig ID	104060_1.R1011
5'-most EST	uC-zmflb73047c06b1

Seq. No.	280302
Contig ID	104068_1.R1011
5'-most EST	xjt700095112.h1

Seq. No.	280303
Contig ID	104076_1.R1011
5'-most EST	uC-zmflB73047e02b1

Seq. No.	280304
Contig ID	104099_1.R1011
5'-most EST	tfd700573732.h1

Seq. No.	280305
Contig ID	104106_1.R1011
5'-most EST	ceu700423808.h1
Method	BLASTX
NCBI GI	g4567225
BLAST score	203
E value	1.0e-15
Match length	58
% identity	69
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	280306
Contig ID	104107_1.R1011
5'-most EST	uC-zmflb73047h01b1
Method	BLASTX
NCBI GI	g4220481
BLAST score	201
E value	1.0e-15
Match length	106
% identity	45
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	280307
Contig ID	104113_1.R1011
5'-most EST	uC-zmflB73047h07b1

Seq. No.	280308
Contig ID	104116_1.R1011
5'-most EST	wyr700244181.h1

Seq. No.	280309
Contig ID	104121_1.R1011
5'-most EST	uC-zmflB73106a03b1

Seq. No.	280310
Contig ID	104127_1.R1011

5'-most EST	uC-zmf1B73106a11b1
Method	BLASTX
NCBI GI	g3036797
BLAST score	303
E value	3.0e-27
Match length	208
% identity	42
NCBI Description	(AL022373) hypothetical protein [Arabidopsis thaliana] >gi_3805859_emb_CAA21479_ (AL031986) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280311
Contig ID	104127_2.R1011
5'-most EST	ymt700218727.h1

Seq. No.	280312
Contig ID	104128_1.R1011
5'-most EST	uwc700150877.h1
Method	BLASTX
NCBI GI	g401621
BLAST score	190
E value	3.0e-14
Match length	134
% identity	38
NCBI Description	HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION >gi_290561 (L10328) o188 [Escherichia coli] >gi_1790149 (AE000448) orf, hypothetical protein [Escherichia coli]

Seq. No.	280313
Contig ID	104148_1.R1011
5'-most EST	uC-zmf1B73106c09b1
Method	BLASTX
NCBI GI	g2388565
BLAST score	347
E value	1.0e-32
Match length	172
% identity	44
NCBI Description	(AC000098) Similar to Prunus pectinesterase (gb_X95991). [Arabidopsis thaliana]

Seq. No.	280314
Contig ID	104150_1.R1011
5'-most EST	uC-zmf1B73106c12b1

Seq. No.	280315
Contig ID	104159_1.R1011
5'-most EST	uC-zmf1B73106d10b1

Seq. No.	280316
Contig ID	104165_1.R1011
5'-most EST	pmx700084694.h1
Method	BLASTX
NCBI GI	g2244834
BLAST score	431
E value	2.0e-42
Match length	135
% identity	61

NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280317
Contig ID	104169_1.R1011
5'-most EST	uC-zmflmo17078e11b1
Method	BLASTX
NCBI GI	g3831440
BLAST score	980
E value	1.0e-106
Match length	308
% identity	64
NCBI Description	(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	280318
Contig ID	104170_1.R1011
5'-most EST	uC-zmflB73106e10b1

Seq. No.	280319
Contig ID	104180_1.R1011
5'-most EST	ymt700223234.h1
Method	BLASTX
NCBI GI	g4582489
BLAST score	286
E value	1.0e-25
Match length	111
% identity	55
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	280320
Contig ID	104185_1.R1011
5'-most EST	rvt700549919.h1
Method	BLASTX
NCBI GI	g4455240
BLAST score	209
E value	2.0e-16
Match length	56
% identity	75
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	280321
Contig ID	104189_1.R1011
5'-most EST	uC-zmflmo17248d10b1
Method	BLASTX
NCBI GI	g136140
BLAST score	224
E value	3.0e-18
Match length	204
% identity	35
NCBI Description	PUTATIVE AC9 TRANSPOSASE >gi_72973_pir__TQZMCA probable transposase - maize transposon Ac9

Seq. No.	280322
Contig ID	104190_1.R1011
5'-most EST	uC-zmflB73106g07b1
Method	BLASTX

NCBI GI	g487006
BLAST score	426
E value	3.0e-57
Match length	155
% identity	76
NCBI Description	protoporphyrin IX magnesium chelatase - garden snapdragon >gi_312129_emb_CAA51664_ (X73144) protoporphyrin IX:Mg Chelatase [Antirrhinum majus]

Seq. No.	280323
Contig ID	104192_1.R1011
5'-most EST	ymt700223904.h1
Method	BLASTX
NCBI GI	g4204912
BLAST score	642
E value	2.0e-70
Match length	188
% identity	70
NCBI Description	(U58918) MEK kinase [Arabidopsis thaliana]

Seq. No.	280324
Contig ID	104217_1.R1011
5'-most EST	uC-zmflB73107b12b2

Seq. No.	280325
Contig ID	104251_2.R1011
5'-most EST	uC-zmflB73107g01b2
Method	BLASTX
NCBI GI	g3283051
BLAST score	155
E value	3.0e-10
Match length	91
% identity	36
NCBI Description	(AF053977) cell division cycle protein 23 [Homo sapiens] >gi_4519431_dbj_BAA75628.1_ (AB011472) CDC23 [Homo sapiens]

Seq. No.	280326
Contig ID	104279_1.R1011
5'-most EST	uC-zmflB73108b10b2

Seq. No.	280327
Contig ID	104282_1.R1011
5'-most EST	nbm700473504.h1

Seq. No.	280328
Contig ID	104283_1.R1011
5'-most EST	uC-zmflB73108c09b2
Method	BLASTX
NCBI GI	g4539296
BLAST score	499
E value	3.0e-50
Match length	150
% identity	59
NCBI Description	(AL049480) putative pathogenesis-related protein [Arabidopsis thaliana]

Seq. No. 280329

Contig ID	104290_1.R1011
5'-most EST	uC-zmflB73108d12b2
Method	BLASTX
NCBI GI	g1345132
BLAST score	292
E value	4.0e-26
Match length	128
% identity	47
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	280330
Contig ID	104304_1.R1011
5'-most EST	uC-zmflB73108g11b2

Seq. No.	280331
Contig ID	104305_1.R1011
5'-most EST	uC-zmflB73108g12b2

Seq. No.	280332
Contig ID	104311_1.R1011
5'-most EST	pmx700086380.h1
Method	BLASTX
NCBI GI	g4567201
BLAST score	607
E value	4.0e-73
Match length	200
% identity	74
NCBI Description	(AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	280333
Contig ID	104336_1.R1011
5'-most EST	ntr700072366.h1
Method	BLASTX
NCBI GI	g4468980
BLAST score	822
E value	4.0e-88
Match length	202
% identity	71
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	280334
Contig ID	104336_2.R1011
5'-most EST	pmx700087173.h1
Method	BLASTX
NCBI GI	g4468980
BLAST score	234
E value	3.0e-19
Match length	47
% identity	83
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	280335
Contig ID	104355_1.R1011

5'-most EST	uC-zmflB73111h10b2
Seq. No.	280336
Contig ID	104366_1.R1011
5'-most EST	uC-zmflB73112b01b2
Seq. No.	280337
Contig ID	104378_1.R1011
5'-most EST	afb700381136.h1
Seq. No.	280338
Contig ID	104381_1.R1011
5'-most EST	xjt700093375.h1
Method	BLASTX
NCBI GI	g3183989
BLAST score	334
E value	5.0e-31
Match length	137
% identity	48
NCBI Description	(AJ005172) P69E protein [Lycopersicon esculentum]
Seq. No.	280339
Contig ID	104384_1.R1011
5'-most EST	uC-zmflB73112d04b2
Method	BLASTX
NCBI GI	g4490316
BLAST score	227
E value	7.0e-35
Match length	138
% identity	56
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.	280340
Contig ID	104400_1.R1011
5'-most EST	uC-zmflb73062f10b1
Method	BLASTX
NCBI GI	g4138912
BLAST score	311
E value	2.0e-28
Match length	93
% identity	60
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]
Seq. No.	280341
Contig ID	104403_1.R1011
5'-most EST	uC-zmflB73112f08b2
Seq. No.	280342
Contig ID	104428_1.R1011
5'-most EST	xsy700214390.h1
Seq. No.	280343
Contig ID	104437_1.R1011
5'-most EST	uC-zmflmo17015h01b1
Method	BLASTX
NCBI GI	g3342249
BLAST score	218

E value	5.0e-19
Match length	73
% identity	62
NCBI Description	(AF047719) GA3 [Arabidopsis thaliana] >gi_3342251 (AF047720) GA3 [Arabidopsis thaliana]

Seq. No.	280344
Contig ID	104464_1.R1011
5'-most EST	uer700582101.h1
Method	BLASTX
NCBI GI	g2132267
BLAST score	199
E value	5.0e-15
Match length	128
% identity	34
NCBI Description	hypothetical protein YPR082c - yeast (Saccharomyces cerevisiae) >gi_1230688 (U51033) Weak similarity to hypothetical E. coli protein (PIR accession number S47687) [Saccharomyces cerevisiae]

Seq. No.	280345
Contig ID	104464_2.R1011
5'-most EST	uC-zmflB73113f10b1

Seq. No.	280346
Contig ID	104476_1.R1011
5'-most EST	uC-zmflB73113h08b1
Method	BLASTX
NCBI GI	g4406808
BLAST score	619
E value	2.0e-64
Match length	202
% identity	61
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	280347
Contig ID	104487_1.R1011
5'-most EST	uC-zmflmo17240e09b1

Seq. No.	280348
Contig ID	104487_4.R1011
5'-most EST	uC-zmflb73200c08b1

Seq. No.	280349
Contig ID	104493_1.R1011
5'-most EST	uC-zmflb73001b02b1
Method	BLASTX
NCBI GI	g1173121
BLAST score	529
E value	1.0e-53
Match length	250
% identity	46
NCBI Description	ATP-DEPENDENT RNA HELICASE ROK1 >gi_2131186_pir__S59649 ATP-dependent RNA helicase ROK1 - yeast (Saccharomyces cerevisiae) >gi_607182_emb_CAA84384_ (Z34901) ATP-dependent RNA helicase [Saccharomyces cerevisiae] >gi_971382_emb_CAA59758_ (X85757) putative ATP dependent

RNA helicase [Saccharomyces cerevisiae]
>gi_1322774_emb_CAA96883_ (Z72693) ORF YGL171w
[Saccharomyces cerevisiae]

Seq. No.	280350
Contig ID	104497_1.R1011
5'-most EST	nbm700469259.h1

Seq. No.	280351
Contig ID	104500_1.R1011
5'-most EST	uC-zmflb73001b09b1
Method	BLASTX
NCBI GI	g3241946
BLAST score	314
E value	9.0e-29
Match length	109
% identity	61
NCBI Description	(AC004625) putative peroxidase [Arabidopsis thaliana]

Seq. No.	280352
Contig ID	104513_1.R1011
5'-most EST	uC-zmflb73001c10b1

Seq. No.	280353
Contig ID	104518_1.R1011
5'-most EST	xmt700266527.h1
Method	BLASTX
NCBI GI	g4455288
BLAST score	1051
E value	1.0e-115
Match length	276
% identity	75
NCBI Description	(AL035527) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	280354
Contig ID	104527_1.R1011
5'-most EST	qmh700026280.f1

Seq. No.	280355
Contig ID	104536_1.R1011
5'-most EST	cat700021408.r1

Seq. No.	280356
Contig ID	104541_1.R1011
5'-most EST	uC-zmflb73001f04b1
Method	BLASTX
NCBI GI	g2245070
BLAST score	172
E value	6.0e-12
Match length	204
% identity	27
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280357
Contig ID	104560_1.R1011
5'-most EST	uC-zmflmo17113g08b1

Method	BLASTX
NCBI GI	g4416302
BLAST score	659
E value	3.0e-69
Match length	135
% identity	92
NCBI Description	(AF105716) copia-type pol polyprotein [Zea mays]

Seq. No.	280358
Contig ID	104560_2.R1011
5'-most EST	uC-zmflb73001h01b1
Method	BLASTX
NCBI GI	g4416302
BLAST score	668
E value	2.0e-70
Match length	134
% identity	93
NCBI Description	(AF105716) copia-type pol polyprotein [Zea mays]

Seq. No.	280359
Contig ID	104566_1.R1011
5'-most EST	uC-zmflb73001h07b1
Method	BLASTX
NCBI GI	g1514643
BLAST score	505
E value	1.0e-58
Match length	203
% identity	56
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	280360
Contig ID	104572_1.R1011
5'-most EST	yyf700348734.h1
Method	BLASTX
NCBI GI	g2829925
BLAST score	442
E value	6.0e-44
Match length	134
% identity	63
NCBI Description	(AC002291) Similar to dnaj-like protein, gp_Y11969_2230757 [Arabidopsis thaliana]

Seq. No.	280361
Contig ID	104577_1.R1011
5'-most EST	uC-zmflMo17009c04b1

Seq. No.	280362
Contig ID	104578_1.R1011
5'-most EST	uC-zmflb73210a05b1

Seq. No.	280363
Contig ID	104589_1.R1011
5'-most EST	pmx700083980.h1
Method	BLASTX
NCBI GI	g1361155
BLAST score	229
E value	1.0e-18

Match length	152
% identity	39
NCBI Description	hypothetical protein o215b - Escherichia coli >gi_537235 (U14003) Kenn Rudd identifies as gpmB [Escherichia coli] >gi_1790856 (AE000509) phosphoglyceromutase 2 [Escherichia coli]

Seq. No.	280364
Contig ID	104594_1.R1011
5'-most EST	uC-zmflb73003c05b1
Method	BLASTX
NCBI GI	g1495259
BLAST score	251
E value	2.0e-21
Match length	89
% identity	52
NCBI Description	(X97826) orf04 [Arabidopsis thaliana]

Seq. No.	280365
Contig ID	104627_1.R1011
5'-most EST	uC-zmrob73005b10b1

Seq. No.	280366
Contig ID	104645_1.R1011
5'-most EST	uC-zmflb73003h04b1
Method	BLASTX
NCBI GI	g1723275
BLAST score	175
E value	1.0e-12
Match length	99
% identity	35
NCBI Description	HYPOTHETICAL 55.6 KD PROTEIN C13F4.15C IN CHROMOSOME I >gi_2130223_pir__S67390 hypothetical protein - fission yeast (Schizosaccharomyces pombe) >gi_3451294_emb_CAA20426_ (AL031322) putative diphthamide biosynthesis protein [Schizosaccharomyces pombe]

Seq. No.	280367
Contig ID	104649_1.R1011
5'-most EST	uC-zmflb73242g01b2
Method	BLASTX
NCBI GI	g2583108
BLAST score	182
E value	2.0e-13
Match length	66
% identity	56
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	280368
Contig ID	104661_1.R1011
5'-most EST	uC-zmflb73008b12b1
Method	BLASTX
NCBI GI	g3063448
BLAST score	290
E value	2.0e-31
Match length	151
% identity	51

NCBI Description (AC003981) F22O13.10 [Arabidopsis thaliana]

Seq. No. 280369
Contig ID 104670_1.R1011
5'-most EST uC-zmflb73029f09b1

Seq. No. 280370
Contig ID 104680_1.R1011
5'-most EST uC-zmflMo17065f11b1
Method BLASTX
NCBI GI g3650036
BLAST score 201
E value 3.0e-15
Match length 100
% identity 43
NCBI Description (AC005396) putative transposase [Arabidopsis thaliana]

Seq. No. 280371
Contig ID 104698_1.R1011
5'-most EST ntr700072433.h2

Seq. No. 280372
Contig ID 104706_1.R1011
5'-most EST uC-zmflb73008f04b1

Seq. No. 280373
Contig ID 104714_1.R1011
5'-most EST uC-zmflb73008f12b1
Method BLASTX
NCBI GI g4467126
BLAST score 464
E value 5.0e-46
Match length 242
% identity 38
NCBI Description (AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No. 280374
Contig ID 104714_2.R1011
5'-most EST uC-zmroteosinte104g06b2

Seq. No. 280375
Contig ID 104734_1.R1011
5'-most EST fC-zmfl700355830f1
Method BLASTX
NCBI GI g2723471
BLAST score 697
E value 1.0e-73
Match length 186
% identity 68
NCBI Description (D87819) sucrose transporter [Oryza sativa]

Seq. No. 280376
Contig ID 104736_1.R1011
5'-most EST uC-zmflmo17335g10b1
Method BLASTX
NCBI GI g2920587

BLAST score	211
E value	2.0e-24
Match length	233
% identity	36
NCBI Description	(AF038362) TBP-associated factor 172 [Homo sapiens] >gi_2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo sapiens]

Seq. No.	280377
Contig ID	104742_1.R1011
5'-most EST	uC-zmflb73011a07b1
Method	BLASTX
NCBI GI	g3334349
BLAST score	624
E value	5.0e-65
Match length	153
% identity	74
NCBI Description	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS) >gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	280378
Contig ID	104749_1.R1011
5'-most EST	uC-zmflb73011b02b1
Method	BLASTX
NCBI GI	g4091117
BLAST score	478
E value	7.0e-48
Match length	127
% identity	69
NCBI Description	(AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No.	280379
Contig ID	104751_1.R1011
5'-most EST	uC-zmflmo17109d01b1

Seq. No.	280380
Contig ID	104771_1.R1011
5'-most EST	uC-zmflmo17054d05b1
Method	BLASTX
NCBI GI	g1706186
BLAST score	661
E value	9.0e-69
Match length	435
% identity	35
NCBI Description	HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR) >gi_110721_pir__A32742 murine ecotropic retrovirus receptor protein - mouse >gi_532612 (M26687) ecotropic retrovirus receptor [Mus musculus]

Seq. No.	280381
Contig ID	104773_1.R1011
5'-most EST	fdz701160602.h1
Method	BLASTX
NCBI GI	g2632252

BLAST score	584
E value	3.0e-60
Match length	125
% identity	93
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	280382
Contig ID	104780_1.R1011
5'-most EST	wen700331966.h1
Method	BLASTX
NCBI GI	g4544386
BLAST score	501
E value	2.0e-50
Match length	249
% identity	44
NCBI Description	(AC007047) putative cell division control protein [Arabidopsis thaliana]

Seq. No.	280383
Contig ID	104787_1.R1011
5'-most EST	wty700170623.h1

Seq. No.	280384
Contig ID	104789_1.R1011
5'-most EST	uC-zmflb73011e09b1

Seq. No.	280385
Contig ID	104789_2.R1011
5'-most EST	uC-zmflb73141d05b1
Method	BLASTX
NCBI GI	g3080417
BLAST score	227
E value	2.0e-18
Match length	63
% identity	75
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	280386
Contig ID	104795_1.R1011
5'-most EST	uC-zmflb73196d04a2

Seq. No.	280387
Contig ID	104795_2.R1011
5'-most EST	uC-zmflb73011f04b1

Seq. No.	280388
Contig ID	104797_1.R1011
5'-most EST	uC-zmflb73011f06b1

Seq. No.	280389
Contig ID	104802_2.R1011
5'-most EST	wyr700242342.h1

Seq. No.	280390
Contig ID	104811_1.R1011
5'-most EST	uC-zmflb73011g09b1

Seq. No.	280391
Contig ID	104813_1.R1011
5'-most EST	rvt700550814.h1

Seq. No.	280392
Contig ID	104839_1.R1011
5'-most EST	xmt700264410.h1

Seq. No.	280393
Contig ID	104843_1.R1011
5'-most EST	wen700334091.h1
Method	BLASTX
NCBI GI	g3882151
BLAST score	303
E value	2.0e-27
Match length	164
% identity	34
NCBI Description	(AB018258) KIAA0715 protein [Homo sapiens]

Seq. No.	280394
Contig ID	104849_1.R1011
5'-most EST	uC-zmflb73012c01b1
Method	BLASTX
NCBI GI	g4585972
BLAST score	746
E value	2.0e-79
Match length	174
% identity	80
NCBI Description	(AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No.	280395
Contig ID	104863_1.R1011
5'-most EST	uC-zmflb73012d06b1
Method	BLASTX
NCBI GI	g4220527
BLAST score	426
E value	8.0e-50
Match length	133
% identity	66
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	280396
Contig ID	104867_1.R1011
5'-most EST	uC-zmflb73012d10b1
Method	BLASTX
NCBI GI	g1168518
BLAST score	634
E value	2.0e-66
Match length	148
% identity	76
NCBI Description	APURINIC ENDONUCLEASE-REDOX PROTEIN (DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE) >gi_472869_emb_CAA54234_ (X76912) ARP protein [Arabidopsis thaliana]

Seq. No.	280397
Contig ID	104878_1.R1011
5'-most EST	uC-zmflb73012e10b1

Seq. No.	280398
Contig ID	104883_1.R1011
5'-most EST	uC-zmflb73012f03b1
Method	BLASTX
NCBI GI	g2252840
BLAST score	365
E value	7.0e-36
Match length	145
% identity	54
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	280399
Contig ID	104884_1.R1011
5'-most EST	fC-zmst1700334279a1

Seq. No.	280400
Contig ID	104909_1.R1011
5'-most EST	ypc700806607.h1

Seq. No.	280401
Contig ID	104929_1.R1011
5'-most EST	uC-zmflb73013b03b1

Seq. No.	280402
Contig ID	104931_1.R1011
5'-most EST	pmx700083601.h1
Method	BLASTX
NCBI GI	g3176660
BLAST score	388
E value	2.0e-37
Match length	122
% identity	58
NCBI Description	(AC004393) Similar to ERECTA receptor protein kinase gb_U47029 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	280403
Contig ID	104935_1.R1011
5'-most EST	uC-zmflb73013b09b1

Seq. No.	280404
Contig ID	104950_1.R1011
5'-most EST	uwc700155805.h1

Seq. No.	280405
Contig ID	104953_1.R1011
5'-most EST	uC-zmflb73060g08b1
Method	BLASTX
NCBI GI	g4262186
BLAST score	1484
E value	1.0e-167
Match length	358
% identity	82
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	280406
Contig ID	105022_1.R1011
5'-most EST	uC-zmflb73014b12b1

Seq. No.	280407
Contig ID	105031_1.R1011
5'-most EST	fwa700100605.h1
Method	BLASTX
NCBI GI	g1769897
BLAST score	266
E value	3.0e-23
Match length	136
% identity	37
NCBI Description	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq. No.	280408
Contig ID	105034_1.R1011
5'-most EST	uC-zmflb73014d01b1
Method	BLASTX
NCBI GI	g3478637
BLAST score	285
E value	3.0e-25
Match length	163
% identity	37
NCBI Description	(AC005546) R29425_1 [Homo sapiens]

Seq. No.	280409
Contig ID	105041_1.R1011
5'-most EST	uC-zmflb73014d08b1

Seq. No.	280410
Contig ID	105044_1.R1011
5'-most EST	ymt700219551.h1

Seq. No.	280411
Contig ID	105045_1.R1011
5'-most EST	uC-zmflb73014e01b1
Method	BLASTX
NCBI GI	g3738310
BLAST score	427
E value	6.0e-42
Match length	167
% identity	49
NCBI Description	(AC005309) putative nuclear protein [Arabidopsis thaliana]

Seq. No.	280412
Contig ID	105080_1.R1011
5'-most EST	uC-zmflb73014h02b1
Method	BLASTX
NCBI GI	g2832625
BLAST score	494
E value	7.0e-50
Match length	153
% identity	58
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	280413

Contig ID	105095_1.R1011
5'-most EST	xmt700261282.h1
Method	BLASTX
NCBI GI	g3355486
BLAST score	351
E value	6.0e-33
Match length	156
% identity	49
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	280414
Contig ID	105103_1.R1011
5'-most EST	uC-zmflmo17019b07a1
Method	BLASTX
NCBI GI	g461999
BLAST score	687
E value	1.0e-105
Match length	241
% identity	77
NCBI Description	ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No.	280415
Contig ID	105104_1.R1011
5'-most EST	uC-zmflb73159e01b2

Seq. No.	280416
Contig ID	105107_1.R1011
5'-most EST	uC-zmflb73015b08b1
Method	BLASTX
NCBI GI	g4006856
BLAST score	212
E value	8.0e-22
Match length	147
% identity	46
NCBI Description	(Z99707) receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	280417
Contig ID	105115_1.R1011
5'-most EST	uC-zmflmo17013c01b1
Method	BLASTX
NCBI GI	g2443329
BLAST score	535
E value	3.0e-54
Match length	360
% identity	39
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	280418
Contig ID	105117_1.R1011
5'-most EST	uwc700154689.h1

Seq. No.	280419
Contig ID	105128_1.R1011
5'-most EST	uC-zmflb73015d08b1

Seq. No.	280420

Contig ID 105130_1.R1011
5'-most EST uC-zmflmo17257c05b1

Seq. No. 280421
Contig ID 105149_1.R1011
5'-most EST uC-zmflb73015f09b1

Seq. No. 280422
Contig ID 105151_1.R1011
5'-most EST uC-zmrob73052g05a1

Seq. No. 280423
Contig ID 105151_2.R1011
5'-most EST xmt700264505.h1

Seq. No. 280424
Contig ID 105153_1.R1011
5'-most EST fC-zmst700335931a4

Seq. No. 280425
Contig ID 105164_1.R1011
5'-most EST cyk700051368.f1

Seq. No. 280426
Contig ID 105171_1.R1011
5'-most EST dyk700102562.h1

Seq. No. 280427
Contig ID 105180_1.R1011
5'-most EST uC-zmflb73016a08a1

Seq. No. 280428
Contig ID 105185_1.R1011
5'-most EST uC-zmflb73016b02b1

Seq. No. 280429
Contig ID 105189_1.R1011
5'-most EST uC-zmflb73016b07b1
Method BLASTX
NCBI GI g4557060
BLAST score 591
E value 4.0e-61
Match length 223
% identity 55
NCBI Description (AC007154) putative chromosome-associated polypeptide, 5' partial [Arabidopsis thaliana]

Seq. No. 280430
Contig ID 105190_1.R1011
5'-most EST uC-zmflb73016b08b1
Method BLASTX
NCBI GI g2827139
BLAST score 332
E value 7.0e-31
Match length 90
% identity 64
NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	280431
Contig ID	105198_1.R1011
5'-most EST	bdu700383049.h1

Seq. No.	280432
Contig ID	105209_1.R1011
5'-most EST	xmt700259228.h1

Seq. No.	280433
Contig ID	105210_1.R1011
5'-most EST	uC-zmflmo17073b02b1
Method	BLASTX
NCBI GI	g3688181
BLAST score	220
E value	1.0e-17
Match length	52
% identity	81
NCBI Description	(AL031804) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	280434
Contig ID	105212_1.R1011
5'-most EST	uC-zmflb73016e03b1

Seq. No.	280435
Contig ID	105214_1.R1011
5'-most EST	uC-zmflb73016e05b1

Seq. No.	280436
Contig ID	105217_1.R1011
5'-most EST	uC-zmflb73016e08b1

Seq. No.	280437
Contig ID	105221_1.R1011
5'-most EST	tzu700202313.h1
Method	BLASTX
NCBI GI	g3204108
BLAST score	348
E value	1.0e-32
Match length	160
% identity	47
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]

Seq. No.	280438
Contig ID	105232_1.R1011
5'-most EST	uC-zmflb73097h06b1

Seq. No.	280439
Contig ID	105248_1.R1011
5'-most EST	uC-zmflb73017a01b1

Seq. No.	280440

09054504.100200

Contig ID	105251_3.R1011
5'-most EST	rvt700553064.h1
Method	BLASTX
NCBI GI	g2494266
BLAST score	366
E value	3.0e-35
Match length	93
% identity	76
NCBI Description	GTP-BINDING PROTEIN LEPA >gi_1653961_dbj_BAA18871_ (D90917) LepA [Synechocystis sp.]

Seq. No.	280441
Contig ID	105261_1.R1011
5'-most EST	uC-zmflb73017b06b1
Method	BLASTX
NCBI GI	g3402690
BLAST score	354
E value	8.0e-34
Match length	94
% identity	68
NCBI Description	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	280442
Contig ID	105273_1.R1011
5'-most EST	rvt700551914.h1
Method	BLASTX
NCBI GI	g3776559
BLAST score	833
E value	1.0e-89
Match length	187
% identity	82
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	280443
Contig ID	105275_1.R1011
5'-most EST	uC-zmflb73017c11b1
Method	BLASTX
NCBI GI	g4140710
BLAST score	253
E value	1.0e-21
Match length	90
% identity	56
NCBI Description	(AF109926) rad21 mitotic cohesin [Drosophila melanogaster]

Seq. No.	280444
Contig ID	105322_1.R1011
5'-most EST	uC-zmflmo17307g01b1

Seq. No.	280445
Contig ID	105325_1.R1011
5'-most EST	uC-zmflb73017h09b1
Method	BLASTX
NCBI GI	g2498329

BLAST score	619
E value	1.0e-64
Match length	136
% identity	89
NCBI Description	PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No.	280446
Contig ID	105328_1.R1011
5'-most EST	uC-zmflb73017h12b1
Method	BLASTX
NCBI GI	g2580440
BLAST score	330
E value	3.0e-52
Match length	166
% identity	73
NCBI Description	(D87261) PCF2 [Oryza sativa]

Seq. No.	280447
Contig ID	105331_1.R1011
5'-most EST	uC-zmflb73018a05b1

Seq. No.	280448
Contig ID	105335_1.R1011
5'-most EST	uC-zmflb73018a09b1

Seq. No.	280449
Contig ID	105339_1.R1011
5'-most EST	uC-zmrob73078b08b1
Method	BLASTX
NCBI GI	g3046815
BLAST score	348
E value	1.0e-32
Match length	77
% identity	82
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	280450
Contig ID	105350_1.R1011
5'-most EST	zla700380558.h1

Seq. No.	280451
Contig ID	105359_1.R1011
5'-most EST	uC-zmflb73018c11b1
Method	BLASTX
NCBI GI	g3688598
BLAST score	380
E value	2.0e-36
Match length	113
% identity	59
NCBI Description	(AB009029) Cycloartenol Synthase [Panax ginseng]

Seq. No.	280452
Contig ID	105365_1.R1011
5'-most EST	ymt700220226.h1

Seq. No.	280453
Contig ID	105380_1.R1011
5'-most EST	uC-zmflb73018e08b1

Seq. No.	280454
Contig ID	105388_1.R1011
5'-most EST	ntr700073485.h1
Method	BLASTX
NCBI GI	g2347207
BLAST score	420
E value	4.0e-41
Match length	160
% identity	49
NCBI Description	(AC002338) APG protein isolog [Arabidopsis thaliana] >gi_3150400 (AC004165) putative APG-like protein [Arabidopsis thaliana]

Seq. No.	280455
Contig ID	105392_1.R1011
5'-most EST	uC-zmflb73018f09b1
Method	BLASTN
NCBI GI	g394735
BLAST score	40
E value	8.0e-13
Match length	48
% identity	96
NCBI Description	Rice lip19 mRNA for basic/leucine zipper protein

Seq. No.	280456
Contig ID	105393_1.R1011
5'-most EST	uC-zmflb73018f10b1

Seq. No.	280457
Contig ID	105395_2.R1011
5'-most EST	fwa700097180.h1
Method	BLASTX
NCBI GI	g2335108
BLAST score	367
E value	4.0e-35
Match length	96
% identity	72
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No.	280458
Contig ID	105399_1.R1011
5'-most EST	uC-zmflb73018g04b1
Method	BLASTX
NCBI GI	g2827705
BLAST score	154
E value	6.0e-10
Match length	136
% identity	28

NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	280459
Contig ID	105400_1.R1011
5'-most EST	gwl700618181.h1
Method	BLASTX
NCBI GI	g2104455
BLAST score	269
E value	5.0e-23
Match length	268
% identity	33
NCBI Description	(Z95397) unknown [Schizosaccharomyces pombe]

Seq. No.	280460
Contig ID	105409_1.R1011
5'-most EST	uC-zmflmo17240e02b1
Method	BLASTX
NCBI GI	g719291
BLAST score	1215
E value	1.0e-134
Match length	378
% identity	65
NCBI Description	(U19134) unknown [Arabidopsis thaliana] >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]

Seq. No.	280461
Contig ID	105437_1.R1011
5'-most EST	uC-zmflb73019b08b1

Seq. No.	280462
Contig ID	105444_1.R1011
5'-most EST	yyf700348705.h1
Method	BLASTX
NCBI GI	g3063710
BLAST score	250
E value	5.0e-21
Match length	133
% identity	44
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	280463
Contig ID	105457_1.R1011
5'-most EST	uC-zmflb73019d07b1
Method	BLASTX
NCBI GI	g4115938
BLAST score	446
E value	3.0e-44
Match length	148
% identity	64
NCBI Description	(AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana]

Seq. No.	280464
Contig ID	105458_1.R1011
5'-most EST	uC-zmflmo17041b05b1

Seq. No.	280465
Contig ID	105469_1.R1011
5'-most EST	uC-zmflb73019e09b1

Seq. No.	280466
Contig ID	105471_1.R1011
5'-most EST	pmx700091085.h1
Method	BLASTX
NCBI GI	g2317910
BLAST score	217
E value	1.0e-27
Match length	140
% identity	49
NCBI Description	(U89959) CER1 protein [Arabidopsis thaliana]

Seq. No.	280467
Contig ID	105480_1.R1011
5'-most EST	uC-zmflmo17113b09b1

Seq. No.	280468
Contig ID	105480_2.R1011
5'-most EST	gct701178338.h1

Seq. No.	280469
Contig ID	105480_3.R1011
5'-most EST	uC-zmflb73019f09b1

Seq. No.	280470
Contig ID	105490_1.R1011
5'-most EST	uC-zmflb73019g07b1
Method	BLASTX
NCBI GI	g4321799
BLAST score	443
E value	9.0e-44
Match length	185
% identity	48
NCBI Description	(AF062387) TAP2 protein [Xenopus laevis]

Seq. No.	280471
Contig ID	105492_1.R1011
5'-most EST	uC-zmflb73019g09b1

Seq. No.	280472
Contig ID	105493_1.R1011
5'-most EST	uC-zmflb73019g10b1
Method	BLASTX
NCBI GI	g4519671
BLAST score	303
E value	2.0e-27
Match length	135
% identity	47
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	280473
Contig ID	105509_1.R1011
5'-most EST	uC-zmflmo17073h01b1
Method	BLASTX

NCBI GI	g1091678
BLAST score	274
E value	1.0e-23
Match length	203
% identity	35
NCBI Description	activator-like transposable element [Pennisetum glaucum]

Seq. No.	280474
Contig ID	105509_2.R1011
5'-most EST	uC-zmflb73038f09a1

Seq. No.	280475
Contig ID	105537_1.R1011
5'-most EST	uC-zmflb73020d03b1

Seq. No.	280476
Contig ID	105541_1.R1011
5'-most EST	uC-zmflMo17009a08b1
Method	BLASTX
NCBI GI	g627468
BLAST score	572
E value	8.0e-59
Match length	227
% identity	49
NCBI Description	hypothetical protein 1 - human >gi_285983_dbj_BAA02799_ (D13635) KIAA0010 [Homo sapiens]

Seq. No.	280477
Contig ID	105543_1.R1011
5'-most EST	uC-zmflm017209e01b1

Seq. No.	280478
Contig ID	105545_1.R1011
5'-most EST	uC-zmflb73020d12b1

Seq. No.	280479
Contig ID	105551_1.R1011
5'-most EST	uC-zmflb73020e07b1
Method	BLASTX
NCBI GI	g3618308
BLAST score	339
E value	9.0e-32
Match length	104
% identity	64
NCBI Description	(AB001882) zinc finger protein [Oryza sativa]

Seq. No.	280480
Contig ID	105565_1.R1011
5'-most EST	nbm700475141.h1

Seq. No.	280481
Contig ID	105580_1.R1011
5'-most EST	uC-zmflb73040d01b1

Seq. No.	280482
Contig ID	105586_1.R1011
5'-most EST	uC-zmflb73020h09b1

Seq. No.	280483
Contig ID	105629_1.R1011
5'-most EST	uC-zmflb73022d07b1
Seq. No.	280484
Contig ID	105686_1.R1011
5'-most EST	uC-zmflb73026a08b1
Seq. No.	280485
Contig ID	105687_1.R1011
5'-most EST	uC-zmflb73026a09b1
Seq. No.	280486
Contig ID	105692_1.R1011
5'-most EST	uC-zmflmo17132g09b1
Method	BLASTX
NCBI GI	g3641837
BLAST score	427
E value	5.0e-42
Match length	103
% identity	82
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]
Seq. No.	280487
Contig ID	105696_1.R1011
5'-most EST	uC-zmflb73026b07b1
Method	BLASTX
NCBI GI	g2137490
BLAST score	490
E value	3.0e-49
Match length	252
% identity	44
NCBI Description	lymphocyte specific helicase - mouse >gi_805296 (U25691) lymphocyte specific helicase [Mus musculus]
Seq. No.	280488
Contig ID	105701_1.R1011
5'-most EST	uC-zmflb73026b12b1
Seq. No.	280489
Contig ID	105717_1.R1011
5'-most EST	uC-zmflb73317d01b1
Method	BLASTX
NCBI GI	g2160164
BLAST score	186
E value	1.0e-13
Match length	71
% identity	52
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.	280490
Contig ID	105724_1.R1011
5'-most EST	uC-zmflb73026e02b1
Seq. No.	280491

Contig ID	105726_1.R1011
5'-most EST	uC-zmflmo17307e11b1
Seq. No.	280492
Contig ID	105729_1.R1011
5'-most EST	wyr700241260.h1
Method	BLASTX
NCBI GI	g4468986
BLAST score	255
E value	6.0e-22
Match length	146
% identity	39
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]
Seq. No.	280493
Contig ID	105744_1.R1011
5'-most EST	uC-zmflb73026f10b1
Method	BLASTX
NCBI GI	g3415113
BLAST score	414
E value	5.0e-53
Match length	211
% identity	54
NCBI Description	(AF081201) villin 1 [Arabidopsis thaliana]
Seq. No.	280494
Contig ID	105746_1.R1011
5'-most EST	uC-zmflmo17266a12b1
Seq. No.	280495
Contig ID	105752_1.R1011
5'-most EST	uC-zmflb73026g08b1
Method	BLASTX
NCBI GI	g4406819
BLAST score	387
E value	3.0e-46
Match length	225
% identity	49
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]
Seq. No.	280496
Contig ID	105759_1.R1011
5'-most EST	uC-zmflmo17020d12b1
Method	BLASTX
NCBI GI	g4646203
BLAST score	267
E value	5.0e-23
Match length	173
% identity	37
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]
Seq. No.	280497
Contig ID	105766_1.R1011
5'-most EST	uC-zmflb73284a01b1
Seq. No.	280498

Contig ID	105770_1.R1011
5'-most EST	xyt700346657.h1
Method	BLASTX
NCBI GI	g3805842
BLAST score	253
E value	1.0e-21
Match length	102
% identity	57
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	280499
Contig ID	105780_1.R1011
5'-most EST	uC-zmf1b73027b03b1
Method	BLASTX
NCBI GI	g3522942
BLAST score	485
E value	8.0e-49
Match length	141
% identity	62
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280500
Contig ID	105783_1.R1011
5'-most EST	uC-zmf1b73027b07b1
Method	BLASTX
NCBI GI	g2618702
BLAST score	439
E value	2.0e-43
Match length	117
% identity	75
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	280501
Contig ID	105798_1.R1011
5'-most EST	uC-zmroteosinte072f07b2
Method	BLASTX
NCBI GI	g4490736
BLAST score	728
E value	8.0e-77
Match length	273
% identity	39
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	280502
Contig ID	105802_1.R1011
5'-most EST	uC-zmf1b73027d05b1
Method	BLASTX
NCBI GI	g4559368
BLAST score	627
E value	3.0e-65
Match length	221
% identity	55
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280503
Contig ID	105832_1.R1011
5'-most EST	cyk700048522.f1

Method	BLASTX
NCBI GI	g3096922
BLAST score	258
E value	5.0e-22
Match length	67
% identity	76
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	280504
Contig ID	105844_1.R1011
5'-most EST	fdz701159590.h1
Method	BLASTX
NCBI GI	g3309583
BLAST score	485
E value	1.0e-48
Match length	107
% identity	85
NCBI Description	(AF073830) fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No.	280505
Contig ID	105845_1.R1011
5'-most EST	uC-zmflmo17293h01b1

Seq. No.	280506
Contig ID	105854_1.R1011
5'-most EST	uC-zmflb73033f05b1
Method	BLASTX
NCBI GI	g4501955
BLAST score	169
E value	2.0e-11
Match length	192
% identity	29
NCBI Description	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) >gi_190267 (M32721) poly(ADP-ribose) polymerase [Homo sapiens]

Seq. No.	280507
Contig ID	105858_1.R1011
5'-most EST	uC-zmflb73210g03b1
Method	BLASTX
NCBI GI	g4557026
BLAST score	207
E value	3.0e-16
Match length	94
% identity	9
NCBI Description	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 >gi_1477565 (U50078) p532 [Homo sapiens]

Seq. No.	280508
Contig ID	105868_1.R1011
5'-most EST	xjt700096960.h1
Method	BLASTX
NCBI GI	g4503981
BLAST score	247
E value	2.0e-24

Match length	154
% identity	44
NCBI Description	glutamine-fructose-6-phosphate transaminase >gi_544382_sp_Q06210_GFAT_HUMAN GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) >gi_345855_pir__A45055 glutamine--fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - human >gi_183082 (M90516) glutamine:fructose-6-phosphate amidotransferase [Homo sapiens]

Seq. No.	280509
Contig ID	105874_1.R1011
5'-most EST	uC-zmflmo17285d02b1
Method	BLASTX
NCBI GI	g3080420
BLAST score	526
E value	2.0e-53
Match length	127
% identity	78
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	280510
Contig ID	105875_1.R1011
5'-most EST	uC-zmflb73028b12b1

Seq. No.	280511
Contig ID	105878_1.R1011
5'-most EST	ypc700804353.h1

Seq. No.	280512
Contig ID	105899_1.R1011
5'-most EST	uC-zmflmo17012d05b1

Seq. No.	280513
Contig ID	105912_1.R1011
5'-most EST	uC-zmflb73028f05b1

Seq. No.	280514
Contig ID	105917_1.R1011
5'-most EST	uC-zmflb73028f10b1

Seq. No.	280515
Contig ID	105939_1.R1011
5'-most EST	uC-zmflb73028h09b1
Method	BLASTX
NCBI GI	g2642165
BLAST score	164
E value	3.0e-11
Match length	82
% identity	40
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280516
Contig ID	105946_1.R1011

5'-most EST	xyt700344174.h1
Method	BLASTX
NCBI GI	g4587987
BLAST score	1117
E value	1.0e-122
Match length	301
% identity	67
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No.	280517
Contig ID	105955_1.R1011
5'-most EST	gct701168784.h1
Method	BLASTX
NCBI GI	g3367522
BLAST score	160
E value	9.0e-11
Match length	44
% identity	66
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	280518
Contig ID	105956_1.R1011
5'-most EST	wyr700235634.h1
Method	BLASTX
NCBI GI	g4406764
BLAST score	569
E value	2.0e-58
Match length	217
% identity	54
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	280519
Contig ID	105963_1.R1011
5'-most EST	uC-zmflb73192f10b1

Seq. No.	280520
Contig ID	105965_1.R1011
5'-most EST	xyt700344846.h1

Seq. No.	280521
Contig ID	105972_1.R1011
5'-most EST	uC-zmflb73029c08b1
Method	BLASTX
NCBI GI	g3341696
BLAST score	352
E value	3.0e-33
Match length	144
% identity	53
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	280522
Contig ID	105975_1.R1011
5'-most EST	uC-zmflb73284g06b1

Seq. No.	280523
Contig ID	105976_1.R1011
5'-most EST	uC-zmflmo17292c03b1

Seq. No.	280524
Contig ID	105982_1.R1011
5'-most EST	wty700172705.h1

Seq. No.	280525
Contig ID	105991_1.R1011
5'-most EST	uC-zmflb73029e05b1

Seq. No.	280526
Contig ID	106025_1.R1011
5'-most EST	uC-zmflb73041e04b1
Method	BLASTX
NCBI GI	g1345132
BLAST score	911
E value	1.0e-98
Match length	245
% identity	19
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	280527
Contig ID	106056_1.R1011
5'-most EST	uC-zmflmo17240c07b1
Method	BLASTX
NCBI GI	g1360090
BLAST score	604
E value	1.0e-62
Match length	178
% identity	66
NCBI Description	(X95576) C1C-Nt1 [Nicotiana tabacum]

Seq. No.	280528
Contig ID	106056_2.R1011
5'-most EST	pmx700089521.h1
Method	BLASTX
NCBI GI	g1360090
BLAST score	991
E value	1.0e-108
Match length	319
% identity	59
NCBI Description	(X95576) C1C-Nt1 [Nicotiana tabacum]

Seq. No.	280529
Contig ID	106057_2.R1011
5'-most EST	uC-zmflb73030c11b1
Method	BLASTX
NCBI GI	g728905
BLAST score	233
E value	6.0e-33
Match length	217
% identity	40

NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) >gi_171114 (L01795) ATPase [Saccharomyces cerevisiae] >gi_595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]

Seq. No.	280530
Contig ID	106066_1.R1011
5'-most EST	uC-zmflb73030d09b1
Method	BLASTX
NCBI GI	g1209655
BLAST score	360
E value	4.0e-34
Match length	148
% identity	53
NCBI Description	(U37428) gl1 [Zea mays]

Seq. No.	280531
Contig ID	106081_1.R1011
5'-most EST	uC-zmflmo17048c03b1
Method	BLASTX
NCBI GI	g4406756
BLAST score	504
E value	5.0e-51
Match length	147
% identity	65
NCBI Description	(AC006836) putative integral membrane protein A3 [Arabidopsis thaliana]

Seq. No.	280532
Contig ID	106086_1.R1011
5'-most EST	nbm700472943.h1
Method	BLASTX
NCBI GI	g3242717
BLAST score	249
E value	5.0e-21
Match length	154
% identity	31
NCBI Description	(AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No.	280533
Contig ID	106088_1.R1011
5'-most EST	uC-zmflb73030f08b1
Method	BLASTN
NCBI GI	g1657759
BLAST score	119
E value	5.0e-60
Match length	131
% identity	98
NCBI Description	Zea mays retrotransposon Fourf 5' LTR and primer binding site DNA sequence

Seq. No.	280534
Contig ID	106091_1.R1011
5'-most EST	uC-zmflb73030g01b1

Seq. No.	280535
Contig ID	106101_1.R1011
5'-most EST	uC-zmflb73030h02b1

Seq. No.	280536
Contig ID	106105_1.R1011
5'-most EST	uC-zmflm017207h03b1

Seq. No.	280537
Contig ID	106109_1.R1011
5'-most EST	uC-zmflb73361b02a2

Seq. No.	280538
Contig ID	106112_1.R1011
5'-most EST	uC-zmflm017084g07b1

Seq. No.	280539
Contig ID	106116_1.R1011
5'-most EST	uC-zmflb73031a09b1

Seq. No.	280540
Contig ID	106118_1.R1011
5'-most EST	cyk700049927.f1

Seq. No.	280541
Contig ID	106127_1.R1011
5'-most EST	uC-zmflb73031b09b1

Seq. No.	280542
Contig ID	106139_1.R1011
5'-most EST	uC-zmflb73031c10b1

Seq. No.	280543
Contig ID	106142_1.R1011
5'-most EST	rvl700457222.h1
Method	BLASTX
NCBI GI	g3687654
BLAST score	594
E value	1.0e-61
Match length	181
% identity	67
NCBI Description	(AF047975) putative ethylene receptor; ETR2 [Arabidopsis thaliana]

Seq. No.	280544
Contig ID	106151_1.R1011
5'-most EST	uC-zmflmo17293f04b1
Method	BLASTX
NCBI GI	g1888357
BLAST score	553
E value	1.0e-56
Match length	131
% identity	76
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	280545
Contig ID	106155_1.R1011
5'-most EST	uC-zmflb73031e04b1

Seq. No.	280546
Contig ID	106156_1.R1011
5'-most EST	uwc700154056.h1
Method	BLASTX
NCBI GI	g2827143
BLAST score	835
E value	8.0e-90
Match length	182
% identity	85
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	280547
Contig ID	106169_1.R1011
5'-most EST	qmh700026059.f1
Method	BLASTX
NCBI GI	g2979544
BLAST score	189
E value	3.0e-14
Match length	76
% identity	50
NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	280548
Contig ID	106181_1.R1011
5'-most EST	uC-zmflb73031g06b1

Seq. No.	280549
Contig ID	106186_1.R1011
5'-most EST	uC-zmflmo17164h04b1
Method	BLASTX
NCBI GI	g3927830
BLAST score	865
E value	4.0e-93
Match length	260
% identity	69
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280550
Contig ID	106190_1.R1011
5'-most EST	uC-zmflmo17294e12b1
Method	BLASTX
NCBI GI	g4586058
BLAST score	193
E value	2.0e-14
Match length	130
% identity	36
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	280551
Contig ID	106200_1.R1011
5'-most EST	xmt700264919.h1

Seq. No.	280552
Contig ID	106210_1.R1011
5'-most EST	cjh700196436.h1
Seq. No.	280553
Contig ID	106212_1.R1011
5'-most EST	uC-zmflb73032b04b1
Seq. No.	280554
Contig ID	106217_1.R1011
5'-most EST	uC-zmflMo17063b01b1
Method	BLASTX
NCBI GI	g2443329
BLAST score	295
E value	2.0e-26
Match length	169
% identity	45
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]
Seq. No.	280555
Contig ID	106223_1.R1011
5'-most EST	uC-zmflMo17009f05b1
Seq. No.	280556
Contig ID	106238_1.R1011
5'-most EST	uC-zmflb73032d11b1
Seq. No.	280557
Contig ID	106262_1.R1011
5'-most EST	uC-zmflb73032g02b1
Method	BLASTX
NCBI GI	g4580394
BLAST score	448
E value	3.0e-44
Match length	124
% identity	64
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]
Seq. No.	280558
Contig ID	106265_1.R1011
5'-most EST	uC-zmflb73181h02b2
Method	BLASTX
NCBI GI	g4454048
BLAST score	326
E value	8.0e-30
Match length	112
% identity	53
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]
Seq. No.	280559
Contig ID	106267_1.R1011
5'-most EST	wty700167447.h1
Seq. No.	280560
Contig ID	106278_1.R1011

5'-most EST	xtj700378264.h1
Method	BLASTX
NCBI GI	g4559381
BLAST score	497
E value	9.0e-50
Match length	208
% identity	49
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280561
Contig ID	106278_2.R1011
5'-most EST	uC-zmflb73032h08b1
Method	BLASTX
NCBI GI	g2191134
BLAST score	310
E value	5.0e-28
Match length	85
% identity	67
NCBI Description	(AF007269) contains weak similarity to Galectin-3 binding protein [Arabidopsis thaliana]

Seq. No.	280562
Contig ID	106289_1.R1011
5'-most EST	zuv700355767.h1
Method	BLASTX
NCBI GI	g3738306
BLAST score	746
E value	2.0e-79
Match length	164
% identity	87
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	280563
Contig ID	106297_1.R1011
5'-most EST	yyf700352366.h1

Seq. No.	280564
Contig ID	106301_1.R1011
5'-most EST	uC-zmflmo17294f03b1

Seq. No.	280565
Contig ID	106308_1.R1011
5'-most EST	ymt700220961.h1

Seq. No.	280566
Contig ID	106310_1.R1011
5'-most EST	xjt700095288.h1

Seq. No.	280567
Contig ID	106317_1.R1011
5'-most EST	uC-zmflmo17240f02b1

Seq. No.	280568
Contig ID	106330_1.R1011
5'-most EST	nbm700477550.h1
Method	BLASTX
NCBI GI	g4249382

BLAST score	628
E value	2.0e-65
Match length	189
% identity	59
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	280569
Contig ID	106333_1.R1011
5'-most EST	uC-zmflb73033g02b1

Seq. No.	280570
Contig ID	106371_1.R1011
5'-most EST	uC-zmflb73034c01b2

Seq. No.	280571
Contig ID	106381_1.R1011
5'-most EST	uC-zmflb73034c12b2
Method	BLASTX
NCBI GI	g619749
BLAST score	641
E value	8.0e-67
Match length	199
% identity	62
NCBI Description	(U18969) phosphoribosylanthranilate isomerase [Arabidopsis thaliana]

Seq. No.	280572
Contig ID	106390_1.R1011
5'-most EST	fC-zmle700433779r3
Method	BLASTX
NCBI GI	g3150406
BLAST score	281
E value	2.0e-24
Match length	151
% identity	36
NCBI Description	(AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	280573
Contig ID	106400_1.R1011
5'-most EST	uC-zmflb73034e09b2

Seq. No.	280574
Contig ID	106420_1.R1011
5'-most EST	uC-zmflb73034g05b2
Method	BLASTX
NCBI GI	g466170
BLAST score	197
E value	3.0e-15
Match length	44
% identity	93
NCBI Description	GTP-BINDING PROTEIN YPTM1 >gi_283055_pir__A38202 ypt family - maize >gi_287833_emb_CAA44918_ (X63277) yptm1 [Zea mays]

Seq. No. 280575

Contig ID	106431_1.R1011
5'-most EST	uC-zmromo17027f02a1
Method	BLASTX
NCBI GI	g2245021
BLAST score	470
E value	1.0e-46
Match length	149
% identity	59
NCBI Description	(Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]

Seq. No.	280576
Contig ID	106437_1.R1011
5'-most EST	uC-zmflb73034h11b2

Seq. No.	280577
Contig ID	106461_1.R1011
5'-most EST	uC-zmflb73095d02b1

Seq. No.	280578
Contig ID	106484_1.R1011
5'-most EST	uC-zmflb73038a10b1
Method	BLASTX
NCBI GI	g4504787
BLAST score	405
E value	3.0e-39
Match length	174
% identity	44
NCBI Description	integral transmembrane protein 1 >gi_1174469_sp_P46977_STT3_HUMAN OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_624704 (L38961) putative transmembrane protein precursor [Homo sapiens] >gi_1588286_prf__2208301B integral membrane protein [Homo sapiens]

Seq. No.	280579
Contig ID	106510_1.R1011
5'-most EST	uC-zmflb73038d02b1
Method	BLASTX
NCBI GI	g4455338
BLAST score	218
E value	2.0e-17
Match length	186
% identity	32
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	280580
Contig ID	106520_1.R1011
5'-most EST	uC-zmflb73038e01b1
Method	BLASTX
NCBI GI	g2342683
BLAST score	234
E value	3.0e-19
Match length	172
% identity	37
NCBI Description	(AC000106) Contains similarity to Bos beta-mannosidase (gb_U46067). [Arabidopsis thaliana]

Seq. No.	280581
Contig ID	106533_1.R1011
5'-most EST	uC-zmflb73038f06b1
Method	BLASTX
NCBI GI	g3641838
BLAST score	342
E value	4.0e-32
Match length	94
% identity	68
NCBI Description	(AL023094) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	280582
Contig ID	106533_2.R1011
5'-most EST	uC-zmflmo17040d08b1
Method	BLASTX
NCBI GI	g4544403
BLAST score	322
E value	8.0e-30
Match length	131
% identity	48
NCBI Description	(AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]

Seq. No.	280583
Contig ID	106539_1.R1011
5'-most EST	uC-zmflmo17295e05b1
Method	BLASTN
NCBI GI	g3450841
BLAST score	209
E value	1.0e-114
Match length	274
% identity	95
NCBI Description	Oryza sativa mitogen activated protein kinase kinase (MEK1) mRNA, complete cds

Seq. No.	280584
Contig ID	106544_2.R1011
5'-most EST	rvt700550015.h1

Seq. No.	280585
Contig ID	106551_1.R1011
5'-most EST	uC-zmflb73038h02b1

Seq. No.	280586
Contig ID	106552_1.R1011
5'-most EST	bdu700382291.h1

Seq. No.	280587
Contig ID	106557_1.R1011
5'-most EST	uC-zmflb73038h08b1

Seq. No.	280588
Contig ID	106559_1.R1011
5'-most EST	uC-zmflb73038h10b1

Seq. No.	280589
Contig ID	106565_1.R1011
5'-most EST	uC-zmflb73040b05b1

Seq. No.	280590
Contig ID	106565_2.R1011
5'-most EST	tfd700570120.h1

Seq. No.	280591
Contig ID	106568_1.R1011
5'-most EST	uC-zmflb73039a10b1

Seq. No.	280592
Contig ID	106572_2.R1011
5'-most EST	fwa700101742.h1
Method	BLASTX
NCBI GI	g3738324
BLAST score	229
E value	7.0e-19
Match length	98
% identity	45
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No.	280593
Contig ID	106586_1.R1011
5'-most EST	uC-zmflb73039c08b1

Seq. No.	280594
Contig ID	106591_1.R1011
5'-most EST	uC-zmflb73048b05b1
Method	BLASTX
NCBI GI	g4538965
BLAST score	178
E value	7.0e-13
Match length	79
% identity	42
NCBI Description	(AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280595
Contig ID	106603_1.R1011
5'-most EST	wyr700241038.h1
Method	BLASTX
NCBI GI	g2943792
BLAST score	391
E value	1.0e-37
Match length	107
% identity	67
NCBI Description	(AB006809) PV72 [Cucurbita sp.]

Seq. No.	280596
Contig ID	106605_1.R1011
5'-most EST	gct701173543.h1

Seq. No.	280597
Contig ID	106606_1.R1011
5'-most EST	uC-zmrob73053d06a1

Seq. No.	280598
Contig ID	106610_1.R1011
5'-most EST	uC-zmflb73142c09b1
Method	BLASTX
NCBI GI	g2104949
BLAST score	440
E value	2.0e-59
Match length	132
% identity	89
NCBI Description	(U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	280599
Contig ID	106642_1.R1011
5'-most EST	uC-zmflb73039h12b1

Seq. No.	280600
Contig ID	106667_1.R1011
5'-most EST	uC-zmflmo17285f05b1
Method	BLASTX
NCBI GI	g3914005
BLAST score	1022
E value	1.0e-111
Match length	231
% identity	90
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]

Seq. No.	280601
Contig ID	106668_1.R1011
5'-most EST	mwy700439966.h1

Seq. No.	280602
Contig ID	106671_1.R1011
5'-most EST	uC-zmflb73192e02b1

Seq. No.	280603
Contig ID	106687_1.R1011
5'-most EST	uC-zmflmo17202d12b1

Seq. No.	280604
Contig ID	106688_1.R1011
5'-most EST	ymt700220453.h1
Method	BLASTX
NCBI GI	g4102582
BLAST score	209
E value	1.0e-16
Match length	71
% identity	56
NCBI Description	(AF013115) CAO [Arabidopsis thaliana]

Seq. No.	280605
Contig ID	106690_1.R1011
5'-most EST	uC-zmflb73040e08b1
Method	BLASTX
NCBI GI	g4646233
BLAST score	337
E value	3.0e-31

Match length	157
% identity	48
NCBI Description	(AC007266) putative G9a protein [Arabidopsis thaliana]

Seq. No.	280606
Contig ID	106690_2.R1011
5'-most EST	uC-zmflmo17085d05a1

Seq. No.	280607
Contig ID	106691_1.R1011
5'-most EST	xmt700267251.h1

Seq. No.	280608
Contig ID	106694_1.R1011
5'-most EST	afb700381731.h1
Method	BLASTN
NCBI GI	g1899026
BLAST score	37
E value	4.0e-11
Match length	45
% identity	96
NCBI Description	Zea mays superoxide dismutase 4A (sod4A) gene, complete cds

Seq. No.	280609
Contig ID	106702_1.R1011
5'-most EST	xmt700261357.h1
Method	BLASTX
NCBI GI	g3420751
BLAST score	457
E value	2.0e-45
Match length	163
% identity	54
NCBI Description	(AF079448) cytochrome c oxidase assembly protein [Dictyostelium discoideum]

Seq. No.	280610
Contig ID	106708_1.R1011
5'-most EST	uC-zmflb73040g04b1
Method	BLASTX
NCBI GI	g1722855
BLAST score	341
E value	6.0e-32
Match length	153
% identity	47
NCBI Description	CHROMOSOME ASSEMBLY PROTEIN XCAP-C >gi_1079281_pir__A55094 chromosomal protein XCAP-C - African clawed frog >gi_563812 (U13673) XCAP-C [Xenopus laevis]

Seq. No.	280611
Contig ID	106712_1.R1011
5'-most EST	cyk700048424.f1
Method	BLASTX
NCBI GI	g3201680
BLAST score	741
E value	1.0e-78
Match length	287
% identity	52

NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]
Seq. No.	280612
Contig ID	106749_1.R1011
5'-most EST	uC-zmflmo17367c05a1
Seq. No.	280613
Contig ID	106795_1.R1011
5'-most EST	uC-zmflb73041h06b1
Method	BLASTN
NCBI GI	g2062691
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Human sodium phosphate transporter (NPT4) mRNA, complete cds
Seq. No.	280614
Contig ID	106796_1.R1011
5'-most EST	uC-zmflb73041h07b1
Seq. No.	280615
Contig ID	107054_1.R1011
5'-most EST	uC-zmflb73048b06b1
Seq. No.	280616
Contig ID	107056_1.R1011
5'-most EST	uC-zmflb73048b08b1
Seq. No.	280617
Contig ID	107062_1.R1011
5'-most EST	uC-zmflmo17289g04b1
Method	BLASTX
NCBI GI	g2961380
BLAST score	302
E value	1.0e-29
Match length	126
% identity	59
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]
Seq. No.	280618
Contig ID	107077_1.R1011
5'-most EST	uC-zmflb73069a02b1
Method	BLASTX
NCBI GI	g2459432
BLAST score	176
E value	1.0e-12
Match length	104
% identity	40
NCBI Description	(AC002332) CONSTANS-like protein [Arabidopsis thaliana]
Seq. No.	280619
Contig ID	107090_1.R1011
5'-most EST	pmx700087978.h1
Seq. No.	280620

Contig ID 107092_1.R1011
5'-most EST gwl700613224.h1
Method BLASTX
NCBI GI g4204314
BLAST score 180
E value 6.0e-13
Match length 153
% identity 29
NCBI Description (AC003027) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 280621
Contig ID 107097_1.R1011
5'-most EST uC-zmflb73048f05b1

Seq. No. 280622
Contig ID 107104_1.R1011
5'-most EST uC-zmflb73180d10b1
Method BLASTX
NCBI GI g3080426
BLAST score 549
E value 3.0e-56
Match length 186
% identity 56
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 280623
Contig ID 107139_1.R1011
5'-most EST xmt700263992.h1
Method BLASTX
NCBI GI g3483135
BLAST score 213
E value 5.0e-17
Match length 109
% identity 40
NCBI Description (AF051937) GMP synthetase [Lactobacillus rhamnosus]

Seq. No. 280624
Contig ID 107140_1.R1011
5'-most EST uC-zmflb73049a12b1
Method BLASTX
NCBI GI g3056601
BLAST score 163
E value 2.0e-17
Match length 133
% identity 37
NCBI Description (AC004255) T1F9.22 [Arabidopsis thaliana]

Seq. No. 280625
Contig ID 107146_1.R1011
5'-most EST uC-zmflb73049b06b1

Seq. No. 280626
Contig ID 107158_1.R1011
5'-most EST qmh700030260.f1
Method BLASTX
NCBI GI g4572671
BLAST score 416

E value	1.0e-40
Match length	143
% identity	55
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	280627
Contig ID	107162_1.R1011
5'-most EST	uC-zmflb73049d01b1
Method	BLASTX
NCBI GI	g2462834
BLAST score	291
E value	6.0e-26
Match length	111
% identity	55
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280628
Contig ID	107166_1.R1011
5'-most EST	yyf700352503.h1

Seq. No.	280629
Contig ID	107187_1.R1011
5'-most EST	uC-zmflb73049f07b1
Method	BLASTX
NCBI GI	g4235643
BLAST score	176
E value	1.0e-20
Match length	114
% identity	54
NCBI Description	(AF119040) NL0E [Lycopersicon esculentum]

Seq. No.	280630
Contig ID	107188_1.R1011
5'-most EST	uC-zmflb73049f08b1

Seq. No.	280631
Contig ID	107207_1.R1011
5'-most EST	wyr700240367.h1
Method	BLASTX
NCBI GI	g3335372
BLAST score	198
E value	1.0e-27
Match length	162
% identity	44
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No.	280632
Contig ID	107210_1.R1011
5'-most EST	uC-zmflb73050a05b1

Seq. No.	280633
Contig ID	107231_1.R1011
5'-most EST	xsy700217347.h1
Method	BLASTX
NCBI GI	g4512263
BLAST score	421

E value	6.0e-50
Match length	139
% identity	69
NCBI Description	(AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]

Seq. No.	280634
Contig ID	107236_1.R1011
5'-most EST	uC-zmflb73050c07b1
Method	BLASTX
NCBI GI	g4559333
BLAST score	236
E value	2.0e-38
Match length	215
% identity	43
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	280635
Contig ID	107267_1.R1011
5'-most EST	rvl700456460.h1

Seq. No.	280636
Contig ID	107269_1.R1011
5'-most EST	uC-zmflb73186b05b1
Method	BLASTX
NCBI GI	g4582443
BLAST score	177
E value	2.0e-12
Match length	66
% identity	52
NCBI Description	(AC007142) putative auxin-induced protein [Arabidopsis thaliana]

Seq. No.	280637
Contig ID	107269_2.R1011
5'-most EST	uC-zmflb73188g09a1

Seq. No.	280638
Contig ID	107279_1.R1011
5'-most EST	hbs701183154.h1
Method	BLASTX
NCBI GI	g2462834
BLAST score	221
E value	1.0e-17
Match length	132
% identity	36
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280639
Contig ID	107294_1.R1011
5'-most EST	cjh700193063.h1
Method	BLASTX
NCBI GI	g2506931
BLAST score	199
E value	2.0e-15
Match length	114
% identity	36
NCBI Description	APYRASE PRECURSOR (ATP-DIPHOSPHATASE) (ADENOSINE

DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE)
>gi_2129977_pir__JC4616 apyrase (EC 3.6.1.5) - potato
>gi_1381633 (U58597) ATP-diphosphohydrolase [Solanum tuberosum]

Seq. No.	280640
Contig ID	107303_1.R1011
5'-most EST	nbm700468714.h1
Method	BLASTX
NCBI GI	g1717870
BLAST score	344
E value	6.0e-32
Match length	276
% identity	33
NCBI Description	PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C8A4.01C (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)

Seq. No.	280641
Contig ID	107315_1.R1011
5'-most EST	uC-zmflb73051b12b1
Method	BLASTX
NCBI GI	g2288997
BLAST score	820
E value	3.0e-88
Match length	376
% identity	51
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280642
Contig ID	107316_1.R1011
5'-most EST	uC-zmflb73051c01b1
Method	BLASTX
NCBI GI	g3341684
BLAST score	169
E value	1.0e-11
Match length	121
% identity	34
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280643
Contig ID	107324_1.R1011
5'-most EST	uC-zmflb73051c10b1

Seq. No.	280644
Contig ID	107341_1.R1011
5'-most EST	uC-zmflb73051e06b1

Seq. No.	280645
Contig ID	107362_1.R1011
5'-most EST	uC-zmflb73051g03b1

Seq. No.	280646
Contig ID	107372_1.R1011
5'-most EST	uC-zmflb73051h06b1

Seq. No.	280647

Contig ID	107381_1.R1011
5'-most EST	uC-zmflb73222f10b1
Method	BLASTN
NCBI GI	g949979
BLAST score	151
E value	3.0e-79
Match length	263
% identity	89
NCBI Description	Z.mays Glossy2 locus DNA

Seq. No.	280648
Contig ID	107398_1.R1011
5'-most EST	uC-zmflb73147d10b1
Method	BLASTX
NCBI GI	g4630748
BLAST score	798
E value	3.0e-85
Match length	190
% identity	81
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	280649
Contig ID	107398_2.R1011
5'-most EST	uC-zmflb73194b08b2
Method	BLASTX
NCBI GI	g4630748
BLAST score	265
E value	2.0e-37
Match length	108
% identity	78
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	280650
Contig ID	107404_1.R1011
5'-most EST	uC-zmflb73052c11b1
Method	BLASTX
NCBI GI	g4128133
BLAST score	186
E value	5.0e-14
Match length	71
% identity	49
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	280651
Contig ID	107429_1.R1011
5'-most EST	uC-zmflb73137h08b1
Method	BLASTX
NCBI GI	g3242783
BLAST score	1458
E value	1.0e-166
Match length	414
% identity	69
NCBI Description	(AF055354) respiratory burst oxidase protein B [Arabidopsis thaliana]

Seq. No.	280652
Contig ID	107430_1.R1011
5'-most EST	uC-zmflmo17012d04b1
Method	BLASTX
NCBI GI	g3236240
BLAST score	1079
E value	1.0e-118
Match length	342
% identity	62
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	280653
Contig ID	107443_1.R1011
5'-most EST	uC-zmflb73052g11b1
Method	BLASTX
NCBI GI	g4160292
BLAST score	338
E value	2.0e-31
Match length	186
% identity	61
NCBI Description	(Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]

Seq. No.	280654
Contig ID	107456_1.R1011
5'-most EST	uC-zmflb73053a02b2
Method	BLASTX
NCBI GI	g4309734
BLAST score	426
E value	8.0e-42
Match length	189
% identity	46
NCBI Description	(AC006439) putative 26S proteosome regulatory subunit 8 [Arabidopsis thaliana]

Seq. No.	280655
Contig ID	107474_1.R1011
5'-most EST	uC-zmflb73053b09b2
Method	BLASTX
NCBI GI	g3493611
BLAST score	200
E value	2.0e-15
Match length	43
% identity	79
NCBI Description	(AF068318) regulatory subunit of protein kinase CK2; CK2 beta-subunit [Arabidopsis thaliana]

Seq. No.	280656
Contig ID	107500_1.R1011
5'-most EST	uC-zmflb73053e02b2

Seq. No.	280657
Contig ID	107500_2.R1011
5'-most EST	xdb700340763.h1

Seq. No.	280658
Contig ID	107502_2.R1011
5'-most EST	xyt700342461.h1

Method	BLASTX
NCBI GI	g3402685
BLAST score	291
E value	2.0e-26
Match length	93
% identity	58
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	280659
Contig ID	107514_1.R1011
5'-most EST	uC-zmflb73415c11a1

Seq. No.	280660
Contig ID	107528_1.R1011
5'-most EST	uC-zmflb73053h01b2

Seq. No.	280661
Contig ID	107532_1.R1011
5'-most EST	xyt700345041.h1
Method	BLASTX
NCBI GI	g4588012
BLAST score	1020
E value	1.0e-111
Match length	257
% identity	79
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	280662
Contig ID	107559_1.R1011
5'-most EST	uC-zmflmo17195b04b1

Seq. No.	280663
Contig ID	107564_1.R1011
5'-most EST	uC-zmflb73054c06b1
Method	BLASTX
NCBI GI	g3879914
BLAST score	190
E value	3.0e-14
Match length	137
% identity	35
NCBI Description	(Z74043) predicted using Genefinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk343f4.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	280664
Contig ID	107576_1.R1011
5'-most EST	uC-zmflmo17305c03a1
Method	BLASTX
NCBI GI	g2352795
BLAST score	517
E value	1.0e-105
Match length	233
% identity	83
NCBI Description	(AF007793) retinoblastoma-related protein 1 [Zea mays]

Seq. No.	280665
Contig ID	107578_1.R1011
5'-most EST	uC-zmflb73274f01b1
Method	BLASTX
NCBI GI	g4335763
BLAST score	147
E value	3.0e-09
Match length	59
% identity	53
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	280666
Contig ID	107589_1.R1011
5'-most EST	uC-zmflb73054e10b1

Seq. No.	280667
Contig ID	107590_1.R1011
5'-most EST	uC-zmflb73054e11b1

Seq. No.	280668
Contig ID	107600_1.R1011
5'-most EST	uC-zmflb73054f09b1

Seq. No.	280669
Contig ID	107613_1.R1011
5'-most EST	uC-zmflmo17168g03b1
Method	BLASTX
NCBI GI	g3461814
BLAST score	508
E value	3.0e-51
Match length	190
% identity	55
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280670
Contig ID	107613_2.R1011
5'-most EST	uC-zmflmo17244b05a1

Seq. No.	280671
Contig ID	107613_3.R1011
5'-most EST	uC-zmflmo17247a09a1

Seq. No.	280672
Contig ID	107625_1.R1011
5'-most EST	uC-zmflmo17341h04b1

Seq. No.	280673
Contig ID	107626_1.R1011
5'-most EST	gct701173721.h1

Seq. No.	280674
Contig ID	107633_1.R1011
5'-most EST	uC-zmflb73055a12b1
Method	BLASTX
NCBI GI	g4262174
BLAST score	407
E value	1.0e-39

Match length	127
% identity	59
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	280675
Contig ID	107634_1.R1011
5'-most EST	uC-zmflb73055c09b1

Seq. No.	280676
Contig ID	107641_1.R1011
5'-most EST	xdg700405228.h1

Seq. No.	280677
Contig ID	107648_1.R1011
5'-most EST	uC-zmflb73055c06b1
Method	BLASTX
NCBI GI	g3142290
BLAST score	402
E value	6.0e-39
Match length	167
% identity	47
NCBI Description	(AC002411) Contains similarity to gb_Z69902 from C. elegans. [Arabidopsis thaliana]

Seq. No.	280678
Contig ID	107669_1.R1011
5'-most EST	uC-zmflb73055e03b1
Method	BLASTX
NCBI GI	g1001478
BLAST score	369
E value	7.0e-35
Match length	223
% identity	35
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	280679
Contig ID	107722_1.R1011
5'-most EST	uC-zmflb73056b04b1

Seq. No.	280680
Contig ID	107763_1.R1011
5'-most EST	uC-zmflb73056f06b1

Seq. No.	280681
Contig ID	107778_1.R1011
5'-most EST	uC-zmflb73056g10b1
Method	BLASTX
NCBI GI	g3293031
BLAST score	585
E value	2.0e-60
Match length	139
% identity	77
NCBI Description	(AJ007574) amino acid carrier [Ricinus communis]

Seq. No.	280682
Contig ID	107803_1.R1011
5'-most EST	wyr700243751.h1

Seq. No.	280683
Contig ID	107808_1.R1011
5'-most EST	uC-zmflb73057d07b1

Seq. No.	280684
Contig ID	107821_1.R1011
5'-most EST	ymt700220136.h1
Method	BLASTX
NCBI GI	g3249065
BLAST score	553
E value	6.0e-57
Match length	139
% identity	74
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	280685
Contig ID	107841_1.R1011
5'-most EST	uC-zmflb73058b04b1

Seq. No.	280686
Contig ID	107854_1.R1011
5'-most EST	wyr700239377.h1
Method	BLASTX
NCBI GI	g1871181
BLAST score	277
E value	3.0e-24
Match length	115
% identity	54
NCBI Description	(U90439) ring zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	280687
Contig ID	107858_1.R1011
5'-most EST	uC-zmflb73256g05b1

Seq. No.	280688
Contig ID	107876_1.R1011
5'-most EST	xmt700261834.h1

Seq. No.	280689
Contig ID	107884_1.R1011
5'-most EST	uC-zmflmo17031f07b1

Seq. No.	280690
Contig ID	107891_1.R1011
5'-most EST	uC-zmflb73058g01b1
Method	BLASTX
NCBI GI	g4467125
BLAST score	1131
E value	1.0e-124
Match length	250
% identity	80
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	280691
Contig ID	107893_1.R1011
5'-most EST	qmh700027987.f1

Seq. No.	280692
Contig ID	107895_1.R1011
5'-most EST	mwy700438468.h1

Seq. No.	280693
Contig ID	107900_1.R1011
5'-most EST	uC-zmflb73058g12b1

Seq. No.	280694
Contig ID	107904_1.R1011
5'-most EST	xmt700265678.h1
Method	BLASTX
NCBI GI	g4584257
BLAST score	237
E value	1.0e-19
Match length	122
% identity	38
NCBI Description	(Y18472) SINA2p [Vitis vinifera]

Seq. No.	280695
Contig ID	107911_1.R1011
5'-most EST	hvj700620411.h1

Seq. No.	280696
Contig ID	107918_1.R1011
5'-most EST	uC-zmflmo17076d12b1
Method	BLASTX
NCBI GI	g1531758
BLAST score	277
E value	3.0e-24
Match length	90
% identity	63
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	280697
Contig ID	107924_1.R1011
5'-most EST	dyk700104640.h1
Method	BLASTX
NCBI GI	g1076685
BLAST score	302
E value	5.0e-27
Match length	328
% identity	34
NCBI Description	SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_ (D30038) SPF1 protein [Ipomoea batatas]

Seq. No.	280698
Contig ID	107929_1.R1011
5'-most EST	fC-zmfl700469144a2

Seq. No.	280699
Contig ID	107934_1.R1011

5'-most EST	uC-zmflmo17223a04b1
Method	BLASTX
NCBI GI	g2388577
BLAST score	252
E value	1.0e-21
Match length	131
% identity	42
NCBI Description	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No.	280700
Contig ID	107947_1.R1011
5'-most EST	xjt700092385.h1
Method	BLASTX
NCBI GI	g4506043
BLAST score	672
E value	2.0e-70
Match length	229
% identity	55
NCBI Description	prolyl endopeptidase >gi_1346769_sp_P48147_PPCE_HUMAN PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase [Homo sapiens]

Seq. No.	280701
Contig ID	107953_1.R1011
5'-most EST	gw1700614785.h1
Method	BLASTX
NCBI GI	g1946361
BLAST score	261
E value	2.0e-22
Match length	118
% identity	47
NCBI Description	(U93215) C3HC4 zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	280702
Contig ID	107956_1.R1011
5'-most EST	uC-zmflb73059f02b1
Method	BLASTX
NCBI GI	g3297813
BLAST score	170
E value	4.0e-12
Match length	69
% identity	51
NCBI Description	(AL031032) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280703
Contig ID	107964_1.R1011
5'-most EST	uC-zmflb73059f10b1

Seq. No.	280704
Contig ID	107979_1.R1011
5'-most EST	uC-zmflb73252e09b3
Method	BLASTX
NCBI GI	g3152613

BLAST score	258
E value	3.0e-22
Match length	98
% identity	49
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280705
Contig ID	107992_1.R1011
5'-most EST	uC-zmflmo17300f12b1
Method	BLASTX
NCBI GI	g3402690
BLAST score	180
E value	5.0e-13
Match length	64
% identity	56
NCBI Description	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	280706
Contig ID	107993_1.R1011
5'-most EST	uC-zmflmo17294d09b1
Method	BLASTX
NCBI GI	g3063699
BLAST score	428
E value	5.0e-42
Match length	161
% identity	50
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	280707
Contig ID	107993_2.R1011
5'-most EST	uC-zmflb73135h08b2
Method	BLASTX
NCBI GI	g3063699
BLAST score	347
E value	3.0e-32
Match length	201
% identity	40
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	280708
Contig ID	108008_1.R1011
5'-most EST	uC-zmflmo17222h12b1

Seq. No.	280709
Contig ID	108016_1.R1011
5'-most EST	qmh700027289.f1
Method	BLASTX
NCBI GI	g2462744
BLAST score	332
E value	9.0e-31
Match length	147
% identity	48
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	280710
Contig ID	108034_1.R1011

5'-most EST	uC-zmflb73060e10b1
Seq. No.	280711
Contig ID	108039_1.R1011
5'-most EST	uC-zmflb73067a12b1
Seq. No.	280712
Contig ID	108051_1.R1011
5'-most EST	uC-zmflb73060g07b1
Method	BLASTX
NCBI GI	g3687223
BLAST score	297
E value	8.0e-27
Match length	109
% identity	61
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.	280713
Contig ID	108057_1.R1011
5'-most EST	ntr700071720.h1
Method	BLASTX
NCBI GI	g2827704
BLAST score	314
E value	7.0e-29
Match length	98
% identity	62
NCBI Description	(AL021684) LRR-like protein [Arabidopsis thaliana]
Seq. No.	280714
Contig ID	108058_1.R1011
5'-most EST	nbm700473986.h1
Method	BLASTX
NCBI GI	g4454006
BLAST score	203
E value	3.0e-15
Match length	118
% identity	44
NCBI Description	(AL035396) hypothetical protein [Arabidopsis thaliana]
Seq. No.	280715
Contig ID	108062_1.R1011
5'-most EST	uC-zmflb73060h07b1
Method	BLASTX
NCBI GI	g2459424
BLAST score	256
E value	8.0e-22
Match length	171
% identity	36
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]
Seq. No.	280716
Contig ID	108079_1.R1011
5'-most EST	uC-zmflb73061b03b1
Method	BLASTX
NCBI GI	g1708972
BLAST score	548
E value	5.0e-63

Match length	266
% identity	50
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR (HYDROXYNITRILE LYASE 3) ((R)-OXYNITRILASE 3) >gi_1262279 (U51562) (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus serotina] >gi_2343181 (AF013161) (R)-(+)-mandelonitrile lyase isoform MDL3 precursor [Prunus serotina]

Seq. No.	280717
Contig ID	108083_1.R1011
5'-most EST	xsy700207818.h1

Seq. No.	280718
Contig ID	108096_1.R1011
5'-most EST	uC-zmflb73061c11b1

Seq. No.	280719
Contig ID	108129_1.R1011
5'-most EST	uC-zmflb73061g02b1

Seq. No.	280720
Contig ID	108132_1.R1011
5'-most EST	tfd700572454.h1

Seq. No.	280721
Contig ID	108134_1.R1011
5'-most EST	uC-zmroteosinte096a02b2

Seq. No.	280722
Contig ID	108149_2.R1011
5'-most EST	uC-zmflb73061h12b1

Seq. No.	280723
Contig ID	108151_1.R1011
5'-most EST	uC-zmflb73062a02b1
Method	BLASTX
NCBI GI	g3367576
BLAST score	197
E value	3.0e-15
Match length	65
% identity	58
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	280724
Contig ID	108166_1.R1011
5'-most EST	uC-zmflb73062b07b1

Seq. No.	280725
Contig ID	108175_1.R1011
5'-most EST	uC-zmflb73062c06b1

Seq. No.	280726
Contig ID	108179_1.R1011
5'-most EST	uC-zmroteosinte023g11b2

Seq. No.	280727

Contig ID	108185_1.R1011
5'-most EST	uC-zmflb73084f05b2
Method	BLASTX
NCBI GI	g4585972
BLAST score	375
E value	4.0e-44
Match length	218
% identity	47
NCBI Description	(AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No.	280728
Contig ID	108188_1.R1011
5'-most EST	uC-zmflb73062d08b1
Method	BLASTX
NCBI GI	g2245020
BLAST score	305
E value	1.0e-27
Match length	92
% identity	61
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	280729
Contig ID	108198_1.R1011
5'-most EST	uC-zmflb73167e06b2

Seq. No.	280730
Contig ID	108201_1.R1011
5'-most EST	uC-zmflb73062e09b1
Method	BLASTX
NCBI GI	g4581149
BLAST score	398
E value	2.0e-38
Match length	229
% identity	45
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280731
Contig ID	108230_1.R1011
5'-most EST	uC-zmflb73062h04b1
Method	BLASTX
NCBI GI	g1389835
BLAST score	190
E value	4.0e-14
Match length	78
% identity	53
NCBI Description	(U59284) Linum usitatissimum peroxidase (FLXPER3) mRNA, complete cds. [Linum usitatissimum]

Seq. No.	280732
Contig ID	108236_1.R1011
5'-most EST	ymt700220258.h1
Method	BLASTX
NCBI GI	g4249418
BLAST score	191
E value	2.0e-14
Match length	88
% identity	35

NCBI Description	(AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H type domains), 5' partial [Arabidopsis thaliana]

Seq. No.	280733
Contig ID	108244_1.R1011
5'-most EST	uC-zmflb73063a07b1

Seq. No.	280734
Contig ID	108246_1.R1011
5'-most EST	dyk700103173.h1

Seq. No.	280735
Contig ID	108249_1.R1011
5'-most EST	uC-zmflb73063a12b1

Seq. No.	280736
Contig ID	108270_1.R1011
5'-most EST	ntr700071891.h1
Method	BLASTX
NCBI GI	g629769
BLAST score	189
E value	6.0e-14
Match length	71
% identity	55
NCBI Description	histone-like DNA-binding protein PF 1 - oat (strain Gary) >gi_454279 (L24391) DNA-binding protein [Avena sativa]

Seq. No.	280737
Contig ID	108273_1.R1011
5'-most EST	uC-zmflmo17273b08b1
Method	BLASTX
NCBI GI	g3004565
BLAST score	900
E value	2.0e-97
Match length	203
% identity	41
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	280738
Contig ID	108284_1.R1011
5'-most EST	uC-zmflmo17330b09b1

Seq. No.	280739
Contig ID	108292_1.R1011
5'-most EST	uC-zmflb73063e12b1

Seq. No.	280740
Contig ID	108304_2.R1011
5'-most EST	uC-zmflmo17270a02b1

Seq. No.	280741
Contig ID	108307_1.R1011
5'-most EST	uC-zmflb73159a07a2

Seq. No.	280742
Contig ID	108309_1.R1011
5'-most EST	uC-zmflb73063g06b1

Seq. No.	280743
Contig ID	108316_1.R1011
5'-most EST	uC-zmflmo17294f04b1

Seq. No.	280744
Contig ID	108323_1.R1011
5'-most EST	uC-zmflb73063h08b1
Method	BLASTX
NCBI GI	g2105430
BLAST score	184
E value	1.0e-13
Match length	111
% identity	42
NCBI Description	(U97079) U5-116kD [Mus musculus]

Seq. No.	280745
Contig ID	108340_1.R1011
5'-most EST	uC-zmroteosinte102b06b2

Seq. No.	280746
Contig ID	108360_1.R1011
5'-most EST	nbm700468168.h1

Seq. No.	280747
Contig ID	108377_1.R1011
5'-most EST	uC-zmflb73064e04b1
Method	BLASTX
NCBI GI	g3935168
BLAST score	493
E value	9.0e-50
Match length	155
% identity	65
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	280748
Contig ID	108395_1.R1011
5'-most EST	uC-zmflb73064g03b1
Method	BLASTX
NCBI GI	g2982431
BLAST score	293
E value	3.0e-26
Match length	93
% identity	57
NCBI Description	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]

Seq. No.	280749
Contig ID	108408_1.R1011
5'-most EST	xmt700262461.h1
Method	BLASTX
NCBI GI	g3413481
BLAST score	168
E value	2.0e-17
Match length	88
% identity	53
NCBI Description	(AJ006786) serine protease [Lycopersicon esculentum]

Seq. No.	280750
Contig ID	108410_1.R1011
5'-most EST	uC-zmflb73064h09b1
Seq. No.	280751
Contig ID	108413_1.R1011
5'-most EST	uC-zmroteosinte007f06b1
Seq. No.	280752
Contig ID	108425_1.R1011
5'-most EST	uC-zmflb73065b09b1
Seq. No.	280753
Contig ID	108435_2.R1011
5'-most EST	uC-zmflmo17238f02a1
Method	BLASTN
NCBI GI	g4584684
BLAST score	42
E value	3.0e-14
Match length	97
% identity	86
NCBI Description	Hordeum vulgare high light-induced mRNA for putative lectin (18kDa)
Seq. No.	280754
Contig ID	108436_1.R1011
5'-most EST	dyk700102943.h1
Method	BLASTX
NCBI GI	g2894605
BLAST score	214
E value	4.0e-17
Match length	125
% identity	40
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	280755
Contig ID	108470_1.R1011
5'-most EST	uwc700150333.h1
Seq. No.	280756
Contig ID	108473_1.R1011
5'-most EST	uC-zmflb73066a05b1
Seq. No.	280757
Contig ID	108479_1.R1011
5'-most EST	ymt700222622.h1
Method	BLASTX
NCBI GI	g3367583
BLAST score	424
E value	1.0e-41
Match length	94
% identity	86
NCBI Description	(AL031135) NAD+ dependent isocitrate dehydrogenase -like protein [Arabidopsis thaliana]
Seq. No.	280758

Contig ID	108484_1.R1011
5'-most EST	uC-zmflb73160a04b2

Seq. No.	280759
Contig ID	108514_1.R1011
5'-most EST	pmx700087652.h1
Method	BLASTX
NCBI GI	g2827715
BLAST score	1133
E value	1.0e-124
Match length	232
% identity	92
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	280760
Contig ID	108516_1.R1011
5'-most EST	ypc700807059.h1
Method	BLASTX
NCBI GI	g2642156
BLAST score	173
E value	3.0e-12
Match length	87
% identity	40
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280761
Contig ID	108523_1.R1011
5'-most EST	uC-zmflb73099h11b1

Seq. No.	280762
Contig ID	108539_1.R1011
5'-most EST	yyf700351146.h1

Seq. No.	280763
Contig ID	108550_1.R1011
5'-most EST	uC-zmflb73066h08b1
Method	BLASTX
NCBI GI	g2244813
BLAST score	461
E value	7.0e-46
Match length	150
% identity	57
NCBI Description	(Z97336) acylaminoacyl-peptidase homolog [Arabidopsis thaliana]

Seq. No.	280764
Contig ID	108554_1.R1011
5'-most EST	ydl700405372.h1
Method	BLASTX
NCBI GI	g1709039
BLAST score	147
E value	5.0e-21
Match length	157
% identity	44
NCBI Description	MIS5 PROTEIN >gi_829086_dbj_BAA06729_ (D31960) unknown [Schizosaccharomyces pombe]

Seq. No.	280765
Contig ID	108570_1.R1011
5'-most EST	xmt700265234.h1
Method	BLASTX
NCBI GI	g4507315
BLAST score	309
E value	1.0e-27
Match length	191
% identity	35
NCBI Description	suppressor of var1 (S.cerevisiae) 3-like 1 >gi_2801555 (AF042169) putative ATP-dependent mitochondrial RNA helicase [Homo sapiens]

Seq. No.	280766
Contig ID	108580_1.R1011
5'-most EST	uC-zmflb73067c07a1

Seq. No.	280767
Contig ID	108590_1.R1011
5'-most EST	xjt700096136.h1
Method	BLASTX
NCBI GI	g4335745
BLAST score	199
E value	2.0e-15
Match length	83
% identity	49
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	280768
Contig ID	108601_1.R1011
5'-most EST	uC-zmflmo17134h01b1
Method	BLASTN
NCBI GI	g2656029
BLAST score	51
E value	1.0e-19
Match length	71
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	280769
Contig ID	108609_1.R1011
5'-most EST	uC-zmflb73067f06b1
Method	BLASTX
NCBI GI	g3132472
BLAST score	145
E value	7.0e-09
Match length	113
% identity	35
NCBI Description	(AC003096) unknown protein [Arabidopsis thaliana]

Seq. No.	280770
Contig ID	108616_1.R1011
5'-most EST	uC-zmflb73159g11b2

Seq. No.	280771
Contig ID	108618_1.R1011
5'-most EST	xmt700267410.h1

Seq. No.	280772
Contig ID	108629_1.R1011
5'-most EST	uC-zmflb73067h12b1
Method	BLASTX
NCBI GI	g455399
BLAST score	402
E value	6.0e-39
Match length	93
% identity	83
NCBI Description	(D21068) dihydrolipoamide acetyltransferase [Oryza sativa]

Seq. No.	280773
Contig ID	108642_1.R1011
5'-most EST	uC-zmflb73068b05b1

Seq. No.	280774
Contig ID	108645_1.R1011
5'-most EST	uC-zmflb73068b08a1

Seq. No.	280775
Contig ID	108652_1.R1011
5'-most EST	uer700579624.h1

Seq. No.	280776
Contig ID	108677_1.R1011
5'-most EST	uC-zmflb73068e09b1
Method	BLASTX
NCBI GI	g2961378
BLAST score	353
E value	2.0e-33
Match length	87
% identity	36
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	280777
Contig ID	108679_1.R1011
5'-most EST	uC-zmflb73214b08b1

Seq. No.	280778
Contig ID	108689_1.R1011
5'-most EST	uC-zmflb73068f11b1

Seq. No.	280779
Contig ID	108690_1.R1011
5'-most EST	ntr700071866.h1

Seq. No.	280780
Contig ID	108695_1.R1011
5'-most EST	uC-zmflb73088f12b2
Method	BLASTX
NCBI GI	g4008006
BLAST score	324

E value	5.0e-30
Match length	94
% identity	63
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	280781
Contig ID	108695_2.R1011
5'-most EST	uC-zmflb73068g06b1
Method	BLASTX
NCBI GI	g4008006
BLAST score	473
E value	2.0e-47
Match length	140
% identity	60
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	280782
Contig ID	108698_1.R1011
5'-most EST	uC-zmflb73068g09b1

Seq. No.	280783
Contig ID	108700_1.R1011
5'-most EST	gct701174086.h1
Method	BLASTX
NCBI GI	g4454465
BLAST score	160
E value	1.0e-10
Match length	108
% identity	33
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	280784
Contig ID	108709_1.R1011
5'-most EST	rvl700454470.h1

Seq. No.	280785
Contig ID	108716_1.R1011
5'-most EST	uC-zmflb73069a09b1
Method	BLASTX
NCBI GI	g3702316
BLAST score	707
E value	1.0e-74
Match length	179
% identity	70
NCBI Description	(AC005397) putative Cop1 protein, 5' partial [Arabidopsis thaliana]

Seq. No.	280786
Contig ID	108739_1.R1011
5'-most EST	uC-zmflmo17015e03b1
Method	BLASTX
NCBI GI	g2252840
BLAST score	336
E value	2.0e-31
Match length	125

% identity	50
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	280787
Contig ID	108746_1.R1011
5'-most EST	uC-zmflb73069d11b1

Seq. No.	280788
Contig ID	108759_1.R1011
5'-most EST	uC-zmflb73069f08b1
Method	BLASTX
NCBI GI	g541816
BLAST score	984
E value	1.0e-107
Match length	245
% identity	78
NCBI Description	protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	280789
Contig ID	108771_1.R1011
5'-most EST	uer700582716.h1
Method	BLASTX
NCBI GI	g1220453
BLAST score	484
E value	2.0e-48
Match length	158
% identity	58
NCBI Description	(M79328) alpha-amylase [Solanum tuberosum]

Seq. No.	280790
Contig ID	108771_2.R1011
5'-most EST	uC-zmflb73069g08b1

Seq. No.	280791
Contig ID	108774_1.R1011
5'-most EST	uC-zmflb73069g12b1

Seq. No.	280792
Contig ID	108789_1.R1011
5'-most EST	uC-zmflmo17259c04b1
Method	BLASTX
NCBI GI	g2832643
BLAST score	172
E value	8.0e-12
Match length	82
% identity	48
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280793
Contig ID	108798_1.R1011
5'-most EST	uC-zmflMo17007e08b1
Method	BLASTX
NCBI GI	g1174740
BLAST score	739
E value	2.0e-78

Match length	188
% identity	73
NCBI Description	DNA TOPOISOMERASE II >gi_2129576_pir__S53599 DNA topoisomerase II - Arabidopsis thaliana >gi_474890 (L21015) topoisomerase II [Arabidopsis thaliana]

Seq. No.	280794
Contig ID	108800_1.R1011
5'-most EST	uC-zmflb73070b04b1
Method	BLASTX
NCBI GI	g2688111
BLAST score	148
E value	8.0e-11
Match length	154
% identity	29
NCBI Description	(AE001132) gufA protein [Borrelia burgdorferi]

Seq. No.	280795
Contig ID	108803_1.R1011
5'-most EST	uC-zmflb73070b07b1

Seq. No.	280796
Contig ID	108872_1.R1011
5'-most EST	uC-zmflb73071a05b3

Seq. No.	280797
Contig ID	108876_1.R1011
5'-most EST	uC-zmroteosinte073g11b1

Seq. No.	280798
Contig ID	108926_1.R1011
5'-most EST	uC-zmflmo17285a04b1
Method	BLASTX
NCBI GI	g3875410
BLAST score	245
E value	6.0e-36
Match length	235
% identity	37
NCBI Description	(Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	280799
Contig ID	108939_1.R1011
5'-most EST	uC-zmflb73071h01b3

Seq. No.	280800
Contig ID	108942_1.R1011
5'-most EST	uC-zmflmo17301a08b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	280801
Contig ID	108959_1.R1011
5'-most EST	uC-zmflmo17289d03b1
Method	BLASTX
NCBI GI	g3785995
BLAST score	1076
E value	1.0e-118
Match length	277
% identity	80
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	280802
Contig ID	108963_1.R1011
5'-most EST	uC-zmflmo17029h05b1

Seq. No.	280803
Contig ID	108966_1.R1011
5'-most EST	uC-zmroteosinte015c02b1
Method	BLASTX
NCBI GI	g1170619
BLAST score	597
E value	7.0e-72
Match length	417
% identity	37
NCBI Description	KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830 kinesin-related protein katA - Arabidopsis thaliana >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor protein heavy chain [Arabidopsis thaliana] >gi_2911084_emb_CAA17546.1_ (AL021960) kinesin-related protein katA [Arabidopsis thaliana]

Seq. No.	280804
Contig ID	108970_1.R1011
5'-most EST	uC-zmflb73073b12b3
Method	BLASTX
NCBI GI	g4038035
BLAST score	347
E value	2.0e-32
Match length	203
% identity	42
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	280805
Contig ID	108979_1.R1011
5'-most EST	uC-zmflmo17209b11a1
Method	BLASTN
NCBI GI	g2213642
BLAST score	67
E value	4.0e-29
Match length	135
% identity	87
NCBI Description	Oryza sativa glossy1 homolog mRNA, partial cds

Seq. No.	280806
Contig ID	108981_1.R1011
5'-most EST	uC-zmflb73073c11b3

Method	BLASTX
NCBI GI	g3450842
BLAST score	552
E value	1.0e-56
Match length	162
% identity	71
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	280807
Contig ID	108997_1.R1011
5'-most EST	yyf700349966.h1
Method	BLASTX
NCBI GI	g3355487
BLAST score	219
E value	6.0e-20
Match length	202
% identity	36
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	280808
Contig ID	109015_1.R1011
5'-most EST	uC-zmflb73073f10b3
Method	BLASTX
NCBI GI	g2258469
BLAST score	291
E value	4.0e-26
Match length	113
% identity	55
NCBI Description	(AF009179) replication protein A1 [Oryza sativa]

Seq. No.	280809
Contig ID	109040_1.R1011
5'-most EST	uC-zmflb73073h11b3

Seq. No.	280810
Contig ID	109071_1.R1011
5'-most EST	wyr700239372.h1
Method	BLASTX
NCBI GI	g3128208
BLAST score	257
E value	2.0e-22
Match length	91
% identity	52
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280811
Contig ID	109073_1.R1011
5'-most EST	uC-zmflb73076e03b2
Method	BLASTX
NCBI GI	g1076742
BLAST score	340
E value	9.0e-32
Match length	73
% identity	84
NCBI Description	cyclin - rice >gi_558621_emb_CAA57555_ (X82035) cyclin [Oryza sativa]

Seq. No.	280812
Contig ID	109094_1.R1011
5'-most EST	uC-zmflb73076g02b2

Seq. No.	280813
Contig ID	109129_1.R1011
5'-most EST	uC-zmflb73077b05b2
Method	BLASTX
NCBI GI	g4038035
BLAST score	184
E value	2.0e-13
Match length	52
% identity	63
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	280814
Contig ID	109183_1.R1011
5'-most EST	xmt700265676.h1

Seq. No.	280815
Contig ID	109189_1.R1011
5'-most EST	uC-zmflb73180f08b1

Seq. No.	280816
Contig ID	109190_1.R1011
5'-most EST	uC-zmflb73077h02b2
Method	BLASTX
NCBI GI	g1169544
BLAST score	543
E value	1.0e-55
Match length	152
% identity	73
NCBI Description	ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) ERD1 protein [Arabidopsis thaliana]

Seq. No.	280817
Contig ID	109194_1.R1011
5'-most EST	ymt700220416.h1

Seq. No.	280818
Contig ID	109244_1.R1011
5'-most EST	cyk700051421.f1
Method	BLASTX
NCBI GI	g2262113
BLAST score	301
E value	5.0e-27
Match length	75
% identity	77
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	280819
Contig ID	109251_1.R1011
5'-most EST	uC-zmflb73078f07b2

Seq. No.	280820
Contig ID	109289_1.R1011
5'-most EST	ymt700219670.h1
Method	BLASTX
NCBI GI	g1841864
BLAST score	159
E value	1.0e-10
Match length	54
% identity	54
NCBI Description	(U87108) nucleic acid binding protein [Trypanosoma equiperdum]

Seq. No.	280821
Contig ID	109289_5.R1011
5'-most EST	xjt700095579.h1

Seq. No.	280822
Contig ID	109289_6.R1011
5'-most EST	fdz701160865.h1

Seq. No.	280823
Contig ID	109293_1.R1011
5'-most EST	xmt700264117.h1

Seq. No.	280824
Contig ID	109309_1.R1011
5'-most EST	uC-zmflb73079d05b2

Seq. No.	280825
Contig ID	109312_1.R1011
5'-most EST	uC-zmflb73079d08b2

Seq. No.	280826
Contig ID	109317_1.R1011
5'-most EST	uC-zmflb73079e02b2

Seq. No.	280827
Contig ID	109324_1.R1011
5'-most EST	uC-zmflb73205e10b2

Seq. No.	280828
Contig ID	109338_1.R1011
5'-most EST	uC-zmflb73079g01b2
Method	BLASTX
NCBI GI	g2829910
BLAST score	750
E value	9.0e-80
Match length	194
% identity	28
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	280829
Contig ID	109349_1.R1011
5'-most EST	uC-zmflb73079h02b2

Seq. No.	280830

Contig ID	109351_1.R1011
5'-most EST	xsy700214859.h1
Method	BLASTX
NCBI GI	g3212865
BLAST score	893
E value	2.0e-96
Match length	241
% identity	70
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	280831
Contig ID	109358_1.R1011
5'-most EST	uC-zmflb73080a04b2
Method	BLASTX
NCBI GI	g3549665
BLAST score	366
E value	1.0e-34
Match length	155
% identity	52
NCBI Description	(AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280832
Contig ID	109364_1.R1011
5'-most EST	uC-zmflb73080a10b2

Seq. No.	280833
Contig ID	109374_1.R1011
5'-most EST	uC-zmflmo17292c09a1
Method	BLASTX
NCBI GI	g2244973
BLAST score	809
E value	1.0e-88
Match length	533
% identity	39
NCBI Description	(Z97340) similarity to extensin class 1 protein [Arabidopsis thaliana]

Seq. No.	280834
Contig ID	109385_1.R1011
5'-most EST	pwf700321631.h1

Seq. No.	280835
Contig ID	109390_1.R1011
5'-most EST	uC-zmflb73080d02b2

Seq. No.	280836
Contig ID	109423_1.R1011
5'-most EST	uC-zmflb73080g06b2

Seq. No.	280837
Contig ID	109429_1.R1011
5'-most EST	uC-zmflmo17201a06b1
Method	BLASTX
NCBI GI	g2529677
BLAST score	501
E value	1.0e-64
Match length	180

% identity	69
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]
Seq. No.	280838
Contig ID	109436_1.R1011
5'-most EST	uC-zmflb73080h09b2
Seq. No.	280839
Contig ID	109444_1.R1011
5'-most EST	uC-zmflb73149f09b1
Method	BLASTX
NCBI GI	g3184291
BLAST score	386
E value	6.0e-37
Match length	251
% identity	39
NCBI Description	(AC004136) putative DNA polymerase III gamma subunit [Arabidopsis thaliana]
Seq. No.	280840
Contig ID	109446_1.R1011
5'-most EST	uC-zmflb73083a08b2
Seq. No.	280841
Contig ID	109448_1.R1011
5'-most EST	nbm700474233.h1
Seq. No.	280842
Contig ID	109453_1.R1011
5'-most EST	uC-zmflb73083b06b2
Seq. No.	280843
Contig ID	109456_1.R1011
5'-most EST	uC-zmflMo17084a06b1
Method	BLASTX
NCBI GI	g218179
BLAST score	1124
E value	1.0e-123
Match length	250
% identity	92
NCBI Description	(D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H ATPase [Oryza sativa]
Seq. No.	280844
Contig ID	109463_1.R1011
5'-most EST	uC-zmflb73083c06b2
Seq. No.	280845
Contig ID	109469_1.R1011
5'-most EST	uC-zmflb73083d02b2
Seq. No.	280846
Contig ID	109472_1.R1011
5'-most EST	uC-zmflm017233c09b1
Seq. No.	280847

Contig ID	109472_2.R1011
5'-most EST	uC-zmflb73083d05b2
Method	BLASTX
NCBI GI	g2408029
BLAST score	177
E value	3.0e-18
Match length	158
% identity	34
NCBI Description	(Z99162) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	280848
Contig ID	109486_1.R1011
5'-most EST	tzu700205368.h1

Seq. No.	280849
Contig ID	109505_1.R1011
5'-most EST	uC-zmflb73083g07b2

Seq. No.	280850
Contig ID	109525_1.R1011
5'-most EST	uer700580909.h1
Method	BLASTX
NCBI GI	g3335348
BLAST score	370
E value	4.0e-35
Match length	113
% identity	65
NCBI Description	(AC004512) T8F5.20 [Arabidopsis thaliana]

Seq. No.	280851
Contig ID	109527_1.R1011
5'-most EST	uC-zmrob73050d04a1

Seq. No.	280852
Contig ID	109532_1.R1011
5'-most EST	uC-zmflb73084b09b2
Method	BLASTX
NCBI GI	g3047114
BLAST score	313
E value	1.0e-28
Match length	171
% identity	39
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	280853
Contig ID	109534_1.R1011
5'-most EST	uC-zmflb73084b11b2

Seq. No.	280854
Contig ID	109534_2.R1011
5'-most EST	uC-zmflmo17339d09a1

Seq. No.	280855
Contig ID	109540_1.R1011
5'-most EST	uC-zmflb73084c06b2

Seq. No.	280856

09604-09605-09606

Contig ID	109552_1.R1011
5'-most EST	uC-zmflb73084d06b2
Method	BLASTX
NCBI GI	g4455199
BLAST score	259
E value	3.0e-22
Match length	134
% identity	46
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	280857
Contig ID	109575_1.R1011
5'-most EST	uC-zmflmo17067c11a1
Method	BLASTX
NCBI GI	g4371296
BLAST score	277
E value	3.0e-24
Match length	117
% identity	51
NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	280858
Contig ID	109586_1.R1011
5'-most EST	uC-zmflb73084h06b2

Seq. No.	280859
Contig ID	109597_1.R1011
5'-most EST	xmt700267033.h1

Seq. No.	280860
Contig ID	109609_1.R1011
5'-most EST	uC-zmflb73218g08b2
Method	BLASTX
NCBI GI	g2739168
BLAST score	590
E value	8.0e-61
Match length	244
% identity	45
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	280861
Contig ID	109673_1.R1011
5'-most EST	hvj700623774.h1

Seq. No.	280862
Contig ID	109681_1.R1011
5'-most EST	uC-zmflb73216a03b2

Seq. No.	280863
Contig ID	109691_1.R1011
5'-most EST	uC-zmflb73086e03b2
Method	BLASTX
NCBI GI	g4585872
BLAST score	342
E value	5.0e-32

Match length	118
% identity	56
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	280864
Contig ID	109695_1.R1011
5'-most EST	xjt700095157.h1
Method	BLASTX
NCBI GI	g4432839
BLAST score	527
E value	2.0e-53
Match length	171
% identity	61
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.	280865
Contig ID	109730_1.R1011
5'-most EST	uC-zmflb73088a09b2
Seq. No.	280866
Contig ID	109742_1.R1011
5'-most EST	nbm700465112.h1
Seq. No.	280867
Contig ID	109742_2.R1011
5'-most EST	uC-zmflb73170b12b2
Seq. No.	280868
Contig ID	109743_1.R1011
5'-most EST	xsy700214471.h1
Method	BLASTX
NCBI GI	g542058
BLAST score	254
E value	6.0e-39
Match length	192
% identity	50
NCBI Description	HSR203J protein - common tobacco >gi_444002_emb_CAA54393_ (X77136) HSR203J [Nicotiana tabacum]
Seq. No.	280869
Contig ID	109777_1.R1011
5'-most EST	uC-zmroteosinte074f01b1
Method	BLASTX
NCBI GI	g3135672
BLAST score	182
E value	6.0e-13
Match length	113
% identity	43
NCBI Description	(AF064070) putative 1-acyl-sn-glycerol-3-phosphate acyltransferase [Burkholderia pseudomallei]
Seq. No.	280870
Contig ID	109783_1.R1011
5'-most EST	uC-zmflb73195h06b1
Method	BLASTX
NCBI GI	g4582446
BLAST score	342

E value	6.0e-32
Match length	142
% identity	50
NCBI Description	(AC007071) putative RING finger protein [Arabidopsis thaliana]

Seq. No.	280871
Contig ID	109783_2.R1011
5'-most EST	uC-zmflb73260d11b2

Seq. No.	280872
Contig ID	109792_1.R1011
5'-most EST	tfd700574322.h2
Method	BLASTX
NCBI GI	g3283051
BLAST score	546
E value	7.0e-56
Match length	172
% identity	59
NCBI Description	(AF053977) cell division cycle protein 23 [Homo sapiens] >gi_4519431_dbj_BAA75628.1_ (AB011472) CDC23 [Homo sapiens]

Seq. No.	280873
Contig ID	109808_1.R1011
5'-most EST	uC-zmflb73091c12b2
Method	BLASTX
NCBI GI	g3885328
BLAST score	800
E value	2.0e-85
Match length	202
% identity	75
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	280874
Contig ID	109819_1.R1011
5'-most EST	uC-zmflb73091e02b2
Method	BLASTX
NCBI GI	g112837
BLAST score	399
E value	1.0e-38
Match length	148
% identity	51
NCBI Description	NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE >gi_99953_pir__S14222 reductase - soybean >gi_18728_emb_CAA39261_ (X55730) reductase [Glycine max]

Seq. No.	280875
Contig ID	109824_1.R1011
5'-most EST	uC-zmflb73091e07b2
Method	BLASTX
NCBI GI	g730431
BLAST score	149
E value	2.0e-09
Match length	113
% identity	33
NCBI Description	PERIODIC TRYPTOPHAN PROTEIN 2 >gi_626864_pir__S44226 PWP2

09604759 - 090604

protein - yeast (Saccharomyces cerevisiae)
>gi_475231_emb_CAA55558_ (X78964) periodic tryptophan protein 2 [Saccharomyces cerevisiae]
>gi_1907198_emb_CAA42286_ (X59720) YCR057c, len:923 [Saccharomyces cerevisiae]

Seq. No.	280876
Contig ID	109825_1.R1011
5'-most EST	uC-zmflb73091e08b2

Seq. No.	280877
Contig ID	109831_1.R1011
5'-most EST	uC-zmflb73091f02b2
Method	BLASTX
NCBI GI	g3367592
BLAST score	295
E value	5.0e-35
Match length	141
% identity	57
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	280878
Contig ID	109839_1.R1011
5'-most EST	uC-zmflb73091f10b2

Seq. No.	280879
Contig ID	109840_1.R1011
5'-most EST	ymt700219656.h1
Method	BLASTX
NCBI GI	g1708095
BLAST score	199
E value	3.0e-15
Match length	60
% identity	60
NCBI Description	DNA GYRASE SUBUNIT B >gi_1107468 (L27512) gyrase B [Mycobacterium tuberculosis]

Seq. No.	280880
Contig ID	109858_1.R1011
5'-most EST	fdz701163830.h1
Method	BLASTX
NCBI GI	g1353157
BLAST score	201
E value	3.0e-17
Match length	152
% identity	37
NCBI Description	HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II >gi_3878900_emb_CAA86774_ (Z46794) similar to vacuolar biogenesis protein (pep5); cDNA EST EMBL:D27614 comes from this gene; cDNA EST EMBL:D34974 comes from this gene [Caenorhabditis elegans]

Seq. No.	280881
Contig ID	109863_1.R1011
5'-most EST	uC-zmflb73092a04b2

Seq. No. 280882

Contig ID	109896_1.R1011
5'-most EST	uC-zmflb73092d04b2
Method	BLASTX
NCBI GI	g4580395
BLAST score	313
E value	9.0e-29
Match length	153
% identity	41
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	280883
Contig ID	109910_1.R1011
5'-most EST	uC-zmflb73092e07b2

Seq. No.	280884
Contig ID	109917_1.R1011
5'-most EST	uC-zmflb73092f04b2

Seq. No.	280885
Contig ID	109917_2.R1011
5'-most EST	uC-zmflmo17171b10b1
Method	BLASTX
NCBI GI	g2589164
BLAST score	488
E value	6.0e-49
Match length	127
% identity	76
NCBI Description	(D88452) aldehyde oxidase-2 [Zea mays]

Seq. No.	280886
Contig ID	109926_1.R1011
5'-most EST	fC-zmle70044419f8
Method	BLASTX
NCBI GI	g3335375
BLAST score	858
E value	1.0e-92
Match length	172
% identity	93
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	280887
Contig ID	109926_2.R1011
5'-most EST	uC-zmflb73092g02b2
Method	BLASTX
NCBI GI	g3335375
BLAST score	649
E value	5.0e-68
Match length	138
% identity	87
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	280888
Contig ID	109929_1.R1011
5'-most EST	uC-zmflb73092g05b2

Seq. No.	280889

Contig ID 109929_2.R1011
5'-most EST gct701l74178.h1

Seq. No. 280890
Contig ID 109950_1.R1011
5'-most EST uC-zmroteosinte095e02b2

Seq. No. 280891
Contig ID 109965_1.R1011
5'-most EST uC-zmroteosinte108h08b3
Method BLASTX
NCBI GI g4455299
BLAST score 855
E value 5.0e-92
Match length 196
% identity 76
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 280892
Contig ID 109969_1.R1011
5'-most EST uC-zmflb73093d01b2
Method BLASTX
NCBI GI g4432794
BLAST score 410
E value 5.0e-40
Match length 163
% identity 47
NCBI Description (AC006437) putative Tnp2 Tam1 transposon protein [Antirrhinum majus] [Arabidopsis thaliana]

Seq. No. 280893
Contig ID 109988_1.R1011
5'-most EST uC-zmflb73093e10b2

Seq. No. 280894
Contig ID 109989_1.R1011
5'-most EST pmx700084435.h1
Method BLASTX
NCBI GI g4582457
BLAST score 284
E value 1.0e-25
Match length 62
% identity 74
NCBI Description (AC007071) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 280895
Contig ID 109990_1.R1011
5'-most EST uC-zmflmo17312b04b1
Method BLASTX
NCBI GI g3451066
BLAST score 209
E value 2.0e-16
Match length 100
% identity 44
NCBI Description (AL031326) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280896
Contig ID	109999_1.R1011
5'-most EST	ceu700428763.h1

Seq. No.	280897
Contig ID	110002_1.R1011
5'-most EST	tzu700201658.h1

Seq. No.	280898
Contig ID	110009_1.R1011
5'-most EST	uC-zmflb73093h06b2
Method	BLASTX
NCBI GI	g4140326
BLAST score	600
E value	5.0e-62
Match length	224
% identity	52
NCBI Description	(AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)bacterial, worm and yeast hypothetical proteins) [Homo sapiens]

Seq. No.	280899
Contig ID	110019_1.R1011
5'-most EST	uC-zmflb73094a10b2
Method	BLASTX
NCBI GI	g4539453
BLAST score	204
E value	8.0e-16
Match length	57
% identity	63
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	280900
Contig ID	110027_1.R1011
5'-most EST	uC-zmflmo17058a01a1

Seq. No.	280901
Contig ID	110036_1.R1011
5'-most EST	uC-zmflmo17320d12b1
Method	BLASTX
NCBI GI	g1621268
BLAST score	368
E value	4.0e-35
Match length	111
% identity	66
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	280902
Contig ID	110037_1.R1011
5'-most EST	pmx700086046.h1
Method	BLASTX
NCBI GI	g4115388
BLAST score	782
E value	4.0e-83
Match length	300
% identity	51
NCBI Description	(AC005967) putative prolylcarboxypeptidase [Arabidopsis

thaliana]

Seq. No.	280903
Contig ID	110037_2.R1011
5'-most EST	uC-zmflb73125e02a1

Seq. No.	280904
Contig ID	110041_2.R1011
5'-most EST	fwa700097034.h1

Seq. No.	280905
Contig ID	110048_1.R1011
5'-most EST	uC-zmflb73208b07b1
Method	BLASTX
NCBI GI	g2292917
BLAST score	469
E value	7.0e-47
Match length	138
% identity	64
NCBI Description	(X99851) galactokinase [Arabidopsis thaliana]

Seq. No.	280906
Contig ID	110058_1.R1011
5'-most EST	uC-zmflb73094g05b2

Seq. No.	280907
Contig ID	110071_1.R1011
5'-most EST	uC-zmflmo17338e09b1

Seq. No.	280908
Contig ID	110084_1.R1011
5'-most EST	xmt700265640.h1

Seq. No.	280909
Contig ID	110105_1.R1011
5'-most EST	uC-zmflb73095f07b1
Method	BLASTX
NCBI GI	g3763932
BLAST score	758
E value	7.0e-81
Match length	155
% identity	92
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	280910
Contig ID	110112_1.R1011
5'-most EST	uC-zmflb73095g05b1

Seq. No.	280911
Contig ID	110114_1.R1011
5'-most EST	uC-zmflb73095g07b1
Method	BLASTX
NCBI GI	g3176874
BLAST score	363
E value	3.0e-34
Match length	274
% identity	34

NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]
Seq. No.	280912
Contig ID	110119_1.R1011
5'-most EST	uC-zmflmo17058f08b1
Seq. No.	280913
Contig ID	110123_1.R1011
5'-most EST	nbm700473706.h1
Seq. No.	280914
Contig ID	110137_1.R1011
5'-most EST	uC-zmflb73096e09b1
Method	BLASTX
NCBI GI	g4006878
BLAST score	219
E value	1.0e-24
Match length	105
% identity	61
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.	280915
Contig ID	110148_1.R1011
5'-most EST	uC-zmflb73096e07b1
Method	BLASTX
NCBI GI	g3581838
BLAST score	195
E value	8.0e-31
Match length	217
% identity	40
NCBI Description	(AL031541) putative secreted arabinosidase [Streptomyces coelicolor]
Seq. No.	280916
Contig ID	110158_1.R1011
5'-most EST	xyt700343455.h1
Seq. No.	280917
Contig ID	110168_1.R1011
5'-most EST	uC-zmflb73096g11b1
Seq. No.	280918
Contig ID	110174_1.R1011
5'-most EST	uC-zmflb73165g09b2
Method	BLASTX
NCBI GI	g3831440
BLAST score	223
E value	4.0e-18
Match length	109
% identity	46
NCBI Description	(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	280919
Contig ID	110185_1.R1011

5'-most EST	tfd700576635.h1
Seq. No.	280920
Contig ID	110204_1.R1011
5'-most EST	wyr700237883.h1
Seq. No.	280921
Contig ID	110211_1.R1011
5'-most EST	uC-zmflb73097e06b1
Seq. No.	280922
Contig ID	110211_2.R1011
5'-most EST	fC-zmle700440692r4
Seq. No.	280923
Contig ID	110216_1.R1011
5'-most EST	kem700610884.h1
Method	BLASTX
NCBI GI	g2245070
BLAST score	306
E value	2.0e-27
Match length	248
% identity	32
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.	280924
Contig ID	110226_1.R1011
5'-most EST	uC-zmflmo17193b01b1
Seq. No.	280925
Contig ID	110226_2.R1011
5'-most EST	uC-zmflb73097g03b1
Seq. No.	280926
Contig ID	110230_1.R1011
5'-most EST	pmx700091635.h1
Method	BLASTX
NCBI GI	g4263784
BLAST score	813
E value	5.0e-87
Match length	201
% identity	76
NCBI Description	(AC006068) putative glycogenin-2 protein [Arabidopsis thaliana]
Seq. No.	280927
Contig ID	110239_1.R1011
5'-most EST	uC-zmrob73075f01b1
Seq. No.	280928
Contig ID	110248_1.R1011
5'-most EST	uC-zmflMo17004e08b1
Method	BLASTX
NCBI GI	g1399277
BLAST score	285
E value	2.0e-25
Match length	121

% identity	46
NCBI Description	(U31836) calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis thaliana]

Seq. No.	280929
Contig ID	110258_1.R1011
5'-most EST	uC-zmflb73098b07b1

Seq. No.	280930
Contig ID	110259_1.R1011
5'-most EST	xjt700094673.h1
Method	BLASTX
NCBI GI	g3057120
BLAST score	487
E value	3.0e-50
Match length	167
% identity	57
NCBI Description	(AF023159) starch synthase DULL1 [Zea mays]

Seq. No.	280931
Contig ID	110266_1.R1011
5'-most EST	pwr700451030.h1

Seq. No.	280932
Contig ID	110269_1.R1011
5'-most EST	hbs701181362.h1

Seq. No.	280933
Contig ID	110272_1.R1011
5'-most EST	uC-zmflb73098c10b1
Method	BLASTX
NCBI GI	g3955021
BLAST score	460
E value	9.0e-46
Match length	112
% identity	79
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No.	280934
Contig ID	110272_2.R1011
5'-most EST	uC-zmflm017084d02b1
Method	BLASTX
NCBI GI	g3955021
BLAST score	263
E value	6.0e-23
Match length	109
% identity	53
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No.	280935
Contig ID	110279_1.R1011
5'-most EST	ymt700223810.h1
Method	BLASTX
NCBI GI	g4063748
BLAST score	365

E value	7.0e-35
Match length	94
% identity	68
NCBI Description	(AC005851) unknown protein [Arabidopsis thaliana]

Seq. No.	280936
Contig ID	110282_1.R1011
5'-most EST	uC-zmflm017211b07b1

Seq. No.	280937
Contig ID	110282_2.R1011
5'-most EST	uC-zmflb73098d09b1

Seq. No.	280938
Contig ID	110289_1.R1011
5'-most EST	uC-zmflb73098e05b1
Method	BLASTX
NCBI GI	g2494034
BLAST score	378
E value	2.0e-36
Match length	117
% identity	61
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	280939
Contig ID	110312_1.R1011
5'-most EST	uC-zmflb73213g11b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	280940
Contig ID	110329_1.R1011
5'-most EST	uC-zmflmo17175h08b1

Seq. No.	280941
Contig ID	110331_1.R1011
5'-most EST	uC-zmflb73099b04b1

Seq. No.	280942
Contig ID	110341_1.R1011
5'-most EST	uC-zmflb73099c04b1

Seq. No.	280943
Contig ID	110357_1.R1011
5'-most EST	uC-zmflmo17122g11a1

Seq. No.	280944
Contig ID	110364_1.R1011
5'-most EST	uC-zmflmo17375c08a1

Method	BLASTX
NCBI GI	g3128203
BLAST score	159
E value	2.0e-10
Match length	40
% identity	80
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	280945
Contig ID	110372_1.R1011
5'-most EST	uC-zmflb73099f06b1

Seq. No.	280946
Contig ID	110399_1.R1011
5'-most EST	uC-zmflmo17294d07b1
Method	BLASTX
NCBI GI	g4138912
BLAST score	285
E value	2.0e-25
Match length	75
% identity	64
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No.	280947
Contig ID	110399_2.R1011
5'-most EST	uC-zmflb73100a03b1
Method	BLASTX
NCBI GI	g4138912
BLAST score	225
E value	2.0e-18
Match length	57
% identity	65
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No.	280948
Contig ID	110407_1.R1011
5'-most EST	uC-zmflb73100b02b1

Seq. No.	280949
Contig ID	110413_1.R1011
5'-most EST	uwc700154332.h1

Seq. No.	280950
Contig ID	110415_1.R1011
5'-most EST	uC-zmflmo17309g05b1
Method	BLASTX
NCBI GI	g3785991
BLAST score	770
E value	1.0e-92
Match length	226
% identity	71
NCBI Description	(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	280951
Contig ID	110420_1.R1011
5'-most EST	uC-zmflb73100c03b1
Method	BLASTX

NCBI GI	g1853968
BLAST score	246
E value	4.0e-21
Match length	79
% identity	65
NCBI Description	(D88121) CPRD12 protein [Vigna unguiculata]

Seq. No.	280952
Contig ID	110423_1.R1011
5'-most EST	uC-zmflb73100c06b1

Seq. No.	280953
Contig ID	110430_1.R1011
5'-most EST	xjt700094428.h1

Seq. No.	280954
Contig ID	110436_1.R1011
5'-most EST	uC-zmflb73279e05a2
Method	BLASTX
NCBI GI	g322774
BLAST score	552
E value	2.0e-56
Match length	240
% identity	46
NCBI Description	cytochrome P450 PET-1 - garden petunia (fragment) >gi_287909_emb_CAA50442_ (X71130) P450 hydroxylase [Petunia x hybrida]

Seq. No.	280955
Contig ID	110440_1.R1011
5'-most EST	uC-zmflb73150g05b1
Method	BLASTX
NCBI GI	g1172704
BLAST score	306
E value	8.0e-28
Match length	161
% identity	41
NCBI Description	PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN) >gi_633940 (L39082) transport protein [Arabidopsis thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine transport protein PTR2-B [Arabidopsis thaliana]

Seq. No.	280956
Contig ID	110449_1.R1011
5'-most EST	uC-zmflmo17312f10b1

Seq. No.	280957
Contig ID	110454_1.R1011
5'-most EST	ntr700076889.h1
Method	BLASTX
NCBI GI	g2864618
BLAST score	251
E value	2.0e-21
Match length	57
% identity	74
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	280958
Contig ID	110471_1.R1011
5'-most EST	uC-zmflmo17241d01b1

Seq. No.	280959
Contig ID	110483_1.R1011
5'-most EST	ymt700219603.h1
Method	BLASTX
NCBI GI	g2498329
BLAST score	179
E value	4.0e-13
Match length	81
% identity	52
NCBI Description	PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No.	280960
Contig ID	110484_1.R1011
5'-most EST	uC-zmflb73114a09b1
Method	BLASTX
NCBI GI	g3522956
BLAST score	331
E value	1.0e-30
Match length	129
% identity	44
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	280961
Contig ID	110492_1.R1011
5'-most EST	uC-zmflb73114b09a2

Seq. No.	280962
Contig ID	110494_1.R1011
5'-most EST	uC-zmflb73114b11b1
Method	BLASTX
NCBI GI	g4490327
BLAST score	320
E value	2.0e-29
Match length	162
% identity	42
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	280963
Contig ID	110495_1.R1011
5'-most EST	uC-zmrob73080g10b1

Seq. No.	280964
Contig ID	110579_1.R1011
5'-most EST	uC-zmflb73201c06b1

Seq. No.	280965
Contig ID	110583_1.R1011
5'-most EST	uC-zmflmo17235b07b1
Method	BLASTX
NCBI GI	g464900
BLAST score	288
E value	2.0e-25
Match length	221
% identity	33
NCBI Description	PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR >gi_539008_pir__S39476 kinase-like transmembrane protein TMKL1 precursor - Arabidopsis thaliana >gi_313190_emb_CAA51385_ (X72863) TMKL1 [Arabidopsis thaliana]

Seq. No.	280966
Contig ID	110601_1.R1011
5'-most EST	uC-zmflb73116f02b2
Method	BLASTX
NCBI GI	g3650037
BLAST score	308
E value	3.0e-44
Match length	132
% identity	67
NCBI Description	(AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	280967
Contig ID	110650_1.R1011
5'-most EST	fdz701166701.h1

Seq. No.	280968
Contig ID	110657_1.R1011
5'-most EST	wyr700237276.h1

Seq. No.	280969
Contig ID	110684_1.R1011
5'-most EST	uC-zmflb73117e07b2
Method	BLASTX
NCBI GI	g2191136
BLAST score	171
E value	5.0e-12
Match length	117
% identity	38
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	280970
Contig ID	110686_1.R1011
5'-most EST	uC-zmflb73117e09b2
Method	BLASTX
NCBI GI	g1723687
BLAST score	232
E value	6.0e-19
Match length	232

% identity	31
NCBI Description	HYPOTHETICAL 140.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC REGION >gi_2132603_pir__S64385 probable membrane protein YGR090w - yeast (Saccharomyces cerevisiae) >gi_1323133_emb_CAA97093_ (Z72875) ORF YGR090w [Saccharomyces cerevisiae]
Seq. No.	280971
Contig ID	110693_1.R1011
5'-most EST	uC-zmroteosinte015c12b1
Method	BLASTX
NCBI GI	g3928084
BLAST score	182
E value	3.0e-13
Match length	109
% identity	39
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]
Seq. No.	280972
Contig ID	110694_1.R1011
5'-most EST	uC-zmflb73181a07b2
Method	BLASTX
NCBI GI	g4455293
BLAST score	153
E value	6.0e-10
Match length	108
% identity	46
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]
Seq. No.	280973
Contig ID	110694_2.R1011
5'-most EST	uC-zmflb73117f06b2
Seq. No.	280974
Contig ID	110709_1.R1011
5'-most EST	uC-zmflmo17043e05a1
Seq. No.	280975
Contig ID	110715_1.R1011
5'-most EST	uC-zmrob73066f09b1
Method	BLASTX
NCBI GI	g2852449
BLAST score	190
E value	5.0e-14
Match length	100
% identity	42
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]
Seq. No.	280976
Contig ID	110725_1.R1011
5'-most EST	uC-zmflb73118a04b1
Seq. No.	280977
Contig ID	110728_1.R1011
5'-most EST	uC-zmflb73118a07b1

Method	BLASTX
NCBI GI	g2130099
BLAST score	576
E value	1.0e-59
Match length	151
% identity	74
NCBI Description	acetyl-CoA carboxylase (EC 6.4.1.2) - wheat >gi_514306 (U10187) acetyl-CoA carboxylase [Triticum aestivum]

Seq. No.	280978
Contig ID	110731_1.R1011
5'-most EST	fC-zmst700335606f4
Method	BLASTX
NCBI GI	g4539452
BLAST score	500
E value	1.0e-50
Match length	143
% identity	66
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	280979
Contig ID	110751_1.R1011
5'-most EST	uC-zmflb73344f05a2

Seq. No.	280980
Contig ID	110752_1.R1011
5'-most EST	nbm700478036.h1
Method	BLASTX
NCBI GI	g2191148
BLAST score	163
E value	4.0e-12
Match length	138
% identity	40
NCBI Description	(AF007269) A_IG002N01.28 gene product [Arabidopsis thaliana]

Seq. No.	280981
Contig ID	110761_1.R1011
5'-most EST	uC-zmflb73118d09b1

Seq. No.	280982
Contig ID	110790_1.R1011
5'-most EST	wyr700243238.h1

Seq. No.	280983
Contig ID	110798_1.R1011
5'-most EST	uC-zmflmo17079a04b1
Method	BLASTX
NCBI GI	g1076746
BLAST score	576
E value	2.0e-59
Match length	151
% identity	77
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	280984
Contig ID	110806_1.R1011
5'-most EST	uC-zmflb73118h12b1
Method	BLASTX
NCBI GI	g4586107
BLAST score	388
E value	1.0e-57
Match length	182
% identity	14
NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	280985
Contig ID	110837_1.R1011
5'-most EST	uC-zmflb73119c12b1
Method	BLASTX
NCBI GI	g3676473
BLAST score	201
E value	2.0e-15
Match length	104
% identity	47
NCBI Description	(AF053886) (R)-(+)-mandelonitrile lyase isoform MDL5 precursor [Prunus serotina]

Seq. No.	280986
Contig ID	110868_1.R1011
5'-most EST	uC-zmflb73119g03b1

Seq. No.	280987
Contig ID	110869_1.R1011
5'-most EST	uC-zmflb73119g05b1

Seq. No.	280988
Contig ID	110879_1.R1011
5'-most EST	uC-zmflb73119h04b1
Method	BLASTX
NCBI GI	g3236261
BLAST score	527
E value	1.0e-53
Match length	141
% identity	69
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	280989
Contig ID	110889_1.R1011
5'-most EST	rvl700455858.h1

Seq. No.	280990
Contig ID	110902_1.R1011
5'-most EST	uC-zmflb73120b04b1
Method	BLASTX
NCBI GI	g4646233
BLAST score	336
E value	2.0e-31
Match length	146

% identity	49
NCBI Description	(AC007266) putative G9a protein [Arabidopsis thaliana]
Seq. No.	280991
Contig ID	110918_1.R1011
5'-most EST	uC-zmflb73120d01b1
Method	BLASTX
NCBI GI	g3329368
BLAST score	682
E value	1.0e-71
Match length	243
% identity	55
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]
Seq. No.	280992
Contig ID	110922_1.R1011
5'-most EST	uC-zmflb73120d05b1
Seq. No.	280993
Contig ID	110928_1.R1011
5'-most EST	uC-zmflmo17057e03b1
Method	BLASTX
NCBI GI	g2809246
BLAST score	214
E value	4.0e-17
Match length	88
% identity	47
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]
Seq. No.	280994
Contig ID	110945_1.R1011
5'-most EST	uC-zmflmo17129g02b1
Seq. No.	280995
Contig ID	110948_1.R1011
5'-most EST	uC-zmflb73120f08b1
Seq. No.	280996
Contig ID	110956_1.R1011
5'-most EST	uC-zmflb73230a05b2
Method	BLASTX
NCBI GI	g3258314
BLAST score	294
E value	3.0e-26
Match length	162
% identity	35
NCBI Description	(AP000007) 432aa long hypothetical protein [Pyrococcus horikoshii]
Seq. No.	280997
Contig ID	110968_1.R1011
5'-most EST	zuv700354463.h1
Method	BLASTX
NCBI GI	g3360289
BLAST score	318
E value	3.0e-29
Match length	118

% identity	52
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	280998
Contig ID	110970_1.R1011
5'-most EST	ntr700076326.h1
Method	BLASTX
NCBI GI	g2190553
BLAST score	221
E value	4.0e-18
Match length	75
% identity	55
NCBI Description	(AC001229) Strong similarity to Arabidopsis zeta-crystallin-like protein (gb_Z49268). [Arabidopsis thaliana]

Seq. No.	280999
Contig ID	110973_1.R1011
5'-most EST	uC-zmflmo17342g10a1

Seq. No.	281000
Contig ID	110982_1.R1011
5'-most EST	xmt700266226.h1

Seq. No.	281001
Contig ID	110992_1.R1011
5'-most EST	uC-zmflb73124d04b1
Method	BLASTX
NCBI GI	g4567228
BLAST score	197
E value	5.0e-15
Match length	94
% identity	50
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	281002
Contig ID	111003_1.R1011
5'-most EST	ymt700222844.h1
Method	BLASTX
NCBI GI	g4510349
BLAST score	174
E value	5.0e-12
Match length	82
% identity	50
NCBI Description	(AC006921) putative bZIP transcription factor [Arabidopsis thaliana]

Seq. No.	281003
Contig ID	111003_2.R1011
5'-most EST	nwy700446957.h1

Seq. No.	281004
Contig ID	111014_1.R1011
5'-most EST	ceu700433102.h1
Method	BLASTX
NCBI GI	g282995

BLAST score 174
E value 2.0e-12
Match length 68
% identity 54
NCBI Description seed protein B32E - barley (fragment)
>gi_1345530_emb_CAA45538_ (X64254) B32E [Hordeum vulgare]

Seq. No. 281005
Contig ID 111042_1.R1011
5'-most EST ymt700221153.h1
Method BLASTX
NCBI GI g2911070
BLAST score 632
E value 7.0e-66
Match length 249
% identity 52
NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No. 281006
Contig ID 111047_1.R1011
5'-most EST uC-zmflb73126c09b1

Seq. No. 281007
Contig ID 111055_1.R1011
5'-most EST uC-zmflb73126d09b1

Seq. No. 281008
Contig ID 111058_1.R1011
5'-most EST xmt700265120.h1

Seq. No. 281009
Contig ID 111075_1.R1011
5'-most EST nbm700471983.h1

Seq. No. 281010
Contig ID 111077_1.R1011
5'-most EST ypc700800595.h1

Seq. No. 281011
Contig ID 111101_1.R1011
5'-most EST fC-zmfl700351289f1
Method BLASTX
NCBI GI g3176662
BLAST score 647
E value 8.0e-68
Match length 171
% identity 65
NCBI Description (AC004393) Similar to mannosyl-oligosaccharide glucosidase gb_X87237 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 281012
Contig ID 111107_1.R1011
5'-most EST uC-zmflmo17201e11b1
Method BLASTX
NCBI GI g1730629
BLAST score 204
E value 7.0e-16

Match length	92
% identity	51
NCBI Description	HYPOTHETICAL 43.0 KD PROTEIN B0361.6 IN CHROMOSOME III >gi_458954 (U00031) similar to H. marismortui hypothetical 23.1 kd protein in HMAL3 5' region [Caenorhabditis elegans]

Seq. No.	281013
Contig ID	111108_1.R1011
5'-most EST	uC-zmflb73128d03b1

Seq. No.	281014
Contig ID	111112_1.R1011
5'-most EST	uC-zmflb73128e01b1
Method	BLASTX
NCBI GI	g3327196
BLAST score	162
E value	7.0e-11
Match length	175
% identity	30
NCBI Description	(AB014591) KIAA0691 protein [Homo sapiens]

Seq. No.	281015
Contig ID	111124_1.R1011
5'-most EST	uC-zmroteosinte003c08b1
Method	BLASTX
NCBI GI	g2654870
BLAST score	574
E value	6.0e-90
Match length	165
% identity	92
NCBI Description	(AF015302) RbohAOsp [Oryza sativa]

Seq. No.	281016
Contig ID	111124_2.R1011
5'-most EST	uC-zmflb73128f03b1
Method	BLASTX
NCBI GI	g2654870
BLAST score	669
E value	2.0e-70
Match length	163
% identity	77
NCBI Description	(AF015302) RbohAOsp [Oryza sativa]

Seq. No.	281017
Contig ID	111127_1.R1011
5'-most EST	uC-zmflb73128f06b1
Method	BLASTX
NCBI GI	g2832629
BLAST score	252
E value	2.0e-21
Match length	207
% identity	33
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	281018
Contig ID	111129_1.R1011

5'-most EST	tzu700205961.h1
Method	BLASTX
NCBI GI	g3785974
BLAST score	248
E value	2.0e-21
Match length	83
% identity	58
NCBI Description	(AC005560) putative DNA recombinase [Arabidopsis thaliana]

Seq. No.	281019
Contig ID	111133_1.R1011
5'-most EST	uC-zmflb73128g07b1
Method	BLASTX
NCBI GI	g4469023
BLAST score	355
E value	8.0e-34
Match length	90
% identity	73
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	281020
Contig ID	111133_2.R1011
5'-most EST	pmx700083803.h1
Method	BLASTX
NCBI GI	g4469023
BLAST score	355
E value	7.0e-34
Match length	82
% identity	78
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	281021
Contig ID	111133_3.R1011
5'-most EST	yyf700347836.h1
Method	BLASTX
NCBI GI	g4469023
BLAST score	279
E value	1.0e-24
Match length	71
% identity	75
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	281022
Contig ID	111134_1.R1011
5'-most EST	xsy700213367.h1

Seq. No.	281023
Contig ID	111140_1.R1011
5'-most EST	xsy700208137.h1
Method	BLASTX
NCBI GI	g4263714
BLAST score	158
E value	6.0e-14
Match length	65
% identity	73
NCBI Description	(AC006223) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	281024
Contig ID	111143_1.R1011
5'-most EST	uC-zmflb73192h05b1

Seq. No.	281025
Contig ID	111149_1.R1011
5'-most EST	uC-zmflb73129c01b1
Method	BLASTX
NCBI GI	g2244772
BLAST score	238
E value	9.0e-20
Match length	65
% identity	72
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	281026
Contig ID	111151_1.R1011
5'-most EST	uC-zmflb73129c04b1

Seq. No.	281027
Contig ID	111165_1.R1011
5'-most EST	pmx700082211.h1
Method	BLASTX
NCBI GI	g2618698
BLAST score	1149
E value	1.0e-126
Match length	363
% identity	61
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	281028
Contig ID	111182_1.R1011
5'-most EST	xsy700214870.h1

Seq. No.	281029
Contig ID	111188_1.R1011
5'-most EST	uC-zmflb73129h05b1

Seq. No.	281030
Contig ID	111190_1.R1011
5'-most EST	uC-zmflb73129h07b1
Method	BLASTX
NCBI GI	g3885334
BLAST score	253
E value	1.0e-21
Match length	88
% identity	52
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	281031
Contig ID	111199_1.R1011
5'-most EST	xjt700093981.h1

Seq. No.	281032
Contig ID	111219_1.R1011

5'-most EST	uC-zmrob73080d02b1
Seq. No.	281033
Contig ID	111221_1.R1011
5'-most EST	uC-zmflb73132d06b1
Method	BLASTX
NCBI GI	g1076289
BLAST score	200
E value	2.0e-15
Match length	48
% identity	73
NCBI Description	amino acid permease AAP5 - Arabidopsis thaliana >gi_608673_emb_CAA54632_ (X77501) amino acid permease [Arabidopsis thaliana]
Seq. No.	281034
Contig ID	111227_1.R1011
5'-most EST	uC-zmflb73132e03b1
Seq. No.	281035
Contig ID	111248_1.R1011
5'-most EST	xyt700345535.h1
Method	BLASTX
NCBI GI	g3877656
BLAST score	242
E value	3.0e-20
Match length	140
% identity	35
NCBI Description	(Z72511) similar to nucleotide translocator [Caenorhabditis elegans]
Seq. No.	281036
Contig ID	111251_1.R1011
5'-most EST	uC-zmflmo17054d10a1
Seq. No.	281037
Contig ID	111265_2.R1011
5'-most EST	xsy700209962.h1
Method	BLASTX
NCBI GI	g2880043
BLAST score	891
E value	1.0e-114
Match length	335
% identity	61
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]
Seq. No.	281038
Contig ID	111271_1.R1011
5'-most EST	clt700043517.f1
Seq. No.	281039
Contig ID	111273_1.R1011
5'-most EST	uC-zmflb73134c11b1
Method	BLASTN
NCBI GI	g2352794
BLAST score	41

E value	8.0e-14
Match length	69
% identity	90
NCBI Description	Zea mays retinoblastoma-related protein 1 (RRB1) mRNA, complete cds

Seq. No.	281040
Contig ID	111282_1.R1011
5'-most EST	uC-zmflb73134b10a2

Seq. No.	281041
Contig ID	111292_1.R1011
5'-most EST	uC-zmflb73134d01b1

Seq. No.	281042
Contig ID	111297_1.R1011
5'-most EST	uC-zmflb73182c03b1

Seq. No.	281043
Contig ID	111298_1.R1011
5'-most EST	uC-zmflb73134e03b1
Method	BLASTX
NCBI GI	g1491638
BLAST score	255
E value	6.0e-22
Match length	110
% identity	45
NCBI Description	(X99922) male sterility protein 2 [Brassica napus]

Seq. No.	281044
Contig ID	111302_1.R1011
5'-most EST	uC-zmflb73134f02b1

Seq. No.	281045
Contig ID	111329_1.R1011
5'-most EST	uC-zmflb73136b01b1
Method	BLASTX
NCBI GI	g3668093
BLAST score	204
E value	8.0e-16
Match length	159
% identity	33
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	281046
Contig ID	111339_1.R1011
5'-most EST	uC-zmflb73136d02b1

Seq. No.	281047
Contig ID	111374_1.R1011
5'-most EST	uC-zmflb73136f03b1

Seq. No.	281048
Contig ID	111382_1.R1011
5'-most EST	uC-zmflb73136g01b1
Method	BLASTX
NCBI GI	g2952433

BLAST score	466
E value	2.0e-46
Match length	155
% identity	63
NCBI Description	(AF051135) putative ubiquitin activating enzyme E1 [Arabidopsis thaliana]

Seq. No.	281049
Contig ID	111391_1.R1011
5'-most EST	uC-zmflmo17292a08b1

Seq. No.	281050
Contig ID	111415_1.R1011
5'-most EST	uC-zmflMo17064b05b1
Method	BLASTN
NCBI GI	g2098817
BLAST score	171
E value	4.0e-91
Match length	237
% identity	97
NCBI Description	Zea mays GLOSSY15 (Gl15) gene, partial cds

Seq. No.	281051
Contig ID	111420_1.R1011
5'-most EST	uC-zmflb73137b07b1

Seq. No.	281052
Contig ID	111426_1.R1011
5'-most EST	uC-zmflb73137c02b1

Seq. No.	281053
Contig ID	111426_2.R1011
5'-most EST	uC-zmflmo17278d10b1

Seq. No.	281054
Contig ID	111429_1.R1011
5'-most EST	uC-zmflb73137c07b1
Method	BLASTX
NCBI GI	g2501555
BLAST score	495
E value	7.0e-50
Match length	127
% identity	70
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	281055
Contig ID	111429_2.R1011
5'-most EST	uC-zmflmo17025f10a1
Method	BLASTX
NCBI GI	g4454042
BLAST score	500
E value	1.0e-58
Match length	156
% identity	67
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	281056
Contig ID	111433_1.R1011
5'-most EST	uC-zmflb73137c11b1

Seq. No.	281057
Contig ID	111443_1.R1011
5'-most EST	rvl700454968.h1
Method	BLASTX
NCBI GI	g282873
BLAST score	442
E value	2.0e-43
Match length	189
% identity	51
NCBI Description	transforming protein (myb) homolog - Arabidopsis thaliana >gi_217859_dbj_BAA01730_ (D10936) ATMYB1 protein [Arabidopsis thaliana]

Seq. No.	281058
Contig ID	111465_1.R1011
5'-most EST	uC-zmflb73137f08b1
Method	BLASTX
NCBI GI	g467698
BLAST score	166
E value	3.0e-11
Match length	91
% identity	42
NCBI Description	(X78326) SUR4 [Saccharomyces cerevisiae]

Seq. No.	281059
Contig ID	111490_1.R1011
5'-most EST	uC-zmflb73137h11b1

Seq. No.	281060
Contig ID	111493_1.R1011
5'-most EST	uC-zmroteosinte064e06b1
Method	BLASTX
NCBI GI	g3152609
BLAST score	163
E value	6.0e-11
Match length	71
% identity	45
NCBI Description	(AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No.	281061
Contig ID	111494_1.R1011
5'-most EST	uC-zmflb73139a03b1

Seq. No.	281062
Contig ID	111495_1.R1011
5'-most EST	uC-zmflb73139a04b1

Seq. No.	281063
Contig ID	111500_1.R1011
5'-most EST	uC-zmflmo17074g11a1

Seq. No. 281064

Contig ID	111502_1.R1011
5'-most EST	uC-zmflb73139a11b1
Seq. No.	281065
Contig ID	111511_1.R1011
5'-most EST	uC-zmflb73139b09b1
Seq. No.	281066
Contig ID	111519_1.R1011
5'-most EST	uC-zmflb73139c08b1
Seq. No.	281067
Contig ID	111524_1.R1011
5'-most EST	uC-zmflb73139d01b1
Seq. No.	281068
Contig ID	111538_1.R1011
5'-most EST	uC-zmflb73139e09b1
Method	BLASTX
NCBI GI	g2281705
BLAST score	601
E value	2.0e-68
Match length	141
% identity	92
NCBI Description	(AF013979) ethylene responsive factor [Oryza sativa]
Seq. No.	281069
Contig ID	111573_1.R1011
5'-most EST	hbs701181257.h1
Method	BLASTX
NCBI GI	g4455177
BLAST score	245
E value	1.0e-20
Match length	93
% identity	55
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]
Seq. No.	281070
Contig ID	111592_1.R1011
5'-most EST	uC-zmflb73140b09b1
Seq. No.	281071
Contig ID	111599_1.R1011
5'-most EST	uC-zmflmo17235e10b1
Seq. No.	281072
Contig ID	111604_1.R1011
5'-most EST	uC-zmflb73140h11b1
Seq. No.	281073
Contig ID	111623_1.R1011
5'-most EST	uC-zmflb73140e06b1
Method	BLASTX
NCBI GI	g2425170
BLAST score	579
E value	6.0e-60
Match length	133

% identity	79
NCBI Description	(AB003195) basic class III chitinase OsChib3b [Oryza sativa]

Seq. No.	281074
Contig ID	111656_1.R1011
5'-most EST	uC-zmflb73140h05b1
Method	BLASTX
NCBI GI	g3643608
BLAST score	246
E value	6.0e-24
Match length	144
% identity	46
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281075
Contig ID	111687_1.R1011
5'-most EST	uC-zmflb73234h09b2
Method	BLASTX
NCBI GI	g2160694
BLAST score	1233
E value	1.0e-136
Match length	294
% identity	79
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	281076
Contig ID	111698_1.R1011
5'-most EST	uC-zmflb73141e02b1

Seq. No.	281077
Contig ID	111714_1.R1011
5'-most EST	nbm700466358.h1

Seq. No.	281078
Contig ID	111717_1.R1011
5'-most EST	uC-zmflmo17179a04b1
Method	BLASTX
NCBI GI	g1314711
BLAST score	303
E value	1.0e-33
Match length	140
% identity	59
NCBI Description	(U54615) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_3068712 (AF049236) calcium dependent protein kinase [Arabidopsis thaliana]

Seq. No.	281079
Contig ID	111739_1.R1011
5'-most EST	uC-zmflb73141h11b1
Method	BLASTX
NCBI GI	g4507007
BLAST score	150
E value	1.0e-09
Match length	107
% identity	37

NCBI Description	calcium binding mitochondrial carrier superfamily member Aralar >gi_3559910_emb_CAA74834_ (Y14494) aralar1 [Homo sapiens]
Seq. No.	281080
Contig ID	111740_1.R1011
5'-most EST	uC-zmflb73141h12b1
Seq. No.	281081
Contig ID	111743_1.R1011
5'-most EST	uC-zmflb73142a04b1
Method	BLASTX
NCBI GI	g4539011
BLAST score	153
E value	1.0e-09
Match length	138
% identity	28
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]
Seq. No.	281082
Contig ID	111745_1.R1011
5'-most EST	uC-zmflb73142a06b1
Method	BLASTX
NCBI GI	g3047114
BLAST score	147
E value	9.0e-16
Match length	94
% identity	54
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	281083
Contig ID	111745_2.R1011
5'-most EST	wen700335393.h1
Method	BLASTX
NCBI GI	g3047114
BLAST score	157
E value	2.0e-11
Match length	50
% identity	67
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	281084
Contig ID	111745_3.R1011
5'-most EST	ntr700075217.h1
Method	BLASTX
NCBI GI	g3047114
BLAST score	184
E value	7.0e-14
Match length	101
% identity	43
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	281085
Contig ID	111754_1.R1011
5'-most EST	uC-zmflb73142b04b1
Method	BLASTX
NCBI GI	g3046997

BLAST score 251
E value 3.0e-21
Match length 147
% identity 42
NCBI Description (AF056718) ash2l1 [Homo sapiens]

Seq. No. 281086
Contig ID 111756_1.R1011
5'-most EST wyr700237505.h1

Seq. No. 281087
Contig ID 111781_1.R1011
5'-most EST nbm700473933.h1
Method BLASTX
NCBI GI g4467111
BLAST score 803
E value 6.0e-86
Match length 209
% identity 68
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 281088
Contig ID 111794_1.R1011
5'-most EST xyt700344908.h1
Method BLASTX
NCBI GI g1353157
BLAST score 250
E value 3.0e-21
Match length 128
% identity 41
NCBI Description HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II >gi_3878900_emb_CAA86774_ (Z46794) similar to vacuolar biogenesis protein (pep5); cDNA EST EMBL:D27614 comes from this gene; cDNA EST EMBL:D34974 comes from this gene [Caenorhabditis elegans]

Seq. No. 281089
Contig ID 111810_1.R1011
5'-most EST vux700162090.h1
Method BLASTX
NCBI GI g2980767
BLAST score 362
E value 2.0e-34
Match length 95
% identity 69
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 281090
Contig ID 111816_1.R1011
5'-most EST ntr700077188.h1

Seq. No. 281091
Contig ID 111832_1.R1011
5'-most EST uC-zmf1b73150g04b1

Seq. No. 281092
Contig ID 111855_1.R1011

5'-most EST	tfd700570029.h1
Method	BLASTX
NCBI GI	g2649624
BLAST score	173
E value	7.0e-12
Match length	230
% identity	28
NCBI Description	(AE001037) acetyl-CoA synthetase (acs-4) [Archaeoglobus fulgidus]

Seq. No.	281093
Contig ID	111858_1.R1011
5'-most EST	uC-zmflmo17262e08b1
Method	BLASTX
NCBI GI	g4337195
BLAST score	510
E value	2.0e-51
Match length	185
% identity	63
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	281094
Contig ID	111858_2.R1011
5'-most EST	uC-zmflb73143d06b1

Seq. No.	281095
Contig ID	111863_1.R1011
5'-most EST	uC-zmflb73143d12b1

Seq. No.	281096
Contig ID	111869_1.R1011
5'-most EST	uC-zmflb73143e06b1

Seq. No.	281097
Contig ID	111876_1.R1011
5'-most EST	tzu700206595.h1
Method	BLASTX
NCBI GI	g3746059
BLAST score	451
E value	1.0e-44
Match length	143
% identity	60
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	281098
Contig ID	111886_1.R1011
5'-most EST	uC-zmflb73210b07b1

Seq. No.	281099
Contig ID	111901_1.R1011
5'-most EST	uC-zmflb73143h04b1

Seq. No.	281100
Contig ID	111904_1.R1011
5'-most EST	uC-zmflb73143h07b1

Seq. No.	281101
Contig ID	111908_1.R1011
5'-most EST	uwc700150084.h1

Seq. No.	281102
Contig ID	111913_1.R1011
5'-most EST	wuj700282113.h1
Method	BLASTX
NCBI GI	g3024577
BLAST score	338
E value	1.0e-31
Match length	86
% identity	79
NCBI Description	HOMEOBOX PROTEIN ROUGH SHEATH 1 >gi_1008879 (L44133) RS1 gene product [Zea mays]

Seq. No.	281103
Contig ID	111944_1.R1011
5'-most EST	uC-zmflb73144d08b1
Method	BLASTX
NCBI GI	g4584539
BLAST score	193
E value	1.0e-14
Match length	54
% identity	63
NCBI Description	(AL049608) extensin-like protein [Arabidopsis thaliana]

Seq. No.	281104
Contig ID	111948_1.R1011
5'-most EST	cyk700049821.f1
Method	BLASTX
NCBI GI	g2462829
BLAST score	468
E value	1.0e-46
Match length	203
% identity	46
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	281105
Contig ID	111982_1.R1011
5'-most EST	vux700162459.h1

Seq. No.	281106
Contig ID	111982_2.R1011
5'-most EST	uC-zmflb73144h03b1

Seq. No.	281107
Contig ID	111986_2.R1011
5'-most EST	fwa700100402.h1

Seq. No.	281108
Contig ID	112052_1.R1011
5'-most EST	uC-zmflmo17306c09b1
Method	BLASTX
NCBI GI	g4490330
BLAST score	1138

E value 1.0e-125
Match length 226
% identity 94
NCBI Description (AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No. 281109
Contig ID 112053_1.R1011
5'-most EST uC-zmflb73146a09b1
Method BLASTX
NCBI GI g3582343
BLAST score 243
E value 2.0e-20
Match length 92
% identity 52
NCBI Description (AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 281110
Contig ID 112059_1.R1011
5'-most EST uC-zmflb73146b03b1

Seq. No. 281111
Contig ID 112061_1.R1011
5'-most EST uC-zmflb73272f02a1
Method BLASTX
NCBI GI g542192
BLAST score 246
E value 8.0e-21
Match length 47
% identity 98
NCBI Description floral homeotic protein ZAG2 - maize (fragment) >gi_309576 (L18925) homologue of Arabidopsis Agamous-like gene [Zea mays]

Seq. No. 281112
Contig ID 112072_1.R1011
5'-most EST uC-zmflb73173g09b1
Method BLASTX
NCBI GI g4539335
BLAST score 1775
E value 0.0e+00
Match length 507
% identity 61
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 281113
Contig ID 112072_2.R1011
5'-most EST uC-zmflb73224c01a1

Seq. No. 281114
Contig ID 112079_1.R1011
5'-most EST uC-zmroteosinte066f10b1

Seq. No. 281115
Contig ID 112090_1.R1011
5'-most EST fC-zmfl700342573a4

Seq. No.	281116
Contig ID	112113_1.R1011
5'-most EST	xmt700264645.h1
Method	BLASTX
NCBI GI	g4512659
BLAST score	801
E value	1.0e-109
Match length	333
% identity	65
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	281117
Contig ID	112132_1.R1011
5'-most EST	uC-zmflb73230d11b2

Seq. No.	281118
Contig ID	112134_1.R1011
5'-most EST	uC-zmflb73147c03b1
Method	BLASTX
NCBI GI	g2792220
BLAST score	416
E value	1.0e-40
Match length	202
% identity	42
NCBI Description	(AF032688) NBS-LRR type resistance protein [Oryza sativa]

Seq. No.	281119
Contig ID	112151_1.R1011
5'-most EST	fwa700100789.h1
Method	BLASTX
NCBI GI	g2655031
BLAST score	621
E value	8.0e-65
Match length	122
% identity	93
NCBI Description	(AF019297) starch synthase isoform zSTSII-2 [Zea mays]

Seq. No.	281120
Contig ID	112154_1.R1011
5'-most EST	uC-zmflb73147e01b1

Seq. No.	281121
Contig ID	112157_1.R1011
5'-most EST	uC-zmflb73147f05b1

Seq. No.	281122
Contig ID	112158_1.R1011
5'-most EST	uC-zmflb73147f07b1

Seq. No.	281123
Contig ID	112167_1.R1011
5'-most EST	ntr700073093.h1
Method	BLASTX
NCBI GI	g2231312

BLAST score	590
E value	5.0e-61
Match length	125
% identity	90
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]

Seq. No.	281124
Contig ID	112167_2.R1011
5'-most EST	pmx700082144.h1
Method	BLASTX
NCBI GI	g2231312
BLAST score	278
E value	7.0e-25
Match length	63
% identity	86
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]

Seq. No.	281125
Contig ID	112179_1.R1011
5'-most EST	uC-zmflmo17151g04b1

Seq. No.	281126
Contig ID	112179_2.R1011
5'-most EST	uC-zmflb73148e01b1

Seq. No.	281127
Contig ID	112180_1.R1011
5'-most EST	nbm700474048.h1

Seq. No.	281128
Contig ID	112188_1.R1011
5'-most EST	uC-zmflb73148f08b1

Seq. No.	281129
Contig ID	112193_1.R1011
5'-most EST	uC-zmflb73292f08a1

Seq. No.	281130
Contig ID	112193_2.R1011
5'-most EST	uC-zmflmo17016e09a1

Seq. No.	281131
Contig ID	112193_3.R1011
5'-most EST	fwa700101205.h1

Seq. No.	281132
Contig ID	112215_1.R1011
5'-most EST	uC-zmflb73149b08b1

Seq. No.	281133
Contig ID	112222_1.R1011
5'-most EST	uC-zmflb73217c07b2

Seq. No.	281134
Contig ID	112224_1.R1011
5'-most EST	uC-zmroteosinte029b01b1
Method	BLASTX

NCBI GI	g2660675
BLAST score	815
E value	3.0e-87
Match length	220
% identity	71
NCBI Description	(AC002342) similar to DNA-damage-inducible protein P [Arabidopsis thaliana]

Seq. No.	281135
Contig ID	112250_1.R1011
5'-most EST	uC-zmflmo17125e03b1
Method	BLASTX
NCBI GI	g1345838
BLAST score	619
E value	2.0e-64
Match length	133
% identity	90
NCBI Description	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) >gi_2130143_pir__S65060 phytoene desaturase precursor - maize >gi_1051180 (U37285) phytoene desaturase [Zea mays]

Seq. No.	281136
Contig ID	112252_1.R1011
5'-most EST	uC-zmflb73149f03b1
Method	BLASTX
NCBI GI	g421954
BLAST score	183
E value	2.0e-18
Match length	148
% identity	39
NCBI Description	hypothetical protein 3 - potato transposon Tst1 >gi_21433_emb_CAA36615_ (X52387) ORF3 [Solanum tuberosum]

Seq. No.	281137
Contig ID	112264_1.R1011
5'-most EST	uC-zmflb73149g03b1
Method	BLASTX
NCBI GI	g125415
BLAST score	185
E value	1.0e-13
Match length	178
% identity	33
NCBI Description	KINESIN HEAVY CHAIN >gi_102714_pir__A35075 kinesin heavy chain - longfin squid >gi_161290 (J05258) kinesin heavy chain [Loligo pealii]

Seq. No.	281138
Contig ID	112271_1.R1011
5'-most EST	fC-zmfl700553382a1
Method	BLASTX
NCBI GI	g4376158
BLAST score	629
E value	2.0e-65
Match length	199
% identity	62
NCBI Description	(X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No.	281139
Contig ID	112280_1.R1011
5'-most EST	uC-zmflb73149h09b1
Method	BLASTX
NCBI GI	g1076764
BLAST score	234
E value	2.0e-19
Match length	144
% identity	38
NCBI Description	AWJL236 protein - wheat >gi_551214_emb_CAA57135_ (X81370) AWJL236 [Triticum aestivum]

Seq. No.	281140
Contig ID	112282_1.R1011
5'-most EST	uC-zmflb73149h11b1

Seq. No.	281141
Contig ID	112284_1.R1011
5'-most EST	uC-zmflb73150b03b1

Seq. No.	281142
Contig ID	112301_1.R1011
5'-most EST	uC-zmflb73150c10b1
Method	BLASTX
NCBI GI	g4220528
BLAST score	217
E value	2.0e-24
Match length	105
% identity	57
NCBI Description	(AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	281143
Contig ID	112302_1.R1011
5'-most EST	uC-zmflb73150b12b1

Seq. No.	281144
Contig ID	112344_1.R1011
5'-most EST	uC-zmflb73150g10b1
Method	BLASTX
NCBI GI	g3608128
BLAST score	314
E value	1.0e-28
Match length	95
% identity	66
NCBI Description	(AC005314) hypothetical protein [Arabidopsis thaliana] >gi_4263794_gb_AAD15454_ (AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281145
Contig ID	112361_1.R1011
5'-most EST	uC-zmroteosinte099c07b2
Method	BLASTX
NCBI GI	g2281088
BLAST score	356
E value	1.0e-33
Match length	172

% identity	47
NCBI Description	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No.	281146
Contig ID	112376_1.R1011
5'-most EST	uC-zmflmo17289g05b1
Method	BLASTX
NCBI GI	g2558654
BLAST score	514
E value	3.0e-52
Match length	168
% identity	60
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	281147
Contig ID	112380_1.R1011
5'-most EST	ntr700074022.h1

Seq. No.	281148
Contig ID	112396_1.R1011
5'-most EST	uC-zmrob73019h07b1

Seq. No.	281149
Contig ID	112397_1.R1011
5'-most EST	uC-zmflb73151c11b1

Seq. No.	281150
Contig ID	112405_1.R1011
5'-most EST	uC-zmflb73151d08b1

Seq. No.	281151
Contig ID	112407_1.R1011
5'-most EST	wyr700235843.h1

Seq. No.	281152
Contig ID	112417_1.R1011
5'-most EST	uC-zmflb73151e08b1
Method	BLASTX
NCBI GI	g100226
BLAST score	218
E value	2.0e-17
Match length	169
% identity	31
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	281153
Contig ID	112424_1.R1011
5'-most EST	uC-zmflmo17222e07b1

Seq. No.	281154
Contig ID	112429_3.R1011
5'-most EST	nbm700468119.h1
Method	BLASTX

NCBI GI g2062175
BLAST score 441
E value 1.0e-43
Match length 155
% identity 59
NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No. 281155
Contig ID 112433_1.R1011
5'-most EST uC-zmflb73151g04b1
Method BLASTX
NCBI GI g4056461
BLAST score 209
E value 2.0e-16
Match length 76
% identity 50
NCBI Description (AC005990) F5O8.34 [Arabidopsis thaliana]

Seq. No. 281156
Contig ID 112434_1.R1011
5'-most EST wyr700239174.h1
Method BLASTX
NCBI GI g4490756
BLAST score 364
E value 6.0e-58
Match length 288
% identity 49
NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 281157
Contig ID 112444_1.R1011
5'-most EST uC-zmflb73151h04b1

Seq. No. 281158
Contig ID 112447_1.R1011
5'-most EST uC-zmflb73151h07b1

Seq. No. 281159
Contig ID 112471_1.R1011
5'-most EST uC-zmrob73071e01b1
Method BLASTX
NCBI GI g2281641
BLAST score 245
E value 2.0e-20
Match length 108
% identity 56
NCBI Description (AF003101) AP2 domain containing protein RAP2.8 [Arabidopsis thaliana]

Seq. No. 281160
Contig ID 112491_1.R1011
5'-most EST uC-zmflb73152d07b1
Method BLASTX
NCBI GI g4432844
BLAST score 334
E value 5.0e-31
Match length 141

% identity	48
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	281161
Contig ID	112492_1.R1011
5'-most EST	fC-zmle700429795a4
Method	BLASTX
NCBI GI	g1934972
BLAST score	681
E value	1.0e-71
Match length	191
% identity	68
NCBI Description	(Y08611) dihydropterin pyrophosphokinase /dihydropteroate synthase [Pisum sativum]

Seq. No.	281162
Contig ID	112530_1.R1011
5'-most EST	cyk700049390.f1

Seq. No.	281163
Contig ID	112541_1.R1011
5'-most EST	uC-zmflb73153a09b1
Method	BLASTX
NCBI GI	g466063
BLAST score	165
E value	3.0e-11
Match length	161
% identity	34
NCBI Description	HYPOTHETICAL 105.6 KD PROTEIN ZK1098.8 IN CHROMOSOME III >gi_482167_pir__S40930 hypothetical protein ZK1098.8 - Caenorhabditis elegans >gi_3881488_emb_CAA80137_ (Z22176) similarity to E. coli RNAase D and human autoantigen PM-SCL-100; cDNA EST EMBL:T01912 comes from this gene; cDNA EST EMBL:D67613 comes from this gene; cDNA EST EMBL:D64565 comes from this gene; cDNA EST EMBL:D68059 com

Seq. No.	281164
Contig ID	112562_1.R1011
5'-most EST	uC-zmflb73153c09b1

Seq. No.	281165
Contig ID	112600_1.R1011
5'-most EST	uC-zmflb73153g02b1
Method	BLASTX
NCBI GI	g4115905
BLAST score	149
E value	2.0e-10
Match length	63
% identity	60
NCBI Description	(AF072131) secondary xylem cellulose synthase [Populus tremuloides]

Seq. No.	281166
Contig ID	112618_1.R1011
5'-most EST	uC-zmflb73184a12b1
Method	BLASTX
NCBI GI	g4204313

BLAST score	262
E value	5.0e-44
Match length	107
% identity	83
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	281167
Contig ID	112618_2.R1011
5'-most EST	uC-zmflb73153h10b1
Method	BLASTX
NCBI GI	g4204313
BLAST score	252
E value	1.0e-21
Match length	56
% identity	82
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	281168
Contig ID	112641_1.R1011
5'-most EST	uC-zmflb73156c01b1

Seq. No.	281169
Contig ID	112643_1.R1011
5'-most EST	uC-zmflb73156c04b1

Seq. No.	281170
Contig ID	112649_1.R1011
5'-most EST	uC-zmflb73156c10b1
Method	BLASTX
NCBI GI	g3608495
BLAST score	503
E value	3.0e-53
Match length	167
% identity	69
NCBI Description	(AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]

Seq. No.	281171
Contig ID	112654_1.R1011
5'-most EST	uC-zmflb73156d04b1
Method	BLASTX
NCBI GI	g2894560
BLAST score	167
E value	2.0e-11
Match length	79
% identity	47
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	281172
Contig ID	112672_1.R1011
5'-most EST	uC-zmflb73156f01b1

Seq. No.	281173
Contig ID	112691_1.R1011

5'-most EST	uC-zmflb73156g12b1
Seq. No.	281174
Contig ID	112708_1.R1011
5'-most EST	uC-zmflb73171a11b1
Method	BLASTX
NCBI GI	g4512666
BLAST score	408
E value	1.0e-39
Match length	147
% identity	56
NCBI Description	(AC006931) putative mei2 protein [Arabidopsis thaliana]
Seq. No.	281175
Contig ID	112712_1.R1011
5'-most EST	uC-zmflmo17152h06b1
Method	BLASTX
NCBI GI	g3935138
BLAST score	275
E value	9.0e-43
Match length	177
% identity	48
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]
Seq. No.	281176
Contig ID	112738_1.R1011
5'-most EST	gct701178687.h1
Seq. No.	281177
Contig ID	112774_1.R1011
5'-most EST	uC-zmflb73173a04b1
Method	BLASTX
NCBI GI	g3913437
BLAST score	604
E value	7.0e-63
Match length	147
% identity	78
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970) RNA helicase [Arabidopsis thaliana]
Seq. No.	281178
Contig ID	112780_1.R1011
5'-most EST	kem700611965.h1
Method	BLASTX
NCBI GI	g2967837
BLAST score	186
E value	1.0e-13
Match length	154
% identity	37
NCBI Description	(AF052641) cyst nematode resistance gene candidate [Triticum aestivum]
Seq. No.	281179
Contig ID	112781_1.R1011
5'-most EST	pmx700081820.h1

Method	BLASTX
NCBI GI	g4415919
BLAST score	469
E value	7.0e-47
Match length	159
% identity	60
NCBI Description	(AC006282) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281180
Contig ID	112813_1.R1011
5'-most EST	uC-zmflmo17248h10b1

Seq. No.	281181
Contig ID	112814_1.R1011
5'-most EST	ntr700074104.h1

Seq. No.	281182
Contig ID	112819_1.R1011
5'-most EST	uC-zmflb73173e11b1

Seq. No.	281183
Contig ID	112826_1.R1011
5'-most EST	uC-zmflb73173f11b1

Seq. No.	281184
Contig ID	112837_1.R1011
5'-most EST	uC-zmflmo17193e12b1

Seq. No.	281185
Contig ID	112845_1.R1011
5'-most EST	xmt700268059.h1
Method	BLASTX
NCBI GI	g1653791
BLAST score	163
E value	5.0e-11
Match length	92
% identity	41
NCBI Description	(D90916) hypothetical protein [Synechocystis sp.]

Seq. No.	281186
Contig ID	112847_1.R1011
5'-most EST	uC-zmflb73207d07b1

Seq. No.	281187
Contig ID	112852_1.R1011
5'-most EST	ymt700218593.h1

Seq. No.	281188
Contig ID	112858_1.R1011
5'-most EST	uC-zmflb73174a09b1

Seq. No.	281189
Contig ID	112863_1.R1011
5'-most EST	uC-zmflb73255f06b1

Seq. No.	281190
Contig ID	112866_1.R1011

5'-most EST	uC-zmflb73174b05b1
Seq. No.	281191
Contig ID	112890_1.R1011
5'-most EST	uC-zmflb73194f02b2
Method	BLASTX
NCBI GI	g3413700
BLAST score	490
E value	2.0e-50
Match length	160
% identity	67
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No.	281192
Contig ID	112899_1.R1011
5'-most EST	uC-zmroteosinte091a03b2
Seq. No.	281193
Contig ID	112899_2.R1011
5'-most EST	uC-zmflb73174e11b1
Seq. No.	281194
Contig ID	112916_1.R1011
5'-most EST	wty700167702.h1
Method	BLASTX
NCBI GI	g4539351
BLAST score	294
E value	5.0e-26
Match length	178
% identity	35
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	281195
Contig ID	112918_1.R1011
5'-most EST	uC-zmflb73167f06b2
Method	BLASTX
NCBI GI	g3844597
BLAST score	158
E value	2.0e-10
Match length	58
% identity	53
NCBI Description	(U28941) contains similarity to human copine I (GB:U83246) [Caenorhabditis elegans]
Seq. No.	281196
Contig ID	112921_1.R1011
5'-most EST	hvj700619237.h1
Seq. No.	281197
Contig ID	112966_1.R1011
5'-most EST	uC-zmflb73175e01b1
Method	BLASTX
NCBI GI	g939779
BLAST score	386
E value	3.0e-37
Match length	75
% identity	100

NCBI Description (L46397) MADS box protein [Zea mays]

Seq. No. 281198
Contig ID 112973_1.R1011
5'-most EST uC-zmflb73175e08b1
Method BLASTX
NCBI GI g3810592
BLAST score 150
E value 1.0e-09
Match length 73
% identity 38
NCBI Description (AC005398) unknown protein [Arabidopsis thaliana]

Seq. No. 281199
Contig ID 112988_1.R1011
5'-most EST uC-zmflb73175f12b1

Seq. No. 281200
Contig ID 113006_1.R1011
5'-most EST uC-zmflb73274e02a1

Seq. No. 281201
Contig ID 113010_1.R1011
5'-most EST uC-zmflb73177a01b1
Method BLASTX
NCBI GI g2344894
BLAST score 757
E value 2.0e-80
Match length 233
% identity 28
NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No. 281202
Contig ID 113021_1.R1011
5'-most EST uC-zmflMo17064d10b1
Method BLASTX
NCBI GI g3608368
BLAST score 194
E value 3.0e-14
Match length 380
% identity 27
NCBI Description (AF045607) origin recognition complex associated protein p81 [Xenopus laevis]

Seq. No. 281203
Contig ID 113085_1.R1011
5'-most EST uC-zmflb73157h11b2
Method BLASTX
NCBI GI g2213592
BLAST score 463
E value 4.0e-46
Match length 154
% identity 29
NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No. 281204
Contig ID 113089_1.R1011

5'-most EST	uC-zmflb73177h04b1
Method	BLASTX
NCBI GI	g2811066
BLAST score	188
E value	1.0e-23
Match length	104
% identity	53
NCBI Description	PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN (MUTATED IN MULTIPLE ADVANCED CANCERS 1) >gi_1916330 (U92437) MMAC1 [Mus musculus]

Seq. No.	281205
Contig ID	113096_1.R1011
5'-most EST	uC-zmflb73177h12b1

Seq. No.	281206
Contig ID	113098_1.R1011
5'-most EST	uC-zmflb73178a02b1
Method	BLASTX
NCBI GI	g2245038
BLAST score	466
E value	1.0e-46
Match length	152
% identity	59
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281207
Contig ID	113102_1.R1011
5'-most EST	uC-zmflb73178a07b1
Method	BLASTX
NCBI GI	g3738315
BLAST score	198
E value	5.0e-15
Match length	51
% identity	69
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	281208
Contig ID	113102_2.R1011
5'-most EST	uer700582837.h1
Method	BLASTX
NCBI GI	g3738315
BLAST score	543
E value	2.0e-55
Match length	168
% identity	64
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	281209
Contig ID	113108_1.R1011
5'-most EST	uC-zmflb73178b01b1

Seq. No.	281210
Contig ID	113112_1.R1011
5'-most EST	uC-zmflb73178b06b1

Seq. No.	281211

Contig ID	113113_1.R1011
5'-most EST	uC-zmflb73178b07b1
Method	BLASTX
NCBI GI	g3445201
BLAST score	387
E value	2.0e-37
Match length	110
% identity	65
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	281212
Contig ID	113120_1.R1011
5'-most EST	uC-zmflb73230f01b2

Seq. No.	281213
Contig ID	113129_1.R1011
5'-most EST	uC-zmflb73178c12b1
Method	BLASTX
NCBI GI	g4580455
BLAST score	556
E value	4.0e-57
Match length	175
% identity	64
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	281214
Contig ID	113130_1.R1011
5'-most EST	uC-zmflb73178d01b1
Method	BLASTX
NCBI GI	g4138583
BLAST score	379
E value	3.0e-36
Match length	81
% identity	91
NCBI Description	(Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No.	281215
Contig ID	113131_1.R1011
5'-most EST	uC-zmflmo17235c12b1
Method	BLASTX
NCBI GI	g2289001
BLAST score	383
E value	6.0e-37
Match length	115
% identity	70
NCBI Description	(AC002335) small nuclear ribonucleoprotein isolog [Arabidopsis thaliana]

Seq. No.	281216
Contig ID	113135_1.R1011
5'-most EST	uC-zmflb73178d06b1
Method	BLASTX
NCBI GI	g4262147
BLAST score	346
E value	1.0e-32
Match length	143
% identity	47

NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	281217
Contig ID	113140_1.R1011
5'-most EST	nbm700475469.h1
Method	BLASTX
NCBI GI	g2244865
BLAST score	230
E value	7.0e-19
Match length	85
% identity	48
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281218
Contig ID	113145_1.R1011
5'-most EST	uC-zmflb73178e05b1
Method	BLASTX
NCBI GI	g3924603
BLAST score	499
E value	1.0e-50
Match length	143
% identity	67
NCBI Description	(AF069442) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No.	281219
Contig ID	113171_1.R1011
5'-most EST	xjt700095575.h1
Method	BLASTX
NCBI GI	g4056507
BLAST score	193
E value	1.0e-14
Match length	98
% identity	42
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	281220
Contig ID	113201_1.R1011
5'-most EST	uC-zmflb73179b09b1

Seq. No.	281221
Contig ID	113229_1.R1011
5'-most EST	uC-zmflb73179f11b1
Method	BLASTX
NCBI GI	g1903019
BLAST score	398
E value	2.0e-38
Match length	223
% identity	42
NCBI Description	(Y10580) polycomb group [Arabidopsis thaliana]

Seq. No.	281222
Contig ID	113234_1.R1011
5'-most EST	qmh700027490.f1

Seq. No.	281223
Contig ID	113245_1.R1011
5'-most EST	uC-zmflb73180a09b1
Method	BLASTN
NCBI GI	g5091496
BLAST score	36
E value	1.0e-10
Match length	104
% identity	84
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	281224
Contig ID	113263_1.R1011
5'-most EST	uC-zmflb73180d04b1

Seq. No.	281225
Contig ID	113269_1.R1011
5'-most EST	ymt700224874.h1

Seq. No.	281226
Contig ID	113270_1.R1011
5'-most EST	uC-zmflb73298f04b1

Seq. No.	281227
Contig ID	113291_1.R1011
5'-most EST	nbm700473587.h1

Seq. No.	281228
Contig ID	113307_1.R1011
5'-most EST	uC-zmflb73181a04b2
Method	BLASTX
NCBI GI	g4539665
BLAST score	274
E value	1.0e-38
Match length	167
% identity	49
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]

Seq. No.	281229
Contig ID	113309_1.R1011
5'-most EST	uC-zmflb73181a11b1

Seq. No.	281230
Contig ID	113315_1.R1011
5'-most EST	uC-zmflb73181b02b2

Seq. No.	281231
Contig ID	113318_1.R1011
5'-most EST	uC-zmflb73181b11b2

Seq. No.	281232
Contig ID	113318_2.R1011
5'-most EST	uC-zmflb73216e07b2

Seq. No.	281233
Contig ID	113336_1.R1011

5'-most EST	uC-zmflmo17261c03b1
Seq. No.	281234
Contig ID	113340_1.R1011
5'-most EST	uC-zmflmo17192b04b1
Method	BLASTX
NCBI GI	g2618721
BLAST score	622
E value	2.0e-64
Match length	160
% identity	77
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]
Seq. No.	281235
Contig ID	113344_1.R1011
5'-most EST	uC-zmflb73181h10b2
Method	BLASTX
NCBI GI	g2289790
BLAST score	266
E value	6.0e-23
Match length	185
% identity	35
NCBI Description	(D88750) beta-galactosidase [Bacillus circulans]
Seq. No.	281236
Contig ID	113354_1.R1011
5'-most EST	uC-zmflb73183a10b1
Seq. No.	281237
Contig ID	113371_1.R1011
5'-most EST	uC-zmflb73183c04b1
Seq. No.	281238
Contig ID	113389_1.R1011
5'-most EST	uC-zmflb73183e02b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	505
E value	3.0e-51
Match length	158
% identity	11
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
Seq. No.	281239
Contig ID	113400_1.R1011
5'-most EST	uC-zmflb73270h10b1
Seq. No.	281240
Contig ID	113405_1.R1011
5'-most EST	uC-zmflb73183f08b1
Method	BLASTX
NCBI GI	g3258278
BLAST score	212
E value	8.0e-17
Match length	162
% identity	37

NCBI Description	(AP000007) 798aa long hypothetical transitional endoplasmic reticulum ATPase [Pyrococcus horikoshii]

Seq. No.	281241
Contig ID	113418_1.R1011
5'-most EST	uC-zmflb73183g09b1

Seq. No.	281242
Contig ID	113437_1.R1011
5'-most EST	wyr700241304.h1

Seq. No.	281243
Contig ID	113449_1.R1011
5'-most EST	uC-zmflb73184b08b1

Seq. No.	281244
Contig ID	113452_1.R1011
5'-most EST	uC-zmflb73192d09a1

Seq. No.	281245
Contig ID	113457_1.R1011
5'-most EST	uC-zmflb73184c07b1

Seq. No.	281246
Contig ID	113459_1.R1011
5'-most EST	uC-zmflb73161b09a1

Seq. No.	281247
Contig ID	113462_1.R1011
5'-most EST	uC-zmflb73176b07b2
Method	BLASTX
NCBI GI	g4433618
BLAST score	267
E value	6.0e-23
Match length	174
% identity	41
NCBI Description	(AF107585) putative myosin heavy chain [Dendrobium grex Madame Thong-IN]

Seq. No.	281248
Contig ID	113469_1.R1011
5'-most EST	ypc700805429.h1

Seq. No.	281249
Contig ID	113507_1.R1011
5'-most EST	uC-zmflb73184h04b1
Method	BLASTX
NCBI GI	g3021336
BLAST score	158
E value	3.0e-10
Match length	61
% identity	61
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	281250
Contig ID	113512_1.R1011
5'-most EST	uC-zmflmo17052c05b1

Seq. No.	281251
Contig ID	113542_1.R1011
5'-most EST	uC-zmflb73185c12b1
Method	BLASTX
NCBI GI	g3402703
BLAST score	309
E value	2.0e-29
Match length	89
% identity	70
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281252
Contig ID	113552_1.R1011
5'-most EST	uC-zmflb73344g07a2

Seq. No.	281253
Contig ID	113561_1.R1011
5'-most EST	uC-zmflb73185f05b1

Seq. No.	281254
Contig ID	113572_1.R1011
5'-most EST	uC-zmflb73186a07b1
Method	BLASTX
NCBI GI	g1174470
BLAST score	167
E value	6.0e-12
Match length	39
% identity	82
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	281255
Contig ID	113596_1.R1011
5'-most EST	uC-zmflb73186c06b1

Seq. No.	281256
Contig ID	113608_1.R1011
5'-most EST	pmx700082244.h1
Method	BLASTX
NCBI GI	g3925363
BLAST score	453
E value	5.0e-45
Match length	176
% identity	56
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	281257
Contig ID	113624_1.R1011
5'-most EST	uC-zmflb73186g06b1

Seq. No.	281258
Contig ID	113635_1.R1011
5'-most EST	uC-zmflb73187a07b1

Seq. No.	281259
Contig ID	113638_1.R1011
5'-most EST	uC-zmflmo17184g12b1

Seq. No.	281260
Contig ID	113638_2.R1011
5'-most EST	uC-zmflmo17292b04b1
Method	BLASTX
NCBI GI	g114336
BLAST score	174
E value	2.0e-12
Match length	49
% identity	82
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)

Seq. No.	281261
Contig ID	113648_1.R1011
5'-most EST	uC-zmflb73187c05b1
Method	BLASTX
NCBI GI	g1432153
BLAST score	269
E value	2.0e-23
Match length	102
% identity	46
NCBI Description	(U61727) cellobiose-specific PTS permease [Klebsiella oxytoca]

Seq. No.	281262
Contig ID	113664_1.R1011
5'-most EST	uC-zmflb73349d11a2

Seq. No.	281263
Contig ID	113670_1.R1011
5'-most EST	uC-zmflb73187h10b1
Method	BLASTX
NCBI GI	g2979562
BLAST score	276
E value	2.0e-24
Match length	120
% identity	46
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana] >gi_3386623 (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	281264
Contig ID	113686_1.R1011
5'-most EST	uC-zmflmo17176h11b1
Method	BLASTX
NCBI GI	g2832625
BLAST score	296
E value	8.0e-28
Match length	102
% identity	64
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	281265
Contig ID	113711_1.R1011

5'-most EST	uC-zmflb73146f06a2
Method	BLASTX
NCBI GI	g4006827
BLAST score	146
E value	4.0e-09
Match length	59
% identity	47
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	281266
Contig ID	113749_1.R1011
5'-most EST	fwa700101765.h1
Method	BLASTX
NCBI GI	g4559327
BLAST score	178
E value	2.0e-24
Match length	203
% identity	34
NCBI Description	(AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281267
Contig ID	113752_1.R1011
5'-most EST	uC-zmflb73189e01b1
Method	BLASTX
NCBI GI	g2864625
BLAST score	378
E value	3.0e-36
Match length	167
% identity	54
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	281268
Contig ID	113754_1.R1011
5'-most EST	uC-zmflb73189e07b1

Seq. No.	281269
Contig ID	113771_1.R1011
5'-most EST	uC-zmflb73190a05b1

Seq. No.	281270
Contig ID	113783_1.R1011
5'-most EST	ymt700223475.h1
Method	BLASTX
NCBI GI	g2792364
BLAST score	186
E value	2.0e-13
Match length	273
% identity	23
NCBI Description	(AF040964) unknown protein IT1 [Homo sapiens]

Seq. No.	281271
Contig ID	113784_1.R1011
5'-most EST	qmh700027172.f1

Seq. No.	281272
Contig ID	113786_1.R1011
5'-most EST	uC-zmflb73190b10b1

Seq. No. 281273
Contig ID 113788_1.R1011
5'-most EST uC-zmflb73192b12b1

Seq. No. 281274
Contig ID 113795_1.R1011
5'-most EST uC-zmflmo17342d02b1

Seq. No. 281275
Contig ID 113797_1.R1011
5'-most EST uC-zmflb73190c12b1
Method BLASTX
NCBI GI g3901268
BLAST score 183
E value 2.0e-13
Match length 126
% identity 37
NCBI Description (AF060173) SV2 related protein [Rattus norvegicus]

Seq. No. 281276
Contig ID 113808_1.R1011
5'-most EST uC-zmflb73253d09b1

Seq. No. 281277
Contig ID 113814_1.R1011
5'-most EST rvt700550660.h1

Seq. No. 281278
Contig ID 113816_1.R1011
5'-most EST uC-zmflb73192e08b1

Seq. No. 281279
Contig ID 113817_1.R1011
5'-most EST uC-zmflb73190e09b1
Method BLASTX
NCBI GI g3885341
BLAST score 175
E value 2.0e-12
Match length 151
% identity 29
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 281280
Contig ID 113825_1.R1011
5'-most EST wyr700243123.h1
Method BLASTX
NCBI GI g2245080
BLAST score 239
E value 7.0e-20
Match length 220
% identity 29
NCBI Description (Z97343) myosin heavy chain homolog [Arabidopsis thaliana]

Seq. No. 281281
Contig ID 113840_1.R1011
5'-most EST uC-zmflb73190h01b1

Seq. No. 281282
Contig ID 113847_1.R1011
5'-most EST uC-zmflb73190h10b1
Method BLASTX
NCBI GI g1335966
BLAST score 1531
E value 1.0e-171
Match length 299
% identity 97
NCBI Description (U58598) acetyl CoA carboxylase [Zea mays]

Seq. No. 281283
Contig ID 113857_1.R1011
5'-most EST xyt700343184.h1

Seq. No. 281284
Contig ID 113857_2.R1011
5'-most EST uC-zmflb73355d12a1

Seq. No. 281285
Contig ID 113857_3.R1011
5'-most EST uC-zmflb73191a12b1

Seq. No. 281286
Contig ID 113892_1.R1011
5'-most EST uC-zmrob73019e10b1
Method BLASTX
NCBI GI g4220518
BLAST score 174
E value 2.0e-12
Match length 85
% identity 42
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No. 281287
Contig ID 113898_1.R1011
5'-most EST uC-zmflmo17391g10a1

Seq. No. 281288
Contig ID 113902_1.R1011
5'-most EST uC-zmflMo17010c02b1
Method BLASTX
NCBI GI g3329506
BLAST score 175
E value 3.0e-12
Match length 115
% identity 40
NCBI Description (AF074723) RNA polymerase transcriptional regulation mediator [Homo sapiens]

Seq. No. 281289
Contig ID 113908_1.R1011
5'-most EST uC-zmflb73192b03b1
Method BLASTX
NCBI GI g1335862
BLAST score 1050

E value	1.0e-115
Match length	206
% identity	97
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	281290
Contig ID	113912_1.R1011
5'-most EST	pmx700086692.h1
Method	BLASTX
NCBI GI	g4263722
BLAST score	793
E value	8.0e-85
Match length	179
% identity	85
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	281291
Contig ID	113913_1.R1011
5'-most EST	pmx700087958.h1

Seq. No.	281292
Contig ID	113914_1.R1011
5'-most EST	wty700164577.h1

Seq. No.	281293
Contig ID	113926_1.R1011
5'-most EST	tzu700206831.h1
Method	BLASTX
NCBI GI	g3912917
BLAST score	439
E value	3.0e-43
Match length	177
% identity	51
NCBI Description	(AF001308) putative NAK-like ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	281294
Contig ID	113938_1.R1011
5'-most EST	uC-zmflb73192d09b1

Seq. No.	281295
Contig ID	113941_1.R1011
5'-most EST	uC-zmflb73161a04b2
Method	BLASTX
NCBI GI	g3915037
BLAST score	429
E value	6.0e-42
Match length	125
% identity	62
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No.	281296
Contig ID	113944_1.R1011
5'-most EST	uC-zmflb73192e03b1
Method	BLASTX

NCBI GI	g4249419
BLAST score	267
E value	3.0e-23
Match length	131
% identity	44
NCBI Description	(AC006072) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	281297
Contig ID	113954_1.R1011
5'-most EST	uC-zmflb73192f01b1

Seq. No.	281298
Contig ID	113959_1.R1011
5'-most EST	wty700171384.h1

Seq. No.	281299
Contig ID	113967_1.R1011
5'-most EST	uC-zmroteosinte024b09b1
Method	BLASTX
NCBI GI	g1172019
BLAST score	500
E value	3.0e-50
Match length	258
% identity	45
NCBI Description	PEROXISOME BIOSYNTHESIS PROTEIN PAS1 (PEROXIN-1) >gi_1076972_pir__A55152 PAS1 protein - yeast (Pichia pastoris) >gi_537420_emb_CAA85450_ (Z36987) PAS1 [Pichia pastoris]

Seq. No.	281300
Contig ID	113981_1.R1011
5'-most EST	wty700168575.h1
Method	BLASTX
NCBI GI	g2194121
BLAST score	204
E value	6.0e-16
Match length	95
% identity	44
NCBI Description	(AC002062) Strong similarity to Arabidopsis cyclin delta-1 (gb_ATCD1). EST gb_ATTS4338 comes from this gene. [Arabidopsis thaliana]

Seq. No.	281301
Contig ID	113984_1.R1011
5'-most EST	uC-zmflb73165a11b2
Method	BLASTX
NCBI GI	g4581164
BLAST score	250
E value	3.0e-21
Match length	140
% identity	45
NCBI Description	(AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No.	281302
Contig ID	113990_1.R1011
5'-most EST	uC-zmflmo17150d11a1

Method	BLASTX
NCBI GI	g2213594
BLAST score	171
E value	6.0e-12
Match length	69
% identity	45
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	281303
Contig ID	114031_1.R1011
5'-most EST	uC-zmflb73193e08b1

Seq. No.	281304
Contig ID	114032_1.R1011
5'-most EST	uC-zmflb73193e09b1
Method	BLASTX
NCBI GI	g116054
BLAST score	370
E value	7.0e-35
Match length	229
% identity	38
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) >gi_280393_pir__A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean >gi_169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]

Seq. No.	281305
Contig ID	114034_1.R1011
5'-most EST	lhp700053352.r1

Seq. No.	281306
Contig ID	114046_1.R1011
5'-most EST	uC-zmflb73193f11b1
Method	BLASTX
NCBI GI	g3420056
BLAST score	190
E value	7.0e-14
Match length	75
% identity	49
NCBI Description	(AC004680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281307
Contig ID	114047_1.R1011
5'-most EST	uC-zmflmo17310e08b1

Seq. No.	281308
Contig ID	114048_1.R1011
5'-most EST	uC-zmflb73193g01b1
Method	BLASTX
NCBI GI	g2982362
BLAST score	399
E value	1.0e-38
Match length	101
% identity	73
NCBI Description	(AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.	281309

Contig ID	114059_1.R1011
5'-most EST	uC-zmflmo17184b05b1
Method	BLASTX
NCBI GI	g4544412
BLAST score	264
E value	2.0e-22
Match length	173
% identity	36
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281310
Contig ID	114059_2.R1011
5'-most EST	xtj700377842.h1

Seq. No.	281311
Contig ID	114072_1.R1011
5'-most EST	uC-zmflb73194a04b2
Method	BLASTN
NCBI GI	g4416300
BLAST score	105
E value	9.0e-52
Match length	137
% identity	94
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	281312
Contig ID	114081_1.R1011
5'-most EST	uC-zmflb73194b03b2
Method	BLASTX
NCBI GI	g2459443
BLAST score	440
E value	1.0e-43
Match length	119
% identity	67
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana]

Seq. No.	281313
Contig ID	114081_2.R1011
5'-most EST	uC-zmrob73076f11b1
Method	BLASTX
NCBI GI	g2459443
BLAST score	267
E value	1.0e-28
Match length	100
% identity	70
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana]

Seq. No.	281314
Contig ID	114083_1.R1011
5'-most EST	wyr700241488.h1
Method	BLASTX
NCBI GI	g1076732
BLAST score	499
E value	2.0e-66

09854500 - 1050900

Match length	147
% identity	81
NCBI Description	type-1 pathogenesis-related protein - barley >gi_732807_emb_CAA88618_ (Z48728) type-1 pathogenesis-related protein [Hordeum vulgare]

Seq. No.	281315
Contig ID	114085_1.R1011
5'-most EST	uC-zmflb73194b07b2

Seq. No.	281316
Contig ID	114130_1.R1011
5'-most EST	fwa700099547.h1
Method	BLASTX
NCBI GI	g3309583
BLAST score	804
E value	1.0e-135
Match length	325
% identity	76
NCBI Description	(AF073830) fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No.	281317
Contig ID	114137_1.R1011
5'-most EST	xjt700095458.h1

Seq. No.	281318
Contig ID	114144_1.R1011
5'-most EST	tfd700574871.h1
Method	BLASTX
NCBI GI	g4033763
BLAST score	185
E value	7.0e-18
Match length	234
% identity	25
NCBI Description	IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5) >gi_2253156_emb_CAA70103_ (Y08890) Ran_GTP binding protein 5 [Homo sapiens]

Seq. No.	281319
Contig ID	114164_1.R1011
5'-most EST	uC-zmroteosinte086b09b1
Method	BLASTX
NCBI GI	g3142297
BLAST score	294
E value	1.0e-43
Match length	211
% identity	47
NCBI Description	(AC002411) Contains similarity to serine/threonine protein phosphatase gb_X83099 from S. cerevisiae. [Arabidopsis thaliana]

Seq. No.	281320
Contig ID	114183_1.R1011
5'-most EST	wyr700242510.h1

Seq. No.	281321

Contig ID	114234_1.R1011
5'-most EST	uC-zmflb73206g03b1
Seq. No.	281322
Contig ID	114248_1.R1011
5'-most EST	uC-zmflb73196b02b1
Method	BLASTX
NCBI GI	g4415932
BLAST score	438
E value	4.0e-43
Match length	224
% identity	42
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana]
Seq. No.	281323
Contig ID	114259_1.R1011
5'-most EST	uC-zmflb73196c01b1
Method	BLASTX
NCBI GI	g4454010
BLAST score	717
E value	8.0e-76
Match length	195
% identity	70
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]
Seq. No.	281324
Contig ID	114261_1.R1011
5'-most EST	uC-zmflb73196c03b1
Method	BLASTX
NCBI GI	g3859659
BLAST score	695
E value	3.0e-73
Match length	223
% identity	58
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]
Seq. No.	281325
Contig ID	114282_1.R1011
5'-most EST	xsy700213407.h1
Seq. No.	281326
Contig ID	114316_1.R1011
5'-most EST	cyk700048903.f1
Seq. No.	281327
Contig ID	114318_1.R1011
5'-most EST	uC-zmflb73197a01b1
Seq. No.	281328
Contig ID	114345_1.R1011
5'-most EST	vfk700404833.h1
Seq. No.	281329
Contig ID	114348_1.R1011
5'-most EST	gct701177490.h1

Seq. No. 281330
Contig ID 114360_1.R1011
5'-most EST uC-zmflb73197e02b1

Seq. No. 281331
Contig ID 114366_1.R1011
5'-most EST uC-zmflmo17336g12b1

Seq. No. 281332
Contig ID 114371_1.R1011
5'-most EST dyk700104466.h1
Method BLASTX
NCBI GI g3702641
BLAST score 188
E value 5.0e-14
Match length 80
% identity 42
NCBI Description (AL031825) similar to human 75k autoantigen [Schizosaccharomyces pombe]

Seq. No. 281333
Contig ID 114377_1.R1011
5'-most EST uC-zmflb73197f09b1
Method BLASTX
NCBI GI g3377803
BLAST score 853
E value 1.0e-91
Match length 286
% identity 65
NCBI Description (AF075597) Similar to (p)ppGpp synthetase; T2H3.9 [Arabidopsis thaliana]

Seq. No. 281334
Contig ID 114395_1.R1011
5'-most EST wyr700240423.h1
Method BLASTX
NCBI GI g2832708
BLAST score 450
E value 7.0e-45
Match length 135
% identity 61
NCBI Description (AL021713) beta-1, 3-glucanase-like protein [Arabidopsis thaliana]

Seq. No. 281335
Contig ID 114438_1.R1011
5'-most EST xmt700265384.h1
Method BLASTX
NCBI GI g3355474
BLAST score 483
E value 3.0e-48
Match length 145
% identity 66
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 281336
Contig ID 114447_1.R1011

5'-most EST	uC-zmflmo17201c11b1
Seq. No.	281337
Contig ID	114449_1.R1011
5'-most EST	uC-zmflb73198f03b1
Seq. No.	281338
Contig ID	114482_1.R1011
5'-most EST	ntr700077404.h1
Seq. No.	281339
Contig ID	114519_1.R1011
5'-most EST	uC-zmflb73199f06b1
Method	BLASTX
NCBI GI	g2245013
BLAST score	390
E value	1.0e-37
Match length	165
% identity	53
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.	281340
Contig ID	114538_1.R1011
5'-most EST	uC-zmroB73020c12b1
Method	BLASTX
NCBI GI	g881625
BLAST score	532
E value	3.0e-54
Match length	125
% identity	78
NCBI Description	(U29432) 22.8 kDa protein [Ipomoea trifida]
Seq. No.	281341
Contig ID	114540_1.R1011
5'-most EST	uC-zmflb73199h07b1
Seq. No.	281342
Contig ID	114564_1.R1011
5'-most EST	uC-zmflb73200b11b1
Seq. No.	281343
Contig ID	114569_1.R1011
5'-most EST	uC-zmflb73200c06b1
Method	BLASTX
NCBI GI	g121341
BLAST score	1506
E value	1.0e-168
Match length	291
% identity	97
NCBI Description	GLUTAMINE SYNTHETASE, CHLOROPLAST PRECURSOR (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_539063_pir__S39482 glutamate--ammonia ligase (EC 6.3.1.2) 1 precursor, chloroplast - maize >gi_434334_emb_CAA46724_ (X65931) glutamine synthetase [Zea mays]
Seq. No.	281344
Contig ID	114574_1.R1011

5'-most EST	xmt700264738.h1
Seq. No.	281345
Contig ID	114584_1.R1011
5'-most EST	uC-zmflb73200d10b1
Method	BLASTX
NCBI GI	g2316016
BLAST score	553
E value	8.0e-57
Match length	160
% identity	67
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
Seq. No.	281346
Contig ID	114597_1.R1011
5'-most EST	uC-zmroteosinte087b08b2
Seq. No.	281347
Contig ID	114608_1.R1011
5'-most EST	uC-zmflb73200g04b1
Method	BLASTX
NCBI GI	g1946355
BLAST score	290
E value	6.0e-26
Match length	115
% identity	42
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.	281348
Contig ID	114631_1.R1011
5'-most EST	ceu700433275.h1
Seq. No.	281349
Contig ID	114631_2.R1011
5'-most EST	tfd700569109.h1
Seq. No.	281350
Contig ID	114631_3.R1011
5'-most EST	clt700042291.f1
Seq. No.	281351
Contig ID	114643_1.R1011
5'-most EST	uC-zmflmo17130b09b1
Method	BLASTX
NCBI GI	g585914
BLAST score	474
E value	2.0e-47
Match length	205
% identity	49
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 135 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 2) >gi_421848_pir__S30228 DNA-directed RNA polymerase (EC 2.7.7.6) II second largest chain - Arabidopsis thaliana >gi_16488_emb_CAA79527_ (Z19120) RNA polymerase II second largest subunit [Arabidopsis thaliana]

Seq. No.	281352
Contig ID	114644_1.R1011
5'-most EST	uC-zmflb73201b08b1

Seq. No.	281353
Contig ID	114647_1.R1011
5'-most EST	uC-zmflb73201b12b1
Method	BLASTX
NCBI GI	g1351945
BLAST score	498
E value	2.0e-50
Match length	105
% identity	88
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA2 >gi_533709 (U12546) APETALA2 protein [Arabidopsis thaliana] >gi_2464888_emb_CAB16765.1_ (Z99707) APETALA2 protein [Arabidopsis thaliana]

Seq. No.	281354
Contig ID	114662_1.R1011
5'-most EST	uC-zmflb73201d04b1
Method	BLASTX
NCBI GI	g4406812
BLAST score	400
E value	8.0e-39
Match length	134
% identity	57
NCBI Description	(AC006201) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	281355
Contig ID	114670_1.R1011
5'-most EST	uC-zmflb73201e01b1

Seq. No.	281356
Contig ID	114672_1.R1011
5'-most EST	cyk700048951.f1

Seq. No.	281357
Contig ID	114691_1.R1011
5'-most EST	rvt700549102.h1
Method	BLASTX
NCBI GI	g4455338
BLAST score	411
E value	7.0e-40
Match length	116
% identity	67
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	281358
Contig ID	114701_1.R1011
5'-most EST	uC-zmflb73201g11b1

Seq. No.	281359
Contig ID	114716_1.R1011
5'-most EST	gct701177363.h1

Method	BLASTX
NCBI GI	g4587554
BLAST score	272
E value	4.0e-24
Match length	94
% identity	52
NCBI Description	(AC006577) Similar to gb_AJ005701 Na/Ca,K-exchanger from Caenorhabditis elegans. ESTs gb_T04173 and gb_AA585918 come from this gene. [Arabidopsis thaliana]

Seq. No.	281360
Contig ID	114717_1.R1011
5'-most EST	xsy700208909.h1

Seq. No.	281361
Contig ID	114726_1.R1011
5'-most EST	uC-zmflb73202b10b1

Seq. No.	281362
Contig ID	114733_1.R1011
5'-most EST	uC-zmflb73202c09b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	9.0e-11
Match length	49
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	281363
Contig ID	114733_2.R1011
5'-most EST	fC-zmle700445820f7

Seq. No.	281364
Contig ID	114748_1.R1011
5'-most EST	tzu700204330.h1

Seq. No.	281365
Contig ID	114748_2.R1011
5'-most EST	pmx700091477.h1

Seq. No.	281366
Contig ID	114775_1.R1011
5'-most EST	uC-zmflb73202g12b1

Seq. No.	281367
Contig ID	114782_1.R1011
5'-most EST	uC-zmflb73202h12b1
Method	BLASTX
NCBI GI	g2245115
BLAST score	218
E value	2.0e-17
Match length	130
% identity	38
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 281368

09654025 - 4704900

Contig ID	114784_1.R1011
5'-most EST	uC-zmflmol7108f06b1
Method	BLASTX
NCBI GI	g4263791
BLAST score	396
E value	2.0e-38
Match length	147
% identity	54
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	281369
Contig ID	114796_1.R1011
5'-most EST	wty700166367.h1
Method	BLASTX
NCBI GI	g3953466
BLAST score	411
E value	2.0e-40
Match length	110
% identity	65
NCBI Description	(AC002328) F20N2.11 [Arabidopsis thaliana]

Seq. No.	281370
Contig ID	114803_1.R1011
5'-most EST	cat700021465.r1
Method	BLASTX
NCBI GI	g4455192
BLAST score	238
E value	6.0e-20
Match length	141
% identity	43
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	281371
Contig ID	114804_1.R1011
5'-most EST	uC-zmroteosinte048f12b1
Method	BLASTX
NCBI GI	g1020095
BLAST score	179
E value	8.0e-13
Match length	65
% identity	52
NCBI Description	(D31838) wee1 tyrosine kinase [Rattus sp.]

Seq. No.	281372
Contig ID	114820_1.R1011
5'-most EST	uC-zmflb73266g03b2

Seq. No.	281373
Contig ID	114826_1.R1011
5'-most EST	uC-zmflb73204f08b1

Seq. No.	281374
Contig ID	114836_1.R1011
5'-most EST	xmt700264092.h1
Method	BLASTN
NCBI GI	g207039

BLAST score	35
E value	4.0e-10
Match length	43
% identity	95
NCBI Description	Rat chondroitin sulfate proteoglycan core protein mRNA, complete cds

Seq. No.	281375
Contig ID	114839_1.R1011
5'-most EST	uC-zmflb73204g12b1

Seq. No.	281376
Contig ID	114841_1.R1011
5'-most EST	afb700381254.h1
Method	BLASTX
NCBI GI	g3776009
BLAST score	428
E value	3.0e-42
Match length	128
% identity	63
NCBI Description	(AJ010468) RNA helicase [Arabidopsis thaliana]

Seq. No.	281377
Contig ID	114856_1.R1011
5'-most EST	uC-zmflb73206a08b1

Seq. No.	281378
Contig ID	114863_1.R1011
5'-most EST	uC-zmflb73206b07b1
Method	BLASTX
NCBI GI	g4539002
BLAST score	205
E value	6.0e-16
Match length	74
% identity	54
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	281379
Contig ID	114880_1.R1011
5'-most EST	uC-zmflb73114b06a2
Method	BLASTX
NCBI GI	g2425101
BLAST score	184
E value	2.0e-13
Match length	87
% identity	46
NCBI Description	(AF019743) cationic peroxidase [Oryza sativa]

Seq. No.	281380
Contig ID	114885_1.R1011
5'-most EST	uC-zmflb73206d09b1

Seq. No.	281381
Contig ID	114888_1.R1011
5'-most EST	nbm700475065.h1
Method	BLASTX
NCBI GI	g2245069

BLAST score	348
E value	6.0e-35
Match length	126
% identity	58
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281382
Contig ID	114898_1.R1011
5'-most EST	uC-zmflmo17360h03a1

Seq. No.	281383
Contig ID	114904_1.R1011
5'-most EST	kem700612168.h1
Method	BLASTX
NCBI GI	g849072
BLAST score	481
E value	1.0e-53
Match length	186
% identity	61
NCBI Description	(D50736) A-type cyclin [Nicotiana tabacum]

Seq. No.	281384
Contig ID	114921_1.R1011
5'-most EST	uC-zmflb73206h02b1
Method	BLASTX
NCBI GI	g3183991
BLAST score	412
E value	2.0e-40
Match length	140
% identity	59
NCBI Description	(AJ005173) P69F protein [Lycopersicon esculentum]

Seq. No.	281385
Contig ID	114942_1.R1011
5'-most EST	uC-zmflb73207b11b1
Method	BLASTX
NCBI GI	g2529677
BLAST score	143
E value	7.0e-09
Match length	43
% identity	63
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No.	281386
Contig ID	114961_1.R1011
5'-most EST	uC-zmflb73207d10b1

Seq. No.	281387
Contig ID	114989_1.R1011
5'-most EST	pwr700453682.h1

Seq. No.	281388
Contig ID	114994_1.R1011
5'-most EST	uC-zmflb73207h12b1
Method	BLASTX
NCBI GI	g3892055

BLAST score	478
E value	4.0e-48
Match length	110
% identity	77
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	281389
Contig ID	115013_1.R1011
5'-most EST	uC-zmflb73208a01b1

Seq. No.	281390
Contig ID	115014_1.R1011
5'-most EST	uC-zmflb73208a02b1
Method	BLASTX
NCBI GI	g2370253
BLAST score	657
E value	7.0e-69
Match length	165
% identity	76
NCBI Description	(Y13273) putative protein kinase [Lycopersicon esculentum]

Seq. No.	281391
Contig ID	115018_1.R1011
5'-most EST	uC-zmflb73208a07b1

Seq. No.	281392
Contig ID	115018_2.R1011
5'-most EST	xsy700209311.h1

Seq. No.	281393
Contig ID	115019_1.R1011
5'-most EST	uC-zmflb73208a08b1

Seq. No.	281394
Contig ID	115042_1.R1011
5'-most EST	yyf700350644.h1
Method	BLASTX
NCBI GI	g1732515
BLAST score	177
E value	3.0e-12
Match length	130
% identity	33
NCBI Description	(U62744) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	281395
Contig ID	115042_2.R1011
5'-most EST	uC-zmflb73208c10b1

Seq. No.	281396
Contig ID	115043_1.R1011
5'-most EST	wyr700237707.h1
Method	BLASTX
NCBI GI	g4415915
BLAST score	398
E value	1.0e-38

Match length	147
% identity	51
NCBI Description	(AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	281397
Contig ID	115048_1.R1011
5'-most EST	uC-zmflb73208d06b1
Method	BLASTX
NCBI GI	g4504629
BLAST score	271
E value	3.0e-23
Match length	328
% identity	27
NCBI Description	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein; IKAP >gi_3757822 (AF044195) IkappaB kinase complex associated protein; IKAP [Homo sapiens]

Seq. No.	281398
Contig ID	115058_1.R1011
5'-most EST	wyr700239284.h1
Method	BLASTX
NCBI GI	g3183347
BLAST score	253
E value	2.0e-21
Match length	168
% identity	38
NCBI Description	HYPOTHETICAL 48.5 KD PROTEIN C23C11.04C IN CHROMOSOME I >gi_2330768_emb_CAB11157_ (Z98559) SPAC23C11.04c; len:421aa, similar eg. to C. elegans Q19683, F21D5.5, (250aa), fasta scores, opt:395, E():1.1e-32, (41.7% identity in 223 aa overlap)also similar eg. to YMR156C, YM31_YEAST, Q03796, hypothetical 27.4 kd

Seq. No.	281399
Contig ID	115059_1.R1011
5'-most EST	uC-zmflb73208e07b1
Method	BLASTX
NCBI GI	g3451069
BLAST score	297
E value	7.0e-27
Match length	145
% identity	43
NCBI Description	(AL031326) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281400
Contig ID	115097_1.R1011
5'-most EST	uC-zmflb73210b01b1
Method	BLASTX
NCBI GI	g3738339
BLAST score	483
E value	2.0e-48
Match length	200
% identity	51
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	281401
Contig ID	115098_1.R1011
5'-most EST	nbm700467852.h1
Method	BLASTX
NCBI GI	g1722856
BLAST score	228
E value	4.0e-19
Match length	98
% identity	46
NCBI Description	CHROMOSOME ASSEMBLY PROTEIN XCAP-E >gi_1079282_pir__B55094 chromosomal protein XCAP-E - African clawed frog >gi_563814 (U13674) XCAP-E [Xenopus laevis]

Seq. No.	281402
Contig ID	115116_1.R1011
5'-most EST	uC-zmflb73210c11b1

Seq. No.	281403
Contig ID	115128_1.R1011
5'-most EST	uC-zmromo17114d10a1

Seq. No.	281404
Contig ID	115134_1.R1011
5'-most EST	pmx700091104.h1

Seq. No.	281405
Contig ID	115135_1.R1011
5'-most EST	xmt700256795.h1

Seq. No.	281406
Contig ID	115139_1.R1011
5'-most EST	uC-zmflb73210f07b1
Method	BLASTX
NCBI GI	g4262186
BLAST score	277
E value	2.0e-24
Match length	90
% identity	60
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	281407
Contig ID	115143_1.R1011
5'-most EST	uC-zmflb73210f11b1

Seq. No.	281408
Contig ID	115148_1.R1011
5'-most EST	uC-zmflb73210g04b1

Seq. No.	281409
Contig ID	115164_1.R1011
5'-most EST	rvt700549375.h1
Method	BLASTX
NCBI GI	g1362084
BLAST score	241
E value	1.0e-23
Match length	111

% identity	51
NCBI Description	probable cell wall-bound EP4 protein, 45K, precursor - carrot (fragment) >gi_886225 (L36957) secreted protein [Daucus carota]
Seq. No.	281410
Contig ID	115166_1.R1011
5'-most EST	uC-zmroteosinte033d09b1
Seq. No.	281411
Contig ID	115177_1.R1011
5'-most EST	uC-zmflb73214b05b1
Seq. No.	281412
Contig ID	115185_1.R1011
5'-most EST	uC-zmflb73214c02b1
Method	BLASTX
NCBI GI	g4218187
BLAST score	385
E value	1.0e-36
Match length	148
% identity	48
NCBI Description	(AJ010165) leghemoglobin activating factor [Glycine max]
Seq. No.	281413
Contig ID	115185_2.R1011
5'-most EST	uC-zmflmo17155d05b1
Method	BLASTX
NCBI GI	g4218187
BLAST score	211
E value	8.0e-17
Match length	71
% identity	51
NCBI Description	(AJ010165) leghemoglobin activating factor [Glycine max]
Seq. No.	281414
Contig ID	115185_3.R1011
5'-most EST	uC-zmflb73325e04a1
Seq. No.	281415
Contig ID	115206_1.R1011
5'-most EST	uC-zmflb73169f08b2
Method	BLASTX
NCBI GI	g2982431
BLAST score	278
E value	2.0e-24
Match length	205
% identity	24
NCBI Description	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
Seq. No.	281416
Contig ID	115222_1.R1011
5'-most EST	uC-zmflmo17187d09b1
Method	BLASTX
NCBI GI	g3928543
BLAST score	247

E value 6.0e-21
Match length 136
% identity 45
NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No. 281417
Contig ID 115253_1.R1011
5'-most EST uC-zmflb73221a06b1
Method BLASTX
NCBI GI g1223579
BLAST score 201
E value 1.0e-15
Match length 85
% identity 47
NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 281418
Contig ID 115282_1.R1011
5'-most EST uC-zmflb73221f04b1

Seq. No. 281419
Contig ID 115285_1.R1011
5'-most EST uC-zmflb73221f08b1

Seq. No. 281420
Contig ID 115287_2.R1011
5'-most EST rvt700552383.h1

Seq. No. 281421
Contig ID 115305_1.R1011
5'-most EST uC-zmflb73221h12b1

Seq. No. 281422
Contig ID 115311_1.R1011
5'-most EST uC-zmflb73222a06b1

Seq. No. 281423
Contig ID 115327_1.R1011
5'-most EST uC-zmflb73222b10b1

Seq. No. 281424
Contig ID 115339_2.R1011
5'-most EST pwr700449050.h1

Seq. No. 281425
Contig ID 115340_1.R1011
5'-most EST uC-zmflb73260g04b2

Seq. No. 281426
Contig ID 115360_1.R1011
5'-most EST uC-zmroteosinte017c10b1
Method BLASTX
NCBI GI g2244855
BLAST score 336
E value 2.0e-31
Match length 130

% identity	52
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281427
Contig ID	115383_1.R1011
5'-most EST	uC-zmflb73222h07b1
Method	BLASTX
NCBI GI	g3341648
BLAST score	554
E value	6.0e-74
Match length	149
% identity	96
NCBI Description	(AJ005343) DNA directed RNA polymerase [Zea mays]

Seq. No.	281428
Contig ID	115389_1.R1011
5'-most EST	uC-zmflb73224a01b1
Method	BLASTX
NCBI GI	g1652919
BLAST score	808
E value	2.0e-87
Match length	174
% identity	98
NCBI Description	(D90909) periplasmic phosphate binding protein [Synechocystis sp.]

Seq. No.	281429
Contig ID	115391_1.R1011
5'-most EST	uC-zmflmo17227a08a1
Method	BLASTX
NCBI GI	g3023956
BLAST score	222
E value	7.0e-18
Match length	168
% identity	6
NCBI Description	VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi_607003 (L28125) beta transducin-like protein [Podospora anserina]

Seq. No.	281430
Contig ID	115392_1.R1011
5'-most EST	uC-zmflb73224a03b1
Method	BLASTX
NCBI GI	g1001164
BLAST score	827
E value	8.0e-89
Match length	160
% identity	99
NCBI Description	(D64001) gamma-glutamyl phosphate reductase [Synechocystis sp.]

Seq. No.	281431
Contig ID	115394_1.R1011
5'-most EST	uC-zmflb73224a04b1
Method	BLASTX
NCBI GI	g1651656
BLAST score	1041
E value	1.0e-132

Match length	237
% identity	93
NCBI Description	(D90899) hypothetical protein [Synechocystis sp.]

Seq. No.	281432
Contig ID	115405_1.R1011
5'-most EST	uC-zmflb73224a10b1
Method	BLASTN
NCBI GI	g1652725
BLAST score	365
E value	0.0e+00
Match length	373
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234

Seq. No.	281433
Contig ID	115405_2.R1011
5'-most EST	uC-zmflmo17227e02b1

Seq. No.	281434
Contig ID	115407_1.R1011
5'-most EST	uC-zmflb73224a11b1
Method	BLASTX
NCBI GI	g1651916
BLAST score	999
E value	1.0e-109
Match length	202
% identity	97
NCBI Description	(D90901) iron transport protein [Synechocystis sp.]

Seq. No.	281435
Contig ID	115410_1.R1011
5'-most EST	uC-zmflb73224b01b1
Method	BLASTX
NCBI GI	g2648839
BLAST score	169
E value	1.0e-11
Match length	109
% identity	38
NCBI Description	(AE000985) type I restriction-modification enzyme, S subunit [Archaeoglobus fulgidus]

Seq. No.	281436
Contig ID	115416_1.R1011
5'-most EST	uC-zmflb73224b06b1
Method	BLASTN
NCBI GI	g1651897
BLAST score	603
E value	0.0e+00
Match length	699
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289

Seq. No.	281437
Contig ID	115418_1.R1011

5'-most EST	uC-zmflb73224b07b1
Method	BLASTN
NCBI GI	g1001102
BLAST score	696
E value	0.0e+00
Match length	708
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794

Seq. No.	281438
Contig ID	115425_1.R1011
5'-most EST	uC-zmflb73224b11b1
Method	BLASTX
NCBI GI	g1001300
BLAST score	1078
E value	1.0e-118
Match length	218
% identity	98
NCBI Description	(D64006) methyl-accepting chemotaxis protein I [Synechocystis sp.]

Seq. No.	281439
Contig ID	115431_1.R1011
5'-most EST	tzu700205951.h1

Seq. No.	281440
Contig ID	115433_1.R1011
5'-most EST	uC-zmflb73224c04b1
Method	BLASTN
NCBI GI	g1001396
BLAST score	551
E value	0.0e+00
Match length	609
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 18/27, 2267260-2392728

Seq. No.	281441
Contig ID	115435_1.R1011
5'-most EST	uC-zmflb73224c05b1
Method	BLASTX
NCBI GI	g1705799
BLAST score	415
E value	1.0e-50
Match length	132
% identity	87
NCBI Description	60 KD CHAPERONIN 2 (PROTEIN CPN60 2) (GROEL HOMOLOG 2) >gi_1001103_dbj_BAA10240_ (D64001) 60kD chaperonin 2 [Synechocystis sp.]

Seq. No.	281442
Contig ID	115443_1.R1011
5'-most EST	uC-zmflb73224c11b1
Method	BLASTX
NCBI GI	g1001593
BLAST score	401

E value	5.0e-39
Match length	84
% identity	95
NCBI Description	(D64000) glucose inhibited division protein A [Synechocystis sp.]

Seq. No.	281443
Contig ID	115445_1.R1011
5'-most EST	uC-zmflb73224c12b1

Seq. No.	281444
Contig ID	115449_1.R1011
5'-most EST	uC-zmflb73224d03b1
Method	BLASTX
NCBI GI	g1651978
BLAST score	864
E value	1.0e-104
Match length	206
% identity	90
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	281445
Contig ID	115450_1.R1011
5'-most EST	wty700167241.h1
Method	BLASTX
NCBI GI	g4006900
BLAST score	636
E value	2.0e-66
Match length	218
% identity	58
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281446
Contig ID	115462_1.R1011
5'-most EST	uC-zmflb73224d10b1
Method	BLASTN
NCBI GI	g1001484
BLAST score	285
E value	1.0e-159
Match length	309
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999

Seq. No.	281447
Contig ID	115466_1.R1011
5'-most EST	uC-zmflb73224d12b1
Method	BLASTX
NCBI GI	g2492511
BLAST score	683
E value	7.0e-72
Match length	223
% identity	67
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG 2 >gi_1652282_dbj_BAA17205_ (D90904) cell division protein FtsH [Synechocystis sp.]

Seq. No.	281448
Contig ID	115469_1.R1011
5'-most EST	uC-zmflb73224e02b1
Method	BLASTX
NCBI GI	g862633
BLAST score	469
E value	9.0e-47
Match length	154
% identity	60
NCBI Description	(U13633) RumB(R391) [IncJ plasmid R391] >gi_1096691_prf__2112258B rumB gene [Escherichia coli]

Seq. No.	281449
Contig ID	115471_1.R1011
5'-most EST	uC-zmflb73224e03b1

Seq. No.	281450
Contig ID	115479_1.R1011
5'-most EST	uC-zmflb73224e07b1
Method	BLASTN
NCBI GI	g1652725
BLAST score	468
E value	0.0e+00
Match length	492
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234

Seq. No.	281451
Contig ID	115481_1.R1011
5'-most EST	uC-zmflb73224e08b1
Method	BLASTX
NCBI GI	g1208454
BLAST score	631
E value	6.0e-66
Match length	153
% identity	82
NCBI Description	(D64004) hypothetical protein [Synechocystis sp.]

Seq. No.	281452
Contig ID	115483_1.R1011
5'-most EST	uC-zmflb73224e09b1
Method	BLASTN
NCBI GI	g1652725
BLAST score	384
E value	0.0e+00
Match length	544
% identity	93
NCBI Description	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234

Seq. No.	281453
Contig ID	115485_1.R1011
5'-most EST	uC-zmflb73224e11b1
Method	BLASTX
NCBI GI	g1001528
BLAST score	1204

E value	1.0e-133
Match length	229
% identity	100
NCBI Description	(D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	281454
Contig ID	115489_1.R1011
5'-most EST	uC-zmflb73224f02b1

Seq. No.	281455
Contig ID	115491_1.R1011
5'-most EST	uC-zmflb73224f03b1
Method	BLASTX
NCBI GI	g1653478
BLAST score	1242
E value	1.0e-137
Match length	243
% identity	99
NCBI Description	(D90914) eukariotic protein kinase [Synechocystis sp.]

Seq. No.	281456
Contig ID	115492_1.R1011
5'-most EST	uC-zmflb73224f03b2

Seq. No.	281457
Contig ID	115493_1.R1011
5'-most EST	uC-zmflb73224f04b1
Method	BLASTX
NCBI GI	g497626
BLAST score	632
E value	1.0e-65
Match length	324
% identity	46
NCBI Description	(D13972) ORF 1 [Synechococcus PCC7002]

Seq. No.	281458
Contig ID	115495_1.R1011
5'-most EST	uC-zmflb73224g04b1
Method	BLASTX
NCBI GI	g443772
BLAST score	226
E value	4.0e-18
Match length	157
% identity	36
NCBI Description	(D17448) ORF1 [Microcystis aeruginosa]

Seq. No.	281459
Contig ID	115497_1.R1011
5'-most EST	uC-zmflb73224f07b1
Method	BLASTX
NCBI GI	g1652740
BLAST score	763
E value	3.0e-81
Match length	152
% identity	97
NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]

Seq. No.	281460
Contig ID	115498_1.R1011
5'-most EST	yyf700350611.h1

Seq. No.	281461
Contig ID	115505_1.R1011
5'-most EST	uC-zmflb73224g01b1
Method	BLASTX
NCBI GI	g1652463
BLAST score	775
E value	7.0e-83
Match length	158
% identity	97
NCBI Description	(D90905) serine protease HtrA [Synechocystis sp.]

Seq. No.	281462
Contig ID	115506_1.R1011
5'-most EST	uC-zmflb73224g01b2
Method	BLASTX
NCBI GI	g2979551
BLAST score	483
E value	2.0e-48
Match length	208
% identity	50
NCBI Description	(AC003680) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	281463
Contig ID	115518_1.R1011
5'-most EST	uC-zmflb73224g07b2
Method	BLASTX
NCBI GI	g3540208
BLAST score	236
E value	4.0e-35
Match length	161
% identity	48
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	281464
Contig ID	115525_1.R1011
5'-most EST	uC-zmflb73224g12b1
Method	BLASTX
NCBI GI	g1652798
BLAST score	768
E value	7.0e-85
Match length	222
% identity	83
NCBI Description	(D90908) GcpE [Synechocystis sp.]

Seq. No.	281465
Contig ID	115531_1.R1011
5'-most EST	uC-zmflb73224h03b1
Method	BLASTX
NCBI GI	g1001193
BLAST score	451
E value	1.0e-44
Match length	170

% identity	78
NCBI Description	(D64001) phosphate transport ATP-binding protein PstB [Synechocystis sp.]
Seq. No.	281466
Contig ID	115538_1.R1011
5'-most EST	uC-zmflb73224h07b1
Method	BLASTN
NCBI GI	g1652956
BLAST score	548
E value	0.0e+00
Match length	595
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592
Seq. No.	281467
Contig ID	115545_1.R1011
5'-most EST	uC-zmflmo17252d10a1
Method	BLASTX
NCBI GI	g1653821
BLAST score	798
E value	1.0e-174
Match length	356
% identity	93
NCBI Description	(D90916) hypothetical protein [Synechocystis sp.]
Seq. No.	281468
Contig ID	115557_1.R1011
5'-most EST	uC-zmflb73225a11b1
Seq. No.	281469
Contig ID	115564_1.R1011
5'-most EST	uC-zmflb73225b08b1
Seq. No.	281470
Contig ID	115565_1.R1011
5'-most EST	uC-zmflmo17e03b1
Seq. No.	281471
Contig ID	115574_1.R1011
5'-most EST	pmx700089741.h1
Seq. No.	281472
Contig ID	115577_1.R1011
5'-most EST	uwc700155030.h1
Method	BLASTX
NCBI GI	g3335363
BLAST score	335
E value	1.0e-30
Match length	273
% identity	16
NCBI Description	(AC003028) hypothetical protein [Arabidopsis thaliana]
Seq. No.	281473
Contig ID	115578_1.R1011
5'-most EST	xyt700345604.h1

Method	BLASTX
NCBI GI	g2353181
BLAST score	201
E value	2.0e-15
Match length	156
% identity	33
NCBI Description	(AF015565) VacA [Dictyostelium discoideum]

Seq. No.	281474
Contig ID	115580_1.R1011
5'-most EST	uC-zmflb73225d03b1
Method	BLASTX
NCBI GI	g3372677
BLAST score	160
E value	1.0e-10
Match length	53
% identity	57
NCBI Description	(AF061749) tumorous imaginal discs protein Tid56 homolog [Homo sapiens]

Seq. No.	281475
Contig ID	115582_1.R1011
5'-most EST	uC-zmflb73225d05b1

Seq. No.	281476
Contig ID	115584_1.R1011
5'-most EST	wty700171733.h1
Method	BLASTX
NCBI GI	g2737882
BLAST score	200
E value	2.0e-15
Match length	129
% identity	44
NCBI Description	(U46014) polyphenol oxidase [Saccharum sp.]

Seq. No.	281477
Contig ID	115596_1.R1011
5'-most EST	uC-zmflb73242a06b2

Seq. No.	281478
Contig ID	115602_1.R1011
5'-most EST	uC-zmflmo17270h02b1

Seq. No.	281479
Contig ID	115604_1.R1011
5'-most EST	uC-zmflb73225f06b1
Method	BLASTX
NCBI GI	g4455192
BLAST score	493
E value	8.0e-50
Match length	143
% identity	65
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	281480
Contig ID	115626_1.R1011
5'-most EST	uC-zmflb73225h09b1

Method	BLASTX
NCBI GI	g1841391
BLAST score	188
E value	5.0e-14
Match length	86
% identity	55
NCBI Description	(D64039) EL3 [Oryza sativa]

Seq. No.	281481
Contig ID	115626_2.R1011
5'-most EST	wyr700238959.h1

Seq. No.	281482
Contig ID	115626_3.R1011
5'-most EST	xsy700213529.h1

Seq. No.	281483
Contig ID	115630_1.R1011
5'-most EST	pmx700082656.h1

Seq. No.	281484
Contig ID	115636_1.R1011
5'-most EST	uC-zmflb73226a07b1

Seq. No.	281485
Contig ID	115656_1.R1011
5'-most EST	uC-zmflb73226c06b1

Seq. No.	281486
Contig ID	115672_1.R1011
5'-most EST	uC-zmflb73226d12b1

Seq. No.	281487
Contig ID	115683_1.R1011
5'-most EST	uC-zmflb73226f02b1

Seq. No.	281488
Contig ID	115686_1.R1011
5'-most EST	uC-zmflmo17306b11b1

Seq. No.	281489
Contig ID	115692_1.R1011
5'-most EST	gwl700614948.h1

Seq. No.	281490
Contig ID	115704_1.R1011
5'-most EST	uC-zmflb73226h02b1
Method	BLASTX
NCBI GI	g3372671
BLAST score	778
E value	4.0e-83
Match length	199
% identity	75
NCBI Description	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No.	281491
Contig ID	115739_2.R1011

5'-most EST	uC-zmroteosinte090g06b2
Method	BLASTX
NCBI GI	g2809385
BLAST score	777
E value	2.0e-89
Match length	226
% identity	76
NCBI Description	(AF024634) NADPH cytochrome P450 reductase [Petroselinum crispum]

Seq. No.	281492
Contig ID	115742_1.R1011
5'-most EST	ymt700224343.h1
Method	BLASTX
NCBI GI	g4586245
BLAST score	552
E value	2.0e-56
Match length	262
% identity	45
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	281493
Contig ID	115747_1.R1011
5'-most EST	qmh700026857.f1

Seq. No.	281494
Contig ID	115750_1.R1011
5'-most EST	uC-zmroteosinte033f12b1
Method	BLASTX
NCBI GI	g3482977
BLAST score	773
E value	5.0e-82
Match length	475
% identity	41
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	281495
Contig ID	115752_1.R1011
5'-most EST	nbm700468448.h1
Method	BLASTX
NCBI GI	g4538965
BLAST score	464
E value	5.0e-46
Match length	225
% identity	41
NCBI Description	(AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281496
Contig ID	115775_1.R1011
5'-most EST	xsy700213387.h1

Seq. No.	281497
Contig ID	115782_1.R1011
5'-most EST	clt700043908.f1
Method	BLASTX
NCBI GI	g4544473
BLAST score	494

E value	5.0e-50
Match length	125
% identity	76
NCBI Description	(AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	281498
Contig ID	115823_1.R1011
5'-most EST	uC-zmflb73233d02b1

Seq. No.	281499
Contig ID	115850_1.R1011
5'-most EST	nbm700473850.h1
Method	BLASTX
NCBI GI	g3687224
BLAST score	201
E value	9.0e-16
Match length	71
% identity	66
NCBI Description	(AC005169) putative N-acetyl-gamma-glutamyl-phosphate reductase [Arabidopsis thaliana]

Seq. No.	281500
Contig ID	115872_1.R1011
5'-most EST	uC-zmflb73236a06b1

Seq. No.	281501
Contig ID	115874_1.R1011
5'-most EST	cyk700050127.f1

Seq. No.	281502
Contig ID	115879_1.R1011
5'-most EST	uC-zmflb73236b02b1
Method	BLASTX
NCBI GI	g3337350
BLAST score	322
E value	1.0e-29
Match length	71
% identity	77
NCBI Description	(AC004481) putative permease [Arabidopsis thaliana]

Seq. No.	281503
Contig ID	115885_1.R1011
5'-most EST	uC-zmflb73236b08b1

Seq. No.	281504
Contig ID	115910_1.R1011
5'-most EST	uC-zmflb73236f06b1

Seq. No.	281505
Contig ID	115913_1.R1011
5'-most EST	uC-zmflb73236f10b1

Seq. No.	281506
Contig ID	115915_1.R1011
5'-most EST	hbs701185568.h1
Method	BLASTX
NCBI GI	g3913218

BLAST score	536
E value	2.0e-70
Match length	204
% identity	75
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi_2318117 (AF014399) Mg-chelatase subunit D [Pisum sativum]

Seq. No.	281507
Contig ID	115924_1.R1011
5'-most EST	nbm700468723.h1
Method	BLASTX
NCBI GI	g3402699
BLAST score	324
E value	6.0e-30
Match length	94
% identity	61
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	281508
Contig ID	115938_1.R1011
5'-most EST	uC-zmflb73253a02b1

Seq. No.	281509
Contig ID	115940_1.R1011
5'-most EST	uC-zmflMo17009g10b1
Method	BLASTX
NCBI GI	g4115925
BLAST score	501
E value	2.0e-50
Match length	151
% identity	63
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	281510
Contig ID	115941_1.R1011
5'-most EST	uC-zmflb73253a06b1

Seq. No.	281511
Contig ID	115961_1.R1011
5'-most EST	rvt700549447.h1

Seq. No.	281512
Contig ID	115969_1.R1011
5'-most EST	uC-zmflb73253d03b1
Method	BLASTX
NCBI GI	g2829904
BLAST score	217
E value	3.0e-17
Match length	78
% identity	63
NCBI Description	(AC002311) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	281513
Contig ID	115970_1.R1011
5'-most EST	ymt700220913.h1

Seq. No.	281514
Contig ID	115978_1.R1011
5'-most EST	uC-zmflb73253e10b1
Method	BLASTX
NCBI GI	g3402679
BLAST score	452
E value	5.0e-45
Match length	158
% identity	54
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	281515
Contig ID	115979_1.R1011
5'-most EST	uC-zmflb73253e12b1

Seq. No.	281516
Contig ID	116001_1.R1011
5'-most EST	uC-zmflmo17245g05b1

Seq. No.	281517
Contig ID	116035_1.R1011
5'-most EST	uC-zmflb73256c12b1
Method	BLASTX
NCBI GI	g3892714
BLAST score	435
E value	7.0e-43
Match length	145
% identity	61
NCBI Description	(AL033545) trehalose-6-phosphate phosphatase - like protein [Arabidopsis thaliana]

Seq. No.	281518
Contig ID	116037_1.R1011
5'-most EST	uC-zmflb73318h05b1
Method	BLASTX
NCBI GI	g2642163
BLAST score	462
E value	8.0e-46
Match length	238
% identity	43
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281519
Contig ID	116052_1.R1011
5'-most EST	uC-zmflb73256e12b1
Method	BLASTX
NCBI GI	g4218121
BLAST score	320
E value	4.0e-29
Match length	143
% identity	45
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	281520
Contig ID	116052_3.R1011
5'-most EST	ypc700800360.h1

Seq. No.	281521
Contig ID	116067_1.R1011
5'-most EST	uC-zmf1b73256g07b1

Seq. No.	281522
Contig ID	116076_1.R1011
5'-most EST	uC-zmflmo17246b11b1

Seq. No.	281523
Contig ID	116077_1.R1011
5'-most EST	uC-zmf1b73256h07b1
Method	BLASTX
NCBI GI	g478809
BLAST score	372
E value	2.0e-35
Match length	178
% identity	44
NCBI Description	protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449) protein kinase [Glycine max] >gi_444789_prf__1908223A protein kinase [Glycine max]

Seq. No.	281524
Contig ID	116077_2.R1011
5'-most EST	ypc700799285.h1

Seq. No.	281525
Contig ID	116078_1.R1011
5'-most EST	uC-zmf1b73220a11b2

Seq. No.	281526
Contig ID	116086_1.R1011
5'-most EST	uC-zmflmo17037h10a1

Seq. No.	281527
Contig ID	116100_1.R1011
5'-most EST	uC-zmf1b73263b10b1
Method	BLASTX
NCBI GI	g464872
BLAST score	180
E value	1.0e-12
Match length	127
% identity	33
NCBI Description	TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA) >gi_345618_pir__JC1442 transcription factor IIIA - American toad >gi_429029_emb_CAA41259_ (X58366) transcription factor IIIA [Bufo americanus]

Seq. No.	281528
Contig ID	116113_1.R1011
5'-most EST	fC-zmle700443661a5

Seq. No.	281529
Contig ID	116116_1.R1011

5'-most EST	uC-zmflb73263d07b1
Seq. No.	281530
Contig ID	116121_1.R1011
5'-most EST	uC-zmroB73020a08b1
Method	BLASTX
NCBI GI	g2746335
BLAST score	167
E value	2.0e-11
Match length	74
% identity	42
NCBI Description	(AF037205) RING zinc finger protein [Mus musculus]
Seq. No.	281531
Contig ID	116121_2.R1011
5'-most EST	uC-zmflb73014d12a1
Method	BLASTN
NCBI GI	g949979
BLAST score	40
E value	6.0e-13
Match length	59
% identity	92
NCBI Description	Z.mays Glossy2 locus DNA
Seq. No.	281532
Contig ID	116139_1.R1011
5'-most EST	uC-zmflb73346d10a2
Seq. No.	281533
Contig ID	116156_1.R1011
5'-most EST	uC-zmflb73263h09b1
Method	BLASTX
NCBI GI	g3983663
BLAST score	653
E value	3.0e-68
Match length	159
% identity	86
NCBI Description	(AB011270) importin-beta1 [Oryza sativa]
Seq. No.	281534
Contig ID	116157_1.R1011
5'-most EST	rvt700553227.h1
Method	BLASTX
NCBI GI	g3152613
BLAST score	142
E value	4.0e-10
Match length	142
% identity	41
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]
Seq. No.	281535
Contig ID	116173_1.R1011
5'-most EST	uC-zmflb73304a12b1
Seq. No.	281536
Contig ID	116181_1.R1011
5'-most EST	uC-zmflb73264c07b1

Seq. No.	281537
Contig ID	116196_1.R1011
5'-most EST	uC-zmflmo17223f11b1
Method	BLASTN
NCBI GI	g3511235
BLAST score	51
E value	2.0e-19
Match length	63
% identity	95
NCBI Description	Zea mays starch branching enzyme IIb (ae) gene, complete cds

Seq. No.	281538
Contig ID	116217_1.R1011
5'-most EST	uC-zmflmo17168h12b1

Seq. No.	281539
Contig ID	116226_1.R1011
5'-most EST	uC-zmflb73264h01b1
Method	BLASTX
NCBI GI	g4417291
BLAST score	195
E value	8.0e-15
Match length	157
% identity	34
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281540
Contig ID	116231_1.R1011
5'-most EST	uC-zmflb73264h08b1

Seq. No.	281541
Contig ID	116238_1.R1011
5'-most EST	uC-zmflb73270a04b1
Method	BLASTN
NCBI GI	g507770
BLAST score	35
E value	5.0e-10
Match length	83
% identity	86
NCBI Description	Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete cds

Seq. No.	281542
Contig ID	116240_1.R1011
5'-most EST	uC-zmflb73270a06b1
Method	BLASTX
NCBI GI	g3176659
BLAST score	201
E value	2.0e-15
Match length	135
% identity	39
NCBI Description	(AC004393) Strong similarity to receptor kinase gb_M80238 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	281543

Contig ID	116257_1.R1011
5'-most EST	uC-zmflb73270b12b1
Seq. No.	281544
Contig ID	116259_1.R1011
5'-most EST	uC-zmflb73270c02b1
Seq. No.	281545
Contig ID	116278_1.R1011
5'-most EST	ymt700220810.h1
Method	BLASTX
NCBI GI	g3695063
BLAST score	507
E value	2.0e-51
Match length	125
% identity	80
NCBI Description	(AF064789) rac GTPase activating protein 3 [Lotus japonicus]
Seq. No.	281546
Contig ID	116279_1.R1011
5'-most EST	uC-zmroteosinte118f08b1
Seq. No.	281547
Contig ID	116293_1.R1011
5'-most EST	nbm700468256.h1
Seq. No.	281548
Contig ID	116318_1.R1011
5'-most EST	uC-zmflb73266a11a2
Method	BLASTX
NCBI GI	g4006886
BLAST score	206
E value	3.0e-16
Match length	51
% identity	75
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	281549
Contig ID	116323_1.R1011
5'-most EST	uC-zmflb73272b11b1
Seq. No.	281550
Contig ID	116334_1.R1011
5'-most EST	uC-zmflb73272c12b1
Seq. No.	281551
Contig ID	116340_1.R1011
5'-most EST	uC-zmroteosinte010b10b1
Method	BLASTX
NCBI GI	g4539335
BLAST score	669
E value	2.0e-70
Match length	189
% identity	63
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	281552
Contig ID	116341_1.R1011
5'-most EST	uC-zmflb73272d08b1
Method	BLASTX
NCBI GI	g3810592
BLAST score	252
E value	2.0e-21
Match length	192
% identity	33
NCBI Description	(AC005398) unknown protein [Arabidopsis thaliana]

Seq. No.	281553
Contig ID	116343_1.R1011
5'-most EST	uC-zmflb73272d11b1
Method	BLASTX
NCBI GI	g4455188
BLAST score	254
E value	2.0e-21
Match length	211
% identity	29
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	281554
Contig ID	116369_1.R1011
5'-most EST	ntr700072757.h1

Seq. No.	281555
Contig ID	116375_1.R1011
5'-most EST	wyr700237301.h1
Method	BLASTX
NCBI GI	g3695392
BLAST score	418
E value	1.0e-40
Match length	193
% identity	44
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	281556
Contig ID	116384_1.R1011
5'-most EST	wty700166647.h1

Seq. No.	281557
Contig ID	116386_1.R1011
5'-most EST	vux700162436.h1

Seq. No.	281558
Contig ID	116391_1.R1011
5'-most EST	uC-zmflb73274a09b1
Method	BLASTX
NCBI GI	g1170408
BLAST score	261
E value	2.0e-22
Match length	56
% identity	86
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT14 (HD-ZIP PROTEIN 14) >gi_549885 (U09334) homeobox protein [Arabidopsis thaliana]

Seq. No.	281559
Contig ID	116401_1.R1011
5'-most EST	nbm700472694.h1
Method	BLASTX
NCBI GI	g2462762
BLAST score	525
E value	2.0e-53
Match length	170
% identity	62
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	281560
Contig ID	116411_1.R1011
5'-most EST	nbm700475313.h1

Seq. No.	281561
Contig ID	116424_1.R1011
5'-most EST	ceu700426031.h1
Method	BLASTX
NCBI GI	g3540194
BLAST score	587
E value	1.0e-60
Match length	136
% identity	82
NCBI Description	(AC004260) AtVPS45p [Arabidopsis thaliana]

Seq. No.	281562
Contig ID	116426_1.R1011
5'-most EST	uC-zmflmo17055a10b1
Method	BLASTX
NCBI GI	g3281861
BLAST score	837
E value	1.0e-89
Match length	244
% identity	67
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	281563
Contig ID	116442_1.R1011
5'-most EST	uC-zmflb73274f12b1

Seq. No.	281564
Contig ID	116443_1.R1011
5'-most EST	nbm700464961.h1
Method	BLASTX
NCBI GI	g3386604
BLAST score	254
E value	1.0e-21
Match length	200
% identity	30
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	281565
Contig ID	116449_1.R1011
5'-most EST	uC-zmflb73274h09b1

Seq. No.	281566
Contig ID	116464_1.R1011
5'-most EST	wyr700241275.h1
Method	BLASTX
NCBI GI	g3819697
BLAST score	234
E value	2.0e-19
Match length	179
% identity	37
NCBI Description	(AJ009608) BnMAP4K alpha1 [Brassica napus]

Seq. No.	281567
Contig ID	116480_1.R1011
5'-most EST	uC-zmflb73275b12b1

Seq. No.	281568
Contig ID	116484_1.R1011
5'-most EST	uC-zmflb73275d03b1
Method	BLASTX
NCBI GI	g4585993
BLAST score	645
E value	1.0e-67
Match length	146
% identity	81
NCBI Description	(AC005287) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	281569
Contig ID	116501_1.R1011
5'-most EST	uC-zmflb73275d12b1

Seq. No.	281570
Contig ID	116503_1.R1011
5'-most EST	uC-zmflb73275e02b1

Seq. No.	281571
Contig ID	116511_1.R1011
5'-most EST	uC-zmrob73075c02b1
Method	BLASTX
NCBI GI	g3688173
BLAST score	857
E value	3.0e-92
Match length	276
% identity	58
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	281572
Contig ID	116513_1.R1011
5'-most EST	uC-zmflb73275f05b1
Method	BLASTX
NCBI GI	g3688173
BLAST score	583
E value	3.0e-60
Match length	175
% identity	63
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	281573
Contig ID	116515_1.R1011
5'-most EST	uC-zmflb73275f08b1
Method	BLASTX
NCBI GI	g738309
BLAST score	154
E value	3.0e-10
Match length	87
% identity	41
NCBI Description	nucler protein GRB1 [Homo sapiens]

Seq. No.	281574
Contig ID	116535_1.R1011
5'-most EST	uC-zmflb73275h07b1
Method	BLASTX
NCBI GI	g2642158
BLAST score	372
E value	1.0e-35
Match length	92
% identity	70
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281575
Contig ID	116537_1.R1011
5'-most EST	uC-zmflb73275h09b1
Method	BLASTX
NCBI GI	g4512705
BLAST score	303
E value	4.0e-54
Match length	146
% identity	76
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	281576
Contig ID	116561_1.R1011
5'-most EST	qmh700028546.f1
Method	BLASTX
NCBI GI	g1628482
BLAST score	213
E value	7.0e-17
Match length	180
% identity	8
NCBI Description	(X97570) embryogenesis transmembrane protein [Zea mays]

Seq. No.	281577
Contig ID	116567_1.R1011
5'-most EST	xmt700260992.h1

Seq. No.	281578
Contig ID	116568_1.R1011
5'-most EST	uC-zmflb73276c08b1
Method	BLASTX
NCBI GI	g2924515
BLAST score	258
E value	2.0e-22
Match length	100

% identity	52
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	281579
Contig ID	116580_1.R1011
5'-most EST	pwr700449439.h1
Method	BLASTX
NCBI GI	g4263722
BLAST score	832
E value	4.0e-89
Match length	254
% identity	62
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	281580
Contig ID	116586_1.R1011
5'-most EST	uC-zmflb73276e05b1

Seq. No.	281581
Contig ID	116596_1.R1011
5'-most EST	uC-zmflb73276f05b1
Method	BLASTX
NCBI GI	g1707642
BLAST score	264
E value	4.0e-24
Match length	135
% identity	47
NCBI Description	(Y07748) TMK [Oryza sativa]

Seq. No.	281582
Contig ID	116601_1.R1011
5'-most EST	xmt700264636.h1

Seq. No.	281583
Contig ID	116613_1.R1011
5'-most EST	wty700171887.h1
Method	BLASTX
NCBI GI	g4567304
BLAST score	640
E value	7.0e-67
Match length	218
% identity	57
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	281584
Contig ID	116613_2.R1011
5'-most EST	uC-zmflb73135f04b2
Method	BLASTX
NCBI GI	g4567304
BLAST score	171
E value	4.0e-12
Match length	70
% identity	59
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	281585
Contig ID	116642_1.R1011

5'-most EST	wyr700240246.h1
Seq. No.	281586
Contig ID	116665_1.R1011
5'-most EST	tfd700570164.h1
Method	BLASTX
NCBI GI	g600855
BLAST score	291
E value	7.0e-26
Match length	248
% identity	29
NCBI Description	(U17887) bZIP protein [Arabidopsis thaliana]
Seq. No.	281587
Contig ID	116672_1.R1011
5'-most EST	uC-zmflmo17315e02a1
Method	BLASTX
NCBI GI	g3242783
BLAST score	166
E value	2.0e-11
Match length	48
% identity	62
NCBI Description	(AF055354) respiratory burst oxidase protein B [Arabidopsis thaliana]
Seq. No.	281588
Contig ID	116676_1.R1011
5'-most EST	fC-zmfl700352054y1
Method	BLASTX
NCBI GI	g4512714
BLAST score	197
E value	1.0e-14
Match length	46
% identity	80
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.	281589
Contig ID	116678_1.R1011
5'-most EST	uC-zmflb73278f07b1
Method	BLASTX
NCBI GI	g2494842
BLAST score	301
E value	4.0e-27
Match length	123
% identity	49
NCBI Description	GLUCOSYLTRANSFERASE ALG6 >gi_2131171_pir__S61985 ALG6 protein - yeast (Saccharomyces cerevisiae) >gi_1150997 (U43491) hypothetical protein UNA544 [Saccharomyces cerevisiae] >gi_1420090_emb_CAA99190_ (Z74910) ORF YOR002w [Saccharomyces cerevisiae]
Seq. No.	281590
Contig ID	116685_1.R1011
5'-most EST	rvt700553088.h1
Seq. No.	281591
Contig ID	116711_1.R1011

5'-most EST	uC-zmflb73279a11b1
Seq. No.	281592
Contig ID	116713_1.R1011
5'-most EST	fC-zmle700429503a4
Seq. No.	281593
Contig ID	116726_1.R1011
5'-most EST	uC-zmflb73279c04b1
Method	BLASTX
NCBI GI	g4586246
BLAST score	228
E value	8.0e-19
Match length	58
% identity	64
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]
Seq. No.	281594
Contig ID	116736_1.R1011
5'-most EST	uC-zmroteosinte031h07b1
Seq. No.	281595
Contig ID	116756_1.R1011
5'-most EST	uC-zmroteosinte074d06b1
Seq. No.	281596
Contig ID	116760_1.R1011
5'-most EST	uC-zmflb73279g06b1
Method	BLASTX
NCBI GI	g4580389
BLAST score	339
E value	1.0e-31
Match length	93
% identity	69
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.	281597
Contig ID	116765_1.R1011
5'-most EST	uC-zmflb73279g11b1
Method	BLASTX
NCBI GI	g2388583
BLAST score	515
E value	3.0e-52
Match length	165
% identity	65
NCBI Description	(AC000098) Similar to Synechocystis hypothetical protein (gb_D90908). [Arabidopsis thaliana]
Seq. No.	281598
Contig ID	116775_1.R1011
5'-most EST	uC-zmflb73284a03b1
Seq. No.	281599
Contig ID	116781_1.R1011
5'-most EST	uC-zmflb73284b02b1
Method	BLASTX
NCBI GI	g2760324

BLAST score 285
E value 6.0e-29
Match length 151
% identity 46
NCBI Description (AC002130) F1N21.9 [Arabidopsis thaliana]

Seq. No. 281600
Contig ID 116785_1.R1011
5'-most EST nbm700470365.h1

Seq. No. 281601
Contig ID 116802_1.R1011
5'-most EST wyr700240807.h1

Seq. No. 281602
Contig ID 116816_1.R1011
5'-most EST xyt700343969.h1

Seq. No. 281603
Contig ID 116819_1.R1011
5'-most EST uC-zmflb73284g05b1
Method BLASTX
NCBI GI g3953466
BLAST score 324
E value 8.0e-30
Match length 120
% identity 53
NCBI Description (AC002328) F20N2.11 [Arabidopsis thaliana]

Seq. No. 281604
Contig ID 116868_1.R1011
5'-most EST wyr700236927.h1

Seq. No. 281605
Contig ID 116873_1.R1011
5'-most EST xsy700210788.h1
Method BLASTX
NCBI GI g4490341
BLAST score 265
E value 6.0e-23
Match length 106
% identity 46
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 281606
Contig ID 116892_1.R1011
5'-most EST uC-zmflb73285h11b1

Seq. No. 281607
Contig ID 116898_1.R1011
5'-most EST wty700167627.h1

Seq. No. 281608
Contig ID 116918_1.R1011
5'-most EST uC-zmflb73286c12b1
Method BLASTX
NCBI GI g4262239

BLAST score	416
E value	5.0e-41
Match length	94
% identity	87
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	281609
Contig ID	116937_1.R1011
5'-most EST	uC-zmflb73286e12b1
Method	BLASTX
NCBI GI	g3004565
BLAST score	282
E value	8.0e-25
Match length	63
% identity	79
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	281610
Contig ID	116937_2.R1011
5'-most EST	xyt700342743.h1
Method	BLASTX
NCBI GI	g3004565
BLAST score	290
E value	1.0e-25
Match length	66
% identity	77
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	281611
Contig ID	116953_1.R1011
5'-most EST	pmx700083042.h1
Method	BLASTX
NCBI GI	g3128231
BLAST score	329
E value	2.0e-30
Match length	219
% identity	21
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana] >gi_3337370 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281612
Contig ID	116957_1.R1011
5'-most EST	uC-zmflb73286g10b1

Seq. No.	281613
Contig ID	116972_1.R1011
5'-most EST	ntr700071777.h1
Method	BLASTX
NCBI GI	g2245108
BLAST score	585
E value	2.0e-60
Match length	156
% identity	68
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	281614
Contig ID	116979_1.R1011
5'-most EST	xmt700258251.h1
Method	BLASTX
NCBI GI	g3132477
BLAST score	705
E value	1.0e-74
Match length	299
% identity	10
NCBI Description	(AC003096) unknown protein [Arabidopsis thaliana]

Seq. No.	281615
Contig ID	116988_1.R1011
5'-most EST	vux700160426.h1
Method	BLASTN
NCBI GI	g2739216
BLAST score	67
E value	4.0e-29
Match length	87
% identity	94
NCBI Description	Hordeum vulgare L41 ribosomal protein

Seq. No.	281616
Contig ID	116995_1.R1011
5'-most EST	uC-zmflb73291h04b1
Method	BLASTX
NCBI GI	g1773014
BLAST score	369
E value	5.0e-35
Match length	101
% identity	74
NCBI Description	(Y10338) chloride channel Stclc1 [Solanum tuberosum]

Seq. No.	281617
Contig ID	117019_1.R1011
5'-most EST	uC-zmflb73287h03b1
Method	BLASTX
NCBI GI	g3341679
BLAST score	403
E value	3.0e-57
Match length	138
% identity	83
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	281618
Contig ID	117030_1.R1011
5'-most EST	pwr700451259.h1

Seq. No.	281619
Contig ID	117031_1.R1011
5'-most EST	pmx700086960.h1
Method	BLASTX
NCBI GI	g2497539
BLAST score	1158
E value	1.0e-127
Match length	345

% identity	66
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	281620
Contig ID	117051_1.R1011
5'-most EST	xmt700266086.h1

Seq. No.	281621
Contig ID	117051_3.R1011
5'-most EST	ceu700432671.h1

Seq. No.	281622
Contig ID	117063_1.R1011
5'-most EST	pmx700085104.h1
Method	BLASTX
NCBI GI	g4544409
BLAST score	474
E value	4.0e-47
Match length	152
% identity	62
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana] >gi_4585920_gb_AAD25580.1_AC007211_2 (AC007211) putative scarecrow homolog [Arabidopsis thaliana]

Seq. No.	281623
Contig ID	117070_1.R1011
5'-most EST	nwy700446738.h1

Seq. No.	281624
Contig ID	117107_1.R1011
5'-most EST	yd1700405339.h1
Method	BLASTX
NCBI GI	g4544399
BLAST score	243
E value	6.0e-21
Match length	81
% identity	57
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	281625
Contig ID	117121_1.R1011
5'-most EST	xyt700343873.h1

Seq. No.	281626
Contig ID	117124_1.R1011
5'-most EST	uC-zmflb73291b01a1

Seq. No.	281627
Contig ID	117154_1.R1011
5'-most EST	uC-zmflb73291h02b1

Seq. No.	281628
Contig ID	117156_1.R1011
5'-most EST	uC-zmflmo17287d12b1
Method	BLASTX

NCBI GI	g4220527
BLAST score	208
E value	2.0e-16
Match length	162
% identity	32
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	281629
Contig ID	117161_1.R1011
5'-most EST	cyk700050209.f1

Seq. No.	281630
Contig ID	117173_1.R1011
5'-most EST	uC-zmflb73291h08b1
Method	BLASTX
NCBI GI	g3075391
BLAST score	300
E value	5.0e-27
Match length	172
% identity	44
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	281631
Contig ID	117174_1.R1011
5'-most EST	uC-zmflb73291h09b1

Seq. No.	281632
Contig ID	117177_1.R1011
5'-most EST	uC-zmflb73292a03b1
Method	BLASTX
NCBI GI	g3041883
BLAST score	192
E value	4.0e-14
Match length	153
% identity	35
NCBI Description	(AF037256) ES2 protein [Mus musculus]

Seq. No.	281633
Contig ID	117213_1.R1011
5'-most EST	uC-zmflMo17016d07b1
Method	BLASTX
NCBI GI	g4336436
BLAST score	351
E value	4.0e-33
Match length	112
% identity	58
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	281634
Contig ID	117213_2.R1011
5'-most EST	ypc700801224.h1

Seq. No.	281635
Contig ID	117218_1.R1011
5'-most EST	nbm700471103.h1
Method	BLASTX
NCBI GI	g4467147

BLAST score	478
E value	4.0e-48
Match length	131
% identity	68
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	281636
Contig ID	117219_1.R1011
5'-most EST	uC-zmroteosinte040h01b1

Seq. No.	281637
Contig ID	117224_1.R1011
5'-most EST	xyt700346514.h1
Method	BLASTX
NCBI GI	g3695061
BLAST score	876
E value	2.0e-94
Match length	287
% identity	62
NCBI Description	(AF064788) rac GTPase activating protein 2 [Lotus japonicus]

Seq. No.	281638
Contig ID	117243_1.R1011
5'-most EST	xjt700095314.h1
Method	BLASTX
NCBI GI	g3080448
BLAST score	617
E value	4.0e-64
Match length	229
% identity	55
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	281639
Contig ID	117257_1.R1011
5'-most EST	uC-zmflb73294e03b1

Seq. No.	281640
Contig ID	117263_1.R1011
5'-most EST	cyk700051777.f1
Method	BLASTX
NCBI GI	g2760839
BLAST score	234
E value	3.0e-19
Match length	100
% identity	47
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	281641
Contig ID	117264_1.R1011
5'-most EST	uC-zmflmo17100a07b1
Method	BLASTX
NCBI GI	g2392895
BLAST score	936
E value	1.0e-101
Match length	251
% identity	71

NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	281642
Contig ID	117271_1.R1011
5'-most EST	uC-zmflb73106b11a1

Seq. No.	281643
Contig ID	117281_1.R1011
5'-most EST	ceu700431194.h1
Method	BLASTX
NCBI GI	g4049353
BLAST score	553
E value	8.0e-57
Match length	140
% identity	71
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	281644
Contig ID	117300_1.R1011
5'-most EST	uC-zmflb73298b11b1
Method	BLASTX
NCBI GI	g4249388
BLAST score	344
E value	2.0e-32
Match length	108
% identity	59
NCBI Description	(AC005966) Similar to gb_AF025438 Opa-interacting protein (OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	281645
Contig ID	117302_1.R1011
5'-most EST	uC-zmflb73298f07b1

Seq. No.	281646
Contig ID	117308_1.R1011
5'-most EST	uC-zmflb73298c12b1

Seq. No.	281647
Contig ID	117321_1.R1011
5'-most EST	pmx700084070.h1

Seq. No.	281648
Contig ID	117331_1.R1011
5'-most EST	uC-zmflb73298f02b1

Seq. No.	281649
Contig ID	117358_1.R1011
5'-most EST	uC-zmflb73298h10b1
Method	BLASTX
NCBI GI	g2160144
BLAST score	148
E value	2.0e-09
Match length	47
% identity	53
NCBI Description	(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No.	281650
Contig ID	117366_1.R1011
5'-most EST	uC-zmflb73299a08b1
Method	BLASTX
NCBI GI	g868266
BLAST score	180
E value	3.0e-13
Match length	85
% identity	52
NCBI Description	(U29536) F45E12.1 gene product [Caenorhabditis elegans]

Seq. No.	281651
Contig ID	117375_1.R1011
5'-most EST	uC-zmflb73299b08b1
Method	BLASTX
NCBI GI	g2832618
BLAST score	480
E value	6.0e-48
Match length	249
% identity	27
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	281652
Contig ID	117415_1.R1011
5'-most EST	uC-zmflMo17093d08b1

Seq. No.	281653
Contig ID	117433_1.R1011
5'-most EST	uC-zmflb73300a11b1
Method	BLASTX
NCBI GI	g3355480
BLAST score	262
E value	2.0e-34
Match length	220
% identity	38
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	281654
Contig ID	117437_1.R1011
5'-most EST	uC-zmflb73300b03b1

Seq. No.	281655
Contig ID	117441_1.R1011
5'-most EST	uC-zmflb73300b07b1

Seq. No.	281656
Contig ID	117487_1.R1011
5'-most EST	uC-zmflb73300f10b1

Seq. No.	281657
Contig ID	117491_1.R1011
5'-most EST	cat700020125.r1
Method	BLASTX
NCBI GI	g4204313
BLAST score	304

E value	2.0e-27
Match length	81
% identity	73
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	281658
Contig ID	117510_1.R1011
5'-most EST	uC-zmflb73303a10b1

Seq. No.	281659
Contig ID	117520_1.R1011
5'-most EST	uC-zmflb73303c01b1

Seq. No.	281660
Contig ID	117524_1.R1011
5'-most EST	uC-zmflmo17097f07b1
Method	BLASTX
NCBI GI	g2760844
BLAST score	445
E value	5.0e-44
Match length	179
% identity	53
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281661
Contig ID	117525_1.R1011
5'-most EST	uC-zmflb73303d04b1
Method	BLASTN
NCBI GI	g405634
BLAST score	66
E value	1.0e-28
Match length	202
% identity	83
NCBI Description	Z.mays zmcpt mRNA triose phosphate/phosphate translocator

Seq. No.	281662
Contig ID	117526_1.R1011
5'-most EST	uC-zmflmo17158b10b1

Seq. No.	281663
Contig ID	117530_1.R1011
5'-most EST	uC-zmflmo17153g05b1
Method	BLASTX
NCBI GI	g2921323
BLAST score	1010
E value	1.0e-110
Match length	244
% identity	76
NCBI Description	(AF034112) beta-1,3-glucanase 7 [Glycine max]

Seq. No.	281664
Contig ID	117535_1.R1011
5'-most EST	pmx700081872.h1

Seq. No.	281665
Contig ID	117538_1.R1011

5'-most EST	uC-zmflb73356f10a2
Method	BLASTX
NCBI GI	g434759
BLAST score	437
E value	5.0e-43
Match length	202
% identity	66
NCBI Description	(D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]

Seq. No.	281666
Contig ID	117545_1.R1011
5'-most EST	gct701178304.h1

Seq. No.	281667
Contig ID	117547_1.R1011
5'-most EST	uC-zmflb73303f10b1
Method	BLASTX
NCBI GI	g4008551
BLAST score	258
E value	3.0e-22
Match length	128
% identity	41
NCBI Description	(AL034490) pseudouridylate synthase [Schizosaccharomyces pombe]

Seq. No.	281668
Contig ID	117552_1.R1011
5'-most EST	yyf700348457.h1

Seq. No.	281669
Contig ID	117559_1.R1011
5'-most EST	wyr700237778.h1

Seq. No.	281670
Contig ID	117582_1.R1011
5'-most EST	uC-zmflb73165a05b2
Method	BLASTX
NCBI GI	g3335359
BLAST score	761
E value	5.0e-81
Match length	217
% identity	68
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	281671
Contig ID	117593_1.R1011
5'-most EST	zuv700356153.h1

Seq. No.	281672
Contig ID	117612_1.R1011
5'-most EST	fwa700098037.h1

Seq. No.	281673
Contig ID	117625_1.R1011
5'-most EST	uC-zmflb73317c08b1
Method	BLASTX

09054506.1400

NCBI GI	g1491638
BLAST score	267
E value	2.0e-36
Match length	175
% identity	47
NCBI Description	(X99922) male sterility protein 2 [Brassica napus]

Seq. No.	281674
Contig ID	117640_1.R1011
5'-most EST	uC-zmflb73317e04b1
Method	BLASTX
NCBI GI	g2829865
BLAST score	177
E value	1.0e-15
Match length	75
% identity	63
NCBI Description	(AC002396) N-terminal region similar to DNA-J proteins [Arabidopsis thaliana]

Seq. No.	281675
Contig ID	117654_1.R1011
5'-most EST	uC-zmflb73317f08b1

Seq. No.	281676
Contig ID	117662_1.R1011
5'-most EST	ypc700800901.h1
Method	BLASTX
NCBI GI	g3885334
BLAST score	285
E value	3.0e-25
Match length	96
% identity	55
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	281677
Contig ID	117664_1.R1011
5'-most EST	uC-zmflb73317g10b1

Seq. No.	281678
Contig ID	117670_1.R1011
5'-most EST	zuv700356108.h1

Seq. No.	281679
Contig ID	117678_1.R1011
5'-most EST	uC-zmflb73224a09a1

Seq. No.	281680
Contig ID	117682_1.R1011
5'-most EST	uC-zmflmo17042f06b1

Seq. No.	281681
Contig ID	117689_1.R1011
5'-most EST	uC-zmflb73318b12b1
Method	BLASTX
NCBI GI	g404690
BLAST score	455

E value	3.0e-45
Match length	181
% identity	49
NCBI Description	(L19075) cytochrome P450 [Catharanthus roseus]

Seq. No.	281682
Contig ID	117696_1.R1011
5'-most EST	uC-zmflb73318c11b1
Method	BLASTX
NCBI GI	g2244971
BLAST score	440
E value	1.0e-43
Match length	168
% identity	58
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281683
Contig ID	117710_1.R1011
5'-most EST	uC-zmflb73318e08b1
Method	BLASTX
NCBI GI	g3450842
BLAST score	217
E value	2.0e-17
Match length	68
% identity	59
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	281684
Contig ID	117727_1.R1011
5'-most EST	uC-zmflmo17055a09b1
Method	BLASTX
NCBI GI	g2271477
BLAST score	772
E value	3.0e-82
Match length	158
% identity	94
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	281685
Contig ID	117740_1.R1011
5'-most EST	uC-zmflb73319a11b1

Seq. No.	281686
Contig ID	117776_1.R1011
5'-most EST	xsy700209437.h1

Seq. No.	281687
Contig ID	117816_1.R1011
5'-most EST	uC-zmflb73235b09b2
Method	BLASTX
NCBI GI	g3928758
BLAST score	845
E value	6.0e-91
Match length	196
% identity	82
NCBI Description	(AB007987) Lipoic acid synthase [Arabidopsis thaliana]

>gi_4454462_gb_AAD20909_ (AC006234) putative lipoic acid synthase [Arabidopsis thaliana]

Seq. No.	281688
Contig ID	117830_1.R1011
5'-most EST	gct701177719.h1

Seq. No.	281689
Contig ID	117841_1.R1011
5'-most EST	uC-zmroB73001d09b1
Method	BLASTX
NCBI GI	g2160694
BLAST score	154
E value	6.0e-10
Match length	96
% identity	35
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	281690
Contig ID	117849_1.R1011
5'-most EST	uC-zmroB73001e05b1
Method	BLASTX
NCBI GI	g4406756
BLAST score	581
E value	4.0e-60
Match length	142
% identity	78
NCBI Description	(AC006836) putative integral membrane protein A3 [Arabidopsis thaliana]

Seq. No.	281691
Contig ID	117884_1.R1011
5'-most EST	ntr700074529.h1

Seq. No.	281692
Contig ID	117886_1.R1011
5'-most EST	uC-zmroB73001h08b1
Method	BLASTX
NCBI GI	g4218537
BLAST score	350
E value	1.0e-32
Match length	180
% identity	36
NCBI Description	(AJ010830) GRAB2 protein [Triticum sp.]

Seq. No.	281693
Contig ID	117919_1.R1011
5'-most EST	uC-zmroB73013e07b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	431
E value	2.0e-42
Match length	165
% identity	54
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	281694
Contig ID	117929_1.R1011
5'-most EST	uC-zmroB73013g03b1

Seq. No.	281695
Contig ID	117990_1.R1011
5'-most EST	uC-zmroB73014d10b1

Seq. No.	281696
Contig ID	118005_1.R1011
5'-most EST	uC-zmroB73014f02b1

Seq. No.	281697
Contig ID	118007_1.R1011
5'-most EST	uC-zmflmo17257e05b1
Method	BLASTX
NCBI GI	g731742
BLAST score	266
E value	4.0e-23
Match length	132
% identity	43
NCBI Description	HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION >gi_626678_pir__S48910 hypothetical protein YHR171w - yeast (Saccharomyces cerevisiae) >gi_458899 (U00027) Yhr171wp [Saccharomyces cerevisiae] >gi_3688625_dbj_BAA33474_ (AB017925) ORF YHR171w [Saccharomyces cerevisiae]

Seq. No.	281698
Contig ID	118019_1.R1011
5'-most EST	wyr700236649.h1
Method	BLASTX
NCBI GI	g1084461
BLAST score	430
E value	4.0e-42
Match length	111
% identity	74
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	281699
Contig ID	118019_2.R1011
5'-most EST	uC-zmroteosinte063a08b1
Method	BLASTX
NCBI GI	g1084461
BLAST score	362
E value	2.0e-34
Match length	113
% identity	66
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	281700
Contig ID	118019_4.R1011
5'-most EST	cyk700048467.f1
Method	BLASTX
NCBI GI	g1084461
BLAST score	197
E value	2.0e-15

Match length	66
% identity	65
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	281701
Contig ID	118024_1.R1011
5'-most EST	wyr700240305.h1

Seq. No.	281702
Contig ID	118026_1.R1011
5'-most EST	uC-zmroteosinte116c04b2
Method	BLASTX
NCBI GI	g3128234
BLAST score	401
E value	7.0e-39
Match length	88
% identity	78
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281703
Contig ID	118035_1.R1011
5'-most EST	uC-zmflmo17100f06b1
Method	BLASTX
NCBI GI	g2245378
BLAST score	326
E value	3.0e-39
Match length	156
% identity	55
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	281704
Contig ID	118040_1.R1011
5'-most EST	uC-zmroB73015a01b1
Method	BLASTX
NCBI GI	g2894599
BLAST score	174
E value	3.0e-26
Match length	150
% identity	49
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	281705
Contig ID	118041_1.R1011
5'-most EST	uC-zmflmo17154b11b1
Method	BLASTX
NCBI GI	g3033398
BLAST score	279
E value	1.0e-24
Match length	74
% identity	74
NCBI Description	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No.	281706
Contig ID	118042_1.R1011
5'-most EST	uC-zmroB73015a03b1
Method	BLASTX

NCBI GI	g3004552
BLAST score	460
E value	7.0e-46
Match length	153
% identity	52
NCBI Description	(AC003673) unknown protein [Arabidopsis thaliana]

Seq. No.	281707
Contig ID	118050_1.R1011
5'-most EST	uC-zmroB73015b01b1
Method	BLASTX
NCBI GI	g4581155
BLAST score	223
E value	4.0e-18
Match length	93
% identity	51
NCBI Description	(AC006919) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	281708
Contig ID	118081_1.R1011
5'-most EST	uwc700151085.h1
Method	BLASTX
NCBI GI	g4098238
BLAST score	193
E value	2.0e-14
Match length	157
% identity	34
NCBI Description	(U76384) o-methyltransferase [Triticum aestivum]

Seq. No.	281709
Contig ID	118095_1.R1011
5'-most EST	dyk700102741.h1
Method	BLASTX
NCBI GI	g2244905
BLAST score	237
E value	9.0e-20
Match length	149
% identity	36
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	281710
Contig ID	118103_1.R1011
5'-most EST	uC-zmroB73015f07b1
Method	BLASTX
NCBI GI	g4415924
BLAST score	162
E value	4.0e-11
Match length	101
% identity	41
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	281711
Contig ID	118111_1.R1011
5'-most EST	wyr700244264.h1
Method	BLASTX

NCBI GI	g4097946
BLAST score	375
E value	6.0e-36
Match length	96
% identity	77
NCBI Description	(U72254) beta-1,3-glucanase precursor [Oryza sativa]

Seq. No.	281712
Contig ID	118122_1.R1011
5'-most EST	uC-zmroB73015h02b1
Method	BLASTX
NCBI GI	g2281102
BLAST score	164
E value	8.0e-11
Match length	114
% identity	34
NCBI Description	(AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No.	281713
Contig ID	118141_1.R1011
5'-most EST	uC-zmroB73017a11b1
Method	BLASTX
NCBI GI	g2894600
BLAST score	210
E value	1.0e-16
Match length	153
% identity	36
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	281714
Contig ID	118153_1.R1011
5'-most EST	wyr700238787.h1
Method	BLASTX
NCBI GI	g1143381
BLAST score	244
E value	2.0e-20
Match length	88
% identity	48
NCBI Description	(Z49063) polygalacturonase inhibitor [Actinidia deliciosa]

Seq. No.	281715
Contig ID	118172_1.R1011
5'-most EST	uC-zmroB73017d06b1

Seq. No.	281716
Contig ID	118185_1.R1011
5'-most EST	uC-zmroB73017e08b1
Method	BLASTX
NCBI GI	g3142289
BLAST score	376
E value	6.0e-36
Match length	103
% identity	67
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	281717

Contig ID 118217_1.R1011
5'-most EST uC-zmroB73017h05b1
Method BLASTX
NCBI GI g1839188
BLAST score 903
E value 1.0e-97
Match length 189
% identity 90
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 281718
Contig ID 118238_1.R1011
5'-most EST uC-zmflmo17122h09a1

Seq. No. 281719
Contig ID 118242_1.R1011
5'-most EST uC-zmflb73028e05a1

Seq. No. 281720
Contig ID 118242_2.R1011
5'-most EST uC-zmroB73020b06b1

Seq. No. 281721
Contig ID 118262_1.R1011
5'-most EST uC-zmroB73020d03b1
Method BLASTX
NCBI GI g4154352
BLAST score 158
E value 2.0e-10
Match length 92
% identity 37
NCBI Description (AF110333) PrMC3 [Pinus radiata]

Seq. No. 281722
Contig ID 118264_1.R1011
5'-most EST uC-zmrob73080h02b1
Method BLASTX
NCBI GI g3600054
BLAST score 184
E value 2.0e-19
Match length 113
% identity 42
NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]

Seq. No. 281723
Contig ID 118278_1.R1011
5'-most EST uC-zmroB73020e07b1
Method BLASTX
NCBI GI g3861068
BLAST score 161
E value 9.0e-11
Match length 72
% identity 39
NCBI Description (AJ235272) unknown [Rickettsia prowazekii]

Seq. No. 281724
Contig ID 118294_1.R1011

5'-most EST	pmx700085383.h1
Method	BLASTX
NCBI GI	g3080437
BLAST score	174
E value	5.0e-12
Match length	51
% identity	57
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	281725
Contig ID	118297_1.R1011
5'-most EST	uC-zmroB73020g02b1
Method	BLASTX
NCBI GI	g4115379
BLAST score	198
E value	8.0e-22
Match length	103
% identity	53
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	281726
Contig ID	118304_1.R1011
5'-most EST	uC-zmroB73020g09b1

Seq. No.	281727
Contig ID	118305_1.R1011
5'-most EST	uC-zmroB73020g10b1

Seq. No.	281728
Contig ID	118311_1.R1011
5'-most EST	uC-zmroB73020h04b1
Method	BLASTX
NCBI GI	g4093155
BLAST score	207
E value	4.0e-16
Match length	119
% identity	45
NCBI Description	(AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana]

Seq. No.	281729
Contig ID	118317_1.R1011
5'-most EST	xjt700093406.h1

Seq. No.	281730
Contig ID	118317_2.R1011
5'-most EST	uC-zmf1b73244h11b2
Method	BLASTX
NCBI GI	g4056467
BLAST score	144
E value	5.0e-09
Match length	59
% identity	49
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256

come from this gene. [Arabidopsis thaliana]

Seq. No.	281731
Contig ID	118320_1.R1011
5'-most EST	cyk700050225.f1
Method	BLASTX
NCBI GI	g4314378
BLAST score	194
E value	1.0e-14
Match length	76
% identity	53
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	281732
Contig ID	118335_1.R1011
5'-most EST	uC-zmroB73028b05b1
Method	BLASTX
NCBI GI	g2731377
BLAST score	393
E value	8.0e-41
Match length	240
% identity	42
NCBI Description	(U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]

Seq. No.	281733
Contig ID	118336_1.R1011
5'-most EST	xjt700095437.h1
Method	BLASTX
NCBI GI	g3426064
BLAST score	202
E value	1.0e-15
Match length	110
% identity	43
NCBI Description	(AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]

Seq. No.	281734
Contig ID	118341_1.R1011
5'-most EST	uC-zmroB73028c01b1
Method	BLASTX
NCBI GI	g3337367
BLAST score	379
E value	4.0e-36
Match length	134
% identity	51
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281735
Contig ID	118342_1.R1011
5'-most EST	uC-zmflb73280g11b2

Seq. No.	281736
Contig ID	118355_1.R1011
5'-most EST	uC-zmroB73028d05b1

Seq. No.	281737
Contig ID	118376_1.R1011
5'-most EST	uC-zmroB73028f03b1

Seq. No.	281738
Contig ID	118377_1.R1011
5'-most EST	uC-zmroB73028f04b1
Method	BLASTX
NCBI GI	g2529663
BLAST score	404
E value	2.0e-63
Match length	158
% identity	73
NCBI Description	(AC002535) putative lysophospholipase [Arabidopsis thaliana] >gi_3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	281739
Contig ID	118379_1.R1011
5'-most EST	uC-zmroB73028f06b1

Seq. No.	281740
Contig ID	118401_1.R1011
5'-most EST	uC-zmroB73028h05b1

Seq. No.	281741
Contig ID	118416_1.R1011
5'-most EST	uC-zmroB73030a09b1
Method	BLASTX
NCBI GI	g1651736
BLAST score	316
E value	5.0e-29
Match length	104
% identity	62
NCBI Description	(D90899) cysteine synthase [Synechocystis sp.]

Seq. No.	281742
Contig ID	118419_1.R1011
5'-most EST	uC-zmflmo17241c04b1
Method	BLASTX
NCBI GI	g3309243
BLAST score	905
E value	1.0e-100
Match length	255
% identity	73
NCBI Description	(AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No.	281743
Contig ID	118421_1.R1011
5'-most EST	uwc700151216.h1
Method	BLASTX
NCBI GI	g295355
BLAST score	443
E value	1.0e-43
Match length	179
% identity	53

NCBI Description	(L13653) peroxidase [Lycopersicon esculentum]

Seq. No.	281744
Contig ID	118430_1.R1011
5'-most EST	uC-zmflmo17104b04a1
Method	BLASTX
NCBI GI	g2088651
BLAST score	707
E value	2.0e-74
Match length	242
% identity	61
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	281745
Contig ID	118434_1.R1011
5'-most EST	uC-zmroB73030c03b1

Seq. No.	281746
Contig ID	118451_1.R1011
5'-most EST	uC-zmroB73030d08b1

Seq. No.	281747
Contig ID	118459_1.R1011
5'-most EST	uC-zmroB73030e04b1
Method	BLASTX
NCBI GI	g4580398
BLAST score	617
E value	4.0e-67
Match length	195
% identity	65
NCBI Description	(AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No.	281748
Contig ID	118463_1.R1011
5'-most EST	fwa700098233.h1

Seq. No.	281749
Contig ID	118477_1.R1011
5'-most EST	qmh700026130.f1

Seq. No.	281750
Contig ID	118478_1.R1011
5'-most EST	uC-zmroB73030g02b1

Seq. No.	281751
Contig ID	118484_1.R1011
5'-most EST	uC-zmroteosinte092b03b2

Seq. No.	281752
Contig ID	118488_1.R1011
5'-most EST	gwl700615385.h1

Seq. No.	281753
Contig ID	118505_1.R1011
5'-most EST	uC-zmroB73070a06b1

Seq. No.	281754
Contig ID	118513_1.R1011
5'-most EST	uC-zmroteosinte042e02b1
Method	BLASTX
NCBI GI	g2980798
BLAST score	445
E value	5.0e-44
Match length	167
% identity	54
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	281755
Contig ID	118528_1.R1011
5'-most EST	uwc700155258.h1

Seq. No.	281756
Contig ID	118536_1.R1011
5'-most EST	uC-zmroB73070d06b1
Method	BLASTX
NCBI GI	g1244566
BLAST score	506
E value	3.0e-51
Match length	141
% identity	70
NCBI Description	(U39321) acetyl-CoA carboxylase [Triticum aestivum] >gi_1588584_prf__2208491A Ac-CoA carboxylase [Triticum aestivum]

Seq. No.	281757
Contig ID	118536_2.R1011
5'-most EST	uC-zmflb73220a05b2
Method	BLASTX
NCBI GI	g2130099
BLAST score	660
E value	3.0e-69
Match length	178
% identity	71
NCBI Description	acetyl-CoA carboxylase (EC 6.4.1.2) - wheat >gi_514306 (U10187) acetyl-CoA carboxylase [Triticum aestivum]

Seq. No.	281758
Contig ID	118541_1.R1011
5'-most EST	wyr700235623.h1

Seq. No.	281759
Contig ID	118545_1.R1011
5'-most EST	uC-zmroB73070e04b1
Method	BLASTX
NCBI GI	g3819699
BLAST score	185
E value	1.0e-13
Match length	89
% identity	45
NCBI Description	(AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No. 281760

Contig ID	118554_1.R1011
5'-most EST	tzu700201676.h1
Seq. No.	281761
Contig ID	118558_1.R1011
5'-most EST	wyr700235250.h1
Method	BLASTX
NCBI GI	g3548810
BLAST score	162
E value	4.0e-11
Match length	89
% identity	40
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
Seq. No.	281762
Contig ID	118565_1.R1011
5'-most EST	dyk700103634.h1
Seq. No.	281763
Contig ID	118583_1.R1011
5'-most EST	uC-zmroB73070h12b1
Method	BLASTX
NCBI GI	g3641661
BLAST score	885
E value	2.0e-95
Match length	209
% identity	83
NCBI Description	(AB008519) high affinity nitrate transporter [Oryza sativa]
Seq. No.	281764
Contig ID	118584_1.R1011
5'-most EST	uC-zmrob73002a01b1
Method	BLASTX
NCBI GI	g1171579
BLAST score	403
E value	2.0e-39
Match length	131
% identity	63
NCBI Description	(X95342) cytochrome P450 [Nicotiana tabacum]
Seq. No.	281765
Contig ID	118586_1.R1011
5'-most EST	uC-zmflmo17329c05a1
Seq. No.	281766
Contig ID	118589_1.R1011
5'-most EST	uC-zmflb73227c09a1
Seq. No.	281767
Contig ID	118605_1.R1011
5'-most EST	uC-zmrob73002c03b1
Seq. No.	281768
Contig ID	118612_1.R1011
5'-most EST	uC-zmrob73002c11b1
Method	BLASTX

NCBI GI	g1723179
BLAST score	236
E value	1.0e-19
Match length	118
% identity	38
NCBI Description	HYPOTHETICAL PROTEIN HI1010 >gi_1074603_pir__B64164 hypothetical protein HI1010 - Haemophilus influenzae (strain Rd KW20) >gi_1574042 (U32782) 3-hydroxyisobutyrate dehydrogenase, putative [Haemophilus influenzae Rd]

Seq. No.	281769
Contig ID	118613_1.R1011
5'-most EST	uwc700154131.h1

Seq. No.	281770
Contig ID	118621_1.R1011
5'-most EST	uC-zmrob73002d12b1
Method	BLASTX
NCBI GI	g4539301
BLAST score	510
E value	2.0e-56
Match length	209
% identity	53
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	281771
Contig ID	118650_1.R1011
5'-most EST	xjt700092548.h1

Seq. No.	281772
Contig ID	118651_1.R1011
5'-most EST	uC-zmrob73002h03b1

Seq. No.	281773
Contig ID	118671_1.R1011
5'-most EST	pwr700450511.h1
Method	BLASTX
NCBI GI	g4586249
BLAST score	347
E value	3.0e-34
Match length	167
% identity	54
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No.	281774
Contig ID	118704_1.R1011
5'-most EST	wyr700240195.h1
Method	BLASTX
NCBI GI	g3522949
BLAST score	328
E value	2.0e-30
Match length	87
% identity	60
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281775
Contig ID	118706_1.R1011
5'-most EST	uC-zmrob73004d11b1

Seq. No.	281776
Contig ID	118708_1.R1011
5'-most EST	uC-zmrob73004f09b1

Seq. No.	281777
Contig ID	118713_1.R1011
5'-most EST	uC-zmrob73004e06b1

Seq. No.	281778
Contig ID	118716_1.R1011
5'-most EST	uC-zmrob73004e09b1
Method	BLASTN
NCBI GI	g786131
BLAST score	73
E value	6.0e-33
Match length	141
% identity	88
NCBI Description	Oryza sativa root-specific RCc3 mRNA, complete cds

Seq. No.	281779
Contig ID	118737_1.R1011
5'-most EST	vux700159634.h2
Method	BLASTX
NCBI GI	g2388561
BLAST score	175
E value	3.0e-12
Match length	65
% identity	54
NCBI Description	(AC000098) Similar to Arabidopsis hypothetical protein PID:e326839 (gb_Z97337). [Arabidopsis thaliana]

Seq. No.	281780
Contig ID	118758_1.R1011
5'-most EST	uC-zmrob73005a03b1
Method	BLASTX
NCBI GI	g4006886
BLAST score	793
E value	1.0e-84
Match length	265
% identity	58
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	281781
Contig ID	118764_1.R1011
5'-most EST	uC-zmrob73005a10b1
Method	BLASTX
NCBI GI	g231536
BLAST score	293
E value	3.0e-26
Match length	104
% identity	54
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL

AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	281782
Contig ID	118767_1.R1011
5'-most EST	uC-zmrob73005b02b1
Method	BLASTX
NCBI GI	g1706958
BLAST score	303
E value	2.0e-27
Match length	111
% identity	83
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	281783
Contig ID	118770_1.R1011
5'-most EST	uC-zmrob73005b07b1
Method	BLASTX
NCBI GI	g4204793
BLAST score	958
E value	1.0e-104
Match length	313
% identity	31
NCBI Description	(U52079) P-glycoprotein [Solanum tuberosum]

Seq. No.	281784
Contig ID	118775_1.R1011
5'-most EST	uC-zmrob73005c01b1
Method	BLASTX
NCBI GI	g3935181
BLAST score	188
E value	9.0e-26
Match length	68
% identity	84
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	281785
Contig ID	118793_1.R1011
5'-most EST	uC-zmrob73005d11b1
Method	BLASTX
NCBI GI	g4432841
BLAST score	169
E value	9.0e-12
Match length	46
% identity	74
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281786
Contig ID	118834_1.R1011
5'-most EST	fwa700098751.h1

Seq. No.	281787
Contig ID	118838_1.R1011
5'-most EST	uwc700153506.h1

Seq. No.	281788
Contig ID	118844_1.R1011
5'-most EST	uC-zmrob73006a12b1

Seq. No.	281789
Contig ID	118851_1.R1011
5'-most EST	uC-zmrob73011c06b1

Seq. No.	281790
Contig ID	118851_2.R1011
5'-most EST	uC-zmrob73006b07b1

Seq. No.	281791
Contig ID	118855_1.R1011
5'-most EST	uC-zmrob73006b11b1

Seq. No.	281792
Contig ID	118857_1.R1011
5'-most EST	uC-zmrob73006f01b1

Seq. No.	281793
Contig ID	118877_1.R1011
5'-most EST	dyk700106819.h1
Method	BLASTX
NCBI GI	g2459446
BLAST score	595
E value	1.0e-61
Match length	205
% identity	55
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	281794
Contig ID	118882_1.R1011
5'-most EST	qmh700026066.f1
Method	BLASTX
NCBI GI	g1263160
BLAST score	204
E value	4.0e-16
Match length	90
% identity	50
NCBI Description	(X89226) leucine-rich repeat/receptor protein kinase [Oryza sativa]

Seq. No.	281795
Contig ID	118884_1.R1011
5'-most EST	uC-zmrob73006e07b1
Method	BLASTX
NCBI GI	g3004565
BLAST score	497
E value	2.0e-50
Match length	140
% identity	40
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	281796

Contig ID	118886_1.R1011
5'-most EST	wty700165467.h1
Method	BLASTX
NCBI GI	g4235430
BLAST score	216
E value	1.0e-24
Match length	92
% identity	66
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	281797
Contig ID	118900_1.R1011
5'-most EST	uC-zmrob73075g09b1

Seq. No.	281798
Contig ID	118920_1.R1011
5'-most EST	uC-zmrob73006h07b1
Method	BLASTX
NCBI GI	g3912917
BLAST score	229
E value	6.0e-19
Match length	86
% identity	49
NCBI Description	(AF001308) putative NAK-like ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	281799
Contig ID	118936_1.R1011
5'-most EST	wyr700239447.h1
Method	BLASTX
NCBI GI	g1001478
BLAST score	193
E value	1.0e-30
Match length	178
% identity	41
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	281800
Contig ID	118942_1.R1011
5'-most EST	uC-zmrob73011b07b1
Method	BLASTX
NCBI GI	g3859775
BLAST score	296
E value	1.0e-26
Match length	121
% identity	47
NCBI Description	(Z54328) putative aminopeptidase p [Schizosaccharomyces pombe]

Seq. No.	281801
Contig ID	118951_1.R1011
5'-most EST	uC-zmrob73011c04b1
Method	BLASTX
NCBI GI	g3600059
BLAST score	331
E value	8.0e-31
Match length	132

% identity	48
NCBI Description	(AF080120) contains similarity to WB domains, G-beta repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03) [Arabidopsis thaliana]
Seq. No.	281802
Contig ID	118955_1.R1011
5'-most EST	uC-zmroteosinte004a11b1
Seq. No.	281803
Contig ID	118958_1.R1011
5'-most EST	uC-zmrob73011c11b1
Method	BLASTX
NCBI GI	g3859112
BLAST score	354
E value	2.0e-33
Match length	96
% identity	69
NCBI Description	(AF031607) male sterility MS5 [Arabidopsis thaliana]
Seq. No.	281804
Contig ID	118963_1.R1011
5'-most EST	tfd700570069.h1
Method	BLASTX
NCBI GI	g4490309
BLAST score	307
E value	4.0e-41
Match length	306
% identity	34
NCBI Description	(AL035678) peroxidase ATP17a-like protein [Arabidopsis thaliana]
Seq. No.	281805
Contig ID	118963_2.R1011
5'-most EST	ntr700077413.h1
Method	BLASTX
NCBI GI	g1086111
BLAST score	143
E value	5.0e-09
Match length	54
% identity	44
NCBI Description	peroxidase (EC 1.11.1.7) - Spirodela polyrrhiza >gi_438245_emb_CAA80502_ (Z22920) peroxidase [Spirodela polyrrhiza]
Seq. No.	281806
Contig ID	118968_1.R1011
5'-most EST	uC-zmflmo17117e02b1
Seq. No.	281807
Contig ID	118974_1.R1011
5'-most EST	xjt700095307.h1
Method	BLASTX
NCBI GI	g4107343
BLAST score	179
E value	4.0e-13
Match length	121

% identity	37
NCBI Description	(AJ224922) ATP citrate lyase [Sordaria macrospora]
Seq. No.	281808
Contig ID	118976_1.R1011
5'-most EST	nbm700467791.h1
Seq. No.	281809
Contig ID	119001_1.R1011
5'-most EST	uC-zmrob73011g09b1
Seq. No.	281810
Contig ID	119005_1.R1011
5'-most EST	qmh700029356.f1
Method	BLASTX
NCBI GI	g2564066
BLAST score	639
E value	1.0e-66
Match length	191
% identity	64
NCBI Description	(D45900) LEDI-3 protein [Lithospermum erythrorhizon]
Seq. No.	281811
Contig ID	119005_2.R1011
5'-most EST	wyr700237340.h1
Method	BLASTX
NCBI GI	g2564066
BLAST score	198
E value	1.0e-15
Match length	51
% identity	71
NCBI Description	(D45900) LEDI-3 protein [Lithospermum erythrorhizon]
Seq. No.	281812
Contig ID	119013_1.R1011
5'-most EST	uC-zmrob73011h09b1
Method	BLASTX
NCBI GI	g1778093
BLAST score	313
E value	7.0e-29
Match length	102
% identity	67
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]
Seq. No.	281813
Contig ID	119019_1.R1011
5'-most EST	uC-zmrob73012a03b1
Seq. No.	281814
Contig ID	119028_1.R1011
5'-most EST	uC-zmrob73012b04b1
Method	BLASTX
NCBI GI	g4490723
BLAST score	344
E value	2.0e-47

09504605.1000

Match length	121
% identity	67
NCBI Description	(AL035709) myb transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	281815
Contig ID	119034_1.R1011
5'-most EST	rvt700550412.h1
Method	BLASTX
NCBI GI	g2435517
BLAST score	405
E value	3.0e-39
Match length	186
% identity	47
NCBI Description	(AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

Seq. No.	281816
Contig ID	119043_1.R1011
5'-most EST	uC-zmflmo17219g01b1
Method	BLASTX
NCBI GI	g2262100
BLAST score	418
E value	6.0e-41
Match length	124
% identity	71
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	281817
Contig ID	119069_1.R1011
5'-most EST	uC-zmrob73012f01b1

Seq. No.	281818
Contig ID	119078_1.R1011
5'-most EST	uC-zmflmo17300b05b1
Method	BLASTX
NCBI GI	g2088658
BLAST score	159
E value	3.0e-10
Match length	125
% identity	38
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	281819
Contig ID	119088_1.R1011
5'-most EST	rvt700553443.h1
Method	BLASTX
NCBI GI	g4558673
BLAST score	205
E value	6.0e-16
Match length	71
% identity	42
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281820
Contig ID	119104_1.R1011
5'-most EST	wyr700239379.h1

Method	BLASTX
NCBI GI	g112802
BLAST score	571
E value	8.0e-59
Match length	171
% identity	70
NCBI Description	4-COUMARATE--COA LIGASE >gi_82454_pir__JU0311 4-coumarate--CoA ligase (EC 6.2.1.12) - rice >gi_20161_emb_CAA36850_ (X52623) 4-coumarate-CoA ligase [Oryza sativa]

Seq. No.	281821
Contig ID	119111_1.R1011
5'-most EST	uwc700154992.h1
Method	BLASTX
NCBI GI	g2921304
BLAST score	571
E value	1.0e-58
Match length	236
% identity	52
NCBI Description	(AF033496) herbicide safener binding protein [Zea mays]

Seq. No.	281822
Contig ID	119112_1.R1011
5'-most EST	uC-zmrob73019a10b1
Method	BLASTX
NCBI GI	g3341468
BLAST score	401
E value	8.0e-39
Match length	112
% identity	65
NCBI Description	(AJ009594) Dof zinc finger protein [Nicotiana tabacum]

Seq. No.	281823
Contig ID	119120_1.R1011
5'-most EST	uC-zmrob73019b06b1

Seq. No.	281824
Contig ID	119148_1.R1011
5'-most EST	uC-zmflmo17068b03b2
Method	BLASTX
NCBI GI	g2224846
BLAST score	735
E value	4.0e-78
Match length	158
% identity	91
NCBI Description	(Y13905) anionic peroxidase [Zea mays]

Seq. No.	281825
Contig ID	119148_2.R1011
5'-most EST	ntr700075815.h1
Method	BLASTX
NCBI GI	g2224846
BLAST score	618
E value	2.0e-84
Match length	161
% identity	100

NCBI Description	(Y13905) anionic peroxidase [Zea mays]

Seq. No.	281826
Contig ID	119180_1.R1011
5'-most EST	uC-zmrob73019g07b1

Seq. No.	281827
Contig ID	119185_1.R1011
5'-most EST	uC-zmrob73019g12b1
Method	BLASTX
NCBI GI	g2947062
BLAST score	155
E value	4.0e-10
Match length	107
% identity	39
NCBI Description	(AC002521) unknown protein [Arabidopsis thaliana]

Seq. No.	281828
Contig ID	119193_1.R1011
5'-most EST	nbm700471526.h1
Method	BLASTX
NCBI GI	g4220541
BLAST score	338
E value	3.0e-31
Match length	257
% identity	32
NCBI Description	(AL035356) Rab geranylgeranyl transferase like protein [Arabidopsis thaliana]

Seq. No.	281829
Contig ID	119194_1.R1011
5'-most EST	ntr700075529.h1

Seq. No.	281830
Contig ID	119197_1.R1011
5'-most EST	uC-zmrob73033a01b1
Method	BLASTX
NCBI GI	g3548810
BLAST score	193
E value	1.0e-14
Match length	92
% identity	45
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	281831
Contig ID	119199_1.R1011
5'-most EST	uC-zmrob73033a04b1

Seq. No.	281832
Contig ID	119211_1.R1011
5'-most EST	uC-zmrob73033b05b1

Seq. No.	281833
Contig ID	119225_1.R1011
5'-most EST	mwy700440982.h1

Seq. No.	281834
Contig ID	119233_1.R1011
5'-most EST	uC-zmrob73033d06b1

Seq. No.	281835
Contig ID	119240_1.R1011
5'-most EST	uC-zmrob73033e07b1

Seq. No.	281836
Contig ID	119260_1.R1011
5'-most EST	uC-zmrob73033f10b1
Method	BLASTX
NCBI GI	g3928084
BLAST score	521
E value	5.0e-53
Match length	174
% identity	60
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No.	281837
Contig ID	119261_1.R1011
5'-most EST	zuv700355912.h1
Method	BLASTX
NCBI GI	g2766450
BLAST score	287
E value	6.0e-26
Match length	96
% identity	68
NCBI Description	(AF029857) cytochrome P450 CYP99A1 [Sorghum bicolor]

Seq. No.	281838
Contig ID	119270_1.R1011
5'-most EST	uC-zmflb73130e04b2
Method	BLASTX
NCBI GI	g2832677
BLAST score	563
E value	1.0e-57
Match length	301
% identity	39
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281839
Contig ID	119296_1.R1011
5'-most EST	wyr700244285.h1

Seq. No.	281840
Contig ID	119299_2.R1011
5'-most EST	uC-zmrob73036b12b1

Seq. No.	281841
Contig ID	119300_1.R1011
5'-most EST	uC-zmrob73036c05b1

Seq. No.	281842
Contig ID	119307_1.R1011
5'-most EST	uer700579803.h1

Seq. No.	281843
Contig ID	119315_1.R1011
5'-most EST	uC-zmrob73024f01a1
Method	BLASTX
NCBI GI	g3337095
BLAST score	337
E value	2.0e-31
Match length	152
% identity	48
NCBI Description	(AB016206) polygalacturonase inhibitor (PGIP) [Citrus iyo]

Seq. No.	281844
Contig ID	119326_1.R1011
5'-most EST	uC-zmrob73080a02b1

Seq. No.	281845
Contig ID	119331_1.R1011
5'-most EST	uC-zmrob73036f04b1
Method	BLASTX
NCBI GI	g3292825
BLAST score	234
E value	2.0e-19
Match length	152
% identity	32
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281846
Contig ID	119348_1.R1011
5'-most EST	fdz701161693.h1

Seq. No.	281847
Contig ID	119354_1.R1011
5'-most EST	uC-zmrob73050a07b1

Seq. No.	281848
Contig ID	119364_1.R1011
5'-most EST	uC-zmrob73050b05b1

Seq. No.	281849
Contig ID	119369_1.R1011
5'-most EST	uC-zmflmo17222c09b1

Seq. No.	281850
Contig ID	119383_1.R1011
5'-most EST	uC-zmrob73050d01b1
Method	BLASTX
NCBI GI	g3924597
BLAST score	249
E value	3.0e-21
Match length	149
% identity	34
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	281851
Contig ID	119388_1.R1011
5'-most EST	uC-zmrob73050d07b1

Method	BLASTX
NCBI GI	g3355487
BLAST score	161
E value	7.0e-11
Match length	120
% identity	38
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	281852
Contig ID	119392_1.R1011
5'-most EST	uC-zmrob73050d11b1
Method	BLASTX
NCBI GI	g3367519
BLAST score	411
E value	6.0e-40
Match length	156
% identity	56
NCBI Description	(AC004392) Contains similarity to gb_U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	281853
Contig ID	119404_1.R1011
5'-most EST	uC-zmrob73050e11b1

Seq. No.	281854
Contig ID	119408_1.R1011
5'-most EST	vux700157638.h1
Method	BLASTX
NCBI GI	g2618699
BLAST score	289
E value	1.0e-25
Match length	144
% identity	36
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	281855
Contig ID	119420_1.R1011
5'-most EST	uC-zmrob73050g03b1
Method	BLASTX
NCBI GI	g1076591
BLAST score	183
E value	2.0e-13
Match length	43
% identity	67
NCBI Description	polygalacturonase inhibitor protein - tomato >gi_469457 (L26529) polygalacturonase inhibitor protein [Lycopersicon esculentum]

Seq. No.	281856
Contig ID	119432_1.R1011
5'-most EST	uC-zmrob73050h04b1
Method	BLASTX
NCBI GI	g3757522
BLAST score	423
E value	1.0e-41
Match length	99

% identity	83
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	281857
Contig ID	119435_1.R1011
5'-most EST	qmh700029439.f1

Seq. No.	281858
Contig ID	119451_1.R1011
5'-most EST	uC-zmrob73055b01b1
Method	BLASTX
NCBI GI	g4585972
BLAST score	260
E value	2.0e-22
Match length	141
% identity	40
NCBI Description	(AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No.	281859
Contig ID	119451_2.R1011
5'-most EST	wty700171690.h1
Method	BLASTX
NCBI GI	g4585972
BLAST score	387
E value	2.0e-37
Match length	130
% identity	52
NCBI Description	(AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No.	281860
Contig ID	119461_1.R1011
5'-most EST	uC-zmrob73055b11b1

Seq. No.	281861
Contig ID	119464_1.R1011
5'-most EST	dyk700105577.h1
Method	BLASTX
NCBI GI	g3618312
BLAST score	278
E value	8.0e-25
Match length	98
% identity	52
NCBI Description	(AB001884) zinc finger protein [Oryza sativa]

Seq. No.	281862
Contig ID	119468_1.R1011
5'-most EST	uC-zmflm017084d05b1
Method	BLASTX
NCBI GI	g4539452
BLAST score	748
E value	2.0e-79
Match length	210
% identity	63
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	281863

Contig ID	119469_1.R1011
5'-most EST	uC-zmrob73055c08b1
Method	BLASTX
NCBI GI	g1514643
BLAST score	835
E value	9.0e-90
Match length	208
% identity	75
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	281864
Contig ID	119475_1.R1011
5'-most EST	uC-zmrob73055d02b1

Seq. No.	281865
Contig ID	119494_1.R1011
5'-most EST	uC-zmrob73055e10b1
Method	BLASTX
NCBI GI	g3075400
BLAST score	249
E value	3.0e-21
Match length	102
% identity	47
NCBI Description	(AC004484) putative thromboxane-A synthase [Arabidopsis thaliana] >gi_3413720 (AC004747) putative thromboxin-A synthase [Arabidopsis thaliana]

Seq. No.	281866
Contig ID	119498_1.R1011
5'-most EST	ymt700218546.h1
Method	BLASTX
NCBI GI	g4468984
BLAST score	260
E value	2.0e-22
Match length	120
% identity	42
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	281867
Contig ID	119508_1.R1011
5'-most EST	uC-zmrob73055f12b1

Seq. No.	281868
Contig ID	119509_1.R1011
5'-most EST	qmh700026002.f1
Method	BLASTX
NCBI GI	g4104060
BLAST score	456
E value	3.0e-45
Match length	217
% identity	46
NCBI Description	(AF031231) S222 [Triticum aestivum]

Seq. No.	281869
Contig ID	119511_1.R1011
5'-most EST	uwc700153213.h1
Method	BLASTX

NCBI GI	g4115379
BLAST score	300
E value	4.0e-27
Match length	133
% identity	50
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	281870
Contig ID	119515_1.R1011
5'-most EST	dyk700103520.h1

Seq. No.	281871
Contig ID	119534_1.R1011
5'-most EST	uC-zmrob73066a02b1
Method	BLASTX
NCBI GI	g3676069
BLAST score	526
E value	2.0e-53
Match length	148
% identity	68
NCBI Description	(Y17899) ERG protein [Antirrhinum majus]

Seq. No.	281872
Contig ID	119562_1.R1011
5'-most EST	rvt700550387.h1
Method	BLASTX
NCBI GI	g4191779
BLAST score	422
E value	3.0e-41
Match length	157
% identity	55
NCBI Description	(AC005917) putative recA protein [Arabidopsis thaliana]

Seq. No.	281873
Contig ID	119575_1.R1011
5'-most EST	xjt700092504.h1

Seq. No.	281874
Contig ID	119578_1.R1011
5'-most EST	uC-zmrob73066d10b1
Method	BLASTX
NCBI GI	g4467125
BLAST score	513
E value	5.0e-52
Match length	180
% identity	56
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	281875
Contig ID	119611_1.R1011
5'-most EST	uC-zmrob73066g09b1

Seq. No.	281876
Contig ID	119629_1.R1011
5'-most EST	uC-zmrob73068a03b1

Seq. No.	281877
Contig ID	119639_1.R1011
5'-most EST	uwc700154272.h1
Method	BLASTX
NCBI GI	g1362162
BLAST score	429
E value	7.0e-42
Match length	242
% identity	38
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	281878
Contig ID	119646_1.R1011
5'-most EST	wyr700238706.h1
Method	BLASTX
NCBI GI	g115583
BLAST score	1039
E value	1.0e-113
Match length	211
% identity	98
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) (CP28) >gi_100758_pir__S18240 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sorghum >gi_22593_emb_CAA42549_ (X59925) phosphoenolpyruvate carboxylase [Sorghum bicolor]

Seq. No.	281879
Contig ID	119675_1.R1011
5'-most EST	uC-zmrob73068f04b1

Seq. No.	281880
Contig ID	119693_1.R1011
5'-most EST	uC-zmrob73068h12b1
Method	BLASTX
NCBI GI	g2935342
BLAST score	197
E value	4.0e-15
Match length	112
% identity	40
NCBI Description	(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 [Arabidopsis thaliana]

Seq. No.	281881
Contig ID	119708_1.R1011
5'-most EST	uC-zmrob73071a05b1
Method	BLASTX
NCBI GI	g4105125
BLAST score	537
E value	5.0e-55
Match length	130
% identity	73
NCBI Description	(AF043347) cell wall invertase; beta-fructosidase; Incw4 [Zea mays]

Seq. No.	281882
Contig ID	119772_1.R1011
5'-most EST	uC-zmrob73075a04b1

Method	BLASTX
NCBI GI	g544018
BLAST score	291
E value	2.0e-40
Match length	141
% identity	66
NCBI Description	NITRATE/CHLORATE TRANSPORTER >gi_1076359_pir__A45772 nitrate-inducible nitrate transporter - Arabidopsis thaliana >gi_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi_3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb_L10357 from A. thaliana. ESTs gb_H37533 and gb_R29790, gb_T46117, gb_T46068, gb_T75688, gb_R29817, gb_R29862, gb_Z34634 and gb_Z34258 come from this gene. [Arabidopsis thaliana]

Seq. No.	281883
Contig ID	119777_1.R1011
5'-most EST	uC-zmflmo17326h05a1

Seq. No.	281884
Contig ID	119781_1.R1011
5'-most EST	wyr700244190.h1
Method	BLASTX
NCBI GI	g4098238
BLAST score	292
E value	5.0e-26
Match length	168
% identity	46
NCBI Description	(U76384) o-methyltransferase [Triticum aestivum]

Seq. No.	281885
Contig ID	119781_2.R1011
5'-most EST	wyr700238841.h1
Method	BLASTX
NCBI GI	g4098238
BLAST score	211
E value	5.0e-17
Match length	78
% identity	59
NCBI Description	(U76384) o-methyltransferase [Triticum aestivum]

Seq. No.	281886
Contig ID	119781_3.R1011
5'-most EST	qmh700026556.f1

Seq. No.	281887
Contig ID	119782_1.R1011
5'-most EST	uC-zmflmo17282a09b1

Seq. No.	281888
Contig ID	119784_1.R1011
5'-most EST	uC-zmrob73075b04b1

Seq. No.	281889
Contig ID	119793_1.R1011
5'-most EST	wyr700236424.h1

Seq. No.	281890
Contig ID	119805_1.R1011
5'-most EST	uC-zmrob73075d01b1
Method	BLASTX
NCBI GI	g1708107
BLAST score	272
E value	6.0e-24
Match length	81
% identity	72
NCBI Description	HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]

Seq. No.	281891
Contig ID	119818_1.R1011
5'-most EST	uC-zmrob73075e02b1

Seq. No.	281892
Contig ID	119830_1.R1011
5'-most EST	uC-zmrob73075f02b1
Method	BLASTX
NCBI GI	g1173367
BLAST score	345
E value	6.0e-39
Match length	169
% identity	54
NCBI Description	SUGI BASIC PROTEIN PRECURSOR (SBP) (MAJOR ALLERGEN CRY J 1) (CRY J I) >gi_541803_pir__JC2123 major allergen Cry j I precursor (clone pCCI-2-2) - Japanese cedar >gi_493632_dbj_BAA05542_ (D26544) Cry j IA precursor [Cryptomeria japonica]

Seq. No.	281893
Contig ID	119831_1.R1011
5'-most EST	uC-zmflmo17159g09b1
Method	BLASTX
NCBI GI	g3006183
BLAST score	183
E value	4.0e-13
Match length	133
% identity	35
NCBI Description	(AL022304) trp-ast repeats containing protein [Schizosaccharomyces pombe]

Seq. No.	281894
Contig ID	119854_1.R1011
5'-most EST	hbs701183193.h1

Seq. No.	281895
Contig ID	119859_1.R1011
5'-most EST	uC-zmflmo17067d05b1

Seq. No.	281896
Contig ID	119878_1.R1011
5'-most EST	uC-zmrob73076b04b1
Method	BLASTX
NCBI GI	g2275215
BLAST score	261
E value	2.0e-22

Match length	83
% identity	70
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281897
Contig ID	119905_1.R1011
5'-most EST	dyk700102026.h1

Seq. No.	281898
Contig ID	119906_1.R1011
5'-most EST	dyk700105959.h1

Seq. No.	281899
Contig ID	119913_1.R1011
5'-most EST	uC-zmrob73076e04b1
Method	BLASTX
NCBI GI	g136125
BLAST score	216
E value	3.0e-17
Match length	184
% identity	28
NCBI Description	PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_ (X05424) ORFa [Zea mays]

Seq. No.	281900
Contig ID	119937_1.R1011
5'-most EST	uwc700155591.h1
Method	BLASTX
NCBI GI	g4115377
BLAST score	222
E value	5.0e-18
Match length	48
% identity	88
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	281901
Contig ID	119941_1.R1011
5'-most EST	uC-zmrob73076g11b1
Method	BLASTX
NCBI GI	g3980397
BLAST score	229
E value	1.0e-18
Match length	117
% identity	45
NCBI Description	(AC004561) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	281902
Contig ID	119947_1.R1011
5'-most EST	ntr700072320.h2
Method	BLASTX
NCBI GI	g3287696
BLAST score	323
E value	8.0e-30
Match length	152
% identity	48
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	281903
Contig ID	119952_1.R1011
5'-most EST	uC-zmrob73076h12b1

Seq. No.	281904
Contig ID	119958_1.R1011
5'-most EST	uC-zmrob73077a05b1

Seq. No.	281905
Contig ID	119961_1.R1011
5'-most EST	uC-zmrob73077a08b1

Seq. No.	281906
Contig ID	119963_1.R1011
5'-most EST	uC-zmrob73077a10b1
Method	BLASTX
NCBI GI	g1652798
BLAST score	187
E value	5.0e-14
Match length	49
% identity	76
NCBI Description	(D90908) GcpE [Synechocystis sp.]

Seq. No.	281907
Contig ID	119964_1.R1011
5'-most EST	ntr700072404.h2

Seq. No.	281908
Contig ID	119964_2.R1011
5'-most EST	hvj700620118.h1

Seq. No.	281909
Contig ID	119968_1.R1011
5'-most EST	uC-zmrob73077b03b1
Method	BLASTX
NCBI GI	g3169883
BLAST score	152
E value	8.0e-10
Match length	43
% identity	72
NCBI Description	(AF033194) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum]

Seq. No.	281910
Contig ID	120002_1.R1011
5'-most EST	uC-zmrob73077e01b1

Seq. No.	281911
Contig ID	120005_1.R1011
5'-most EST	uC-zmrob73077e04b1
Method	BLASTX

NCBI GI	g2245087
BLAST score	179
E value	6.0e-13
Match length	120
% identity	36
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281912
Contig ID	120016_1.R1011
5'-most EST	uC-zmrob73077f03b1
Method	BLASTX
NCBI GI	g2252840
BLAST score	364
E value	1.0e-34
Match length	146
% identity	49
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	281913
Contig ID	120022_1.R1011
5'-most EST	pmx700087190.h1

Seq. No.	281914
Contig ID	120027_1.R1011
5'-most EST	xjt700095525.h1

Seq. No.	281915
Contig ID	120040_1.R1011
5'-most EST	uC-zmrob73077h07b1

Seq. No.	281916
Contig ID	120046_1.R1011
5'-most EST	uC-zmrob73078a01b1

Seq. No.	281917
Contig ID	120064_1.R1011
5'-most EST	uC-zmrob73034d03a1

Seq. No.	281918
Contig ID	120085_1.R1011
5'-most EST	uC-zmrob73078d04b1

Seq. No.	281919
Contig ID	120096_1.R1011
5'-most EST	uC-zmrob73078e04b1
Method	BLASTN
NCBI GI	g4185305
BLAST score	47
E value	3.0e-17
Match length	119
% identity	85
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	281920
Contig ID	120107_1.R1011
5'-most EST	uC-zmrob73078f03b1

Seq. No.	281921
Contig ID	120109_1.R1011
5'-most EST	uC-zmrob73078f10b1

Seq. No.	281922
Contig ID	120112_1.R1011
5'-most EST	uC-zmrob73078f08b1

Seq. No.	281923
Contig ID	120121_1.R1011
5'-most EST	uC-zmrob73078g06b1

Seq. No.	281924
Contig ID	120131_1.R1011
5'-most EST	uC-zmrob73078h04b1

Seq. No.	281925
Contig ID	120139_1.R1011
5'-most EST	uC-zmrob73078h12b1

Seq. No.	281926
Contig ID	120141_1.R1011
5'-most EST	uC-zmrob73079a02b1
Method	BLASTX
NCBI GI	g4115383
BLAST score	429
E value	3.0e-42
Match length	112
% identity	74
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	281927
Contig ID	120183_1.R1011
5'-most EST	wyr700237443.h1
Method	BLASTX
NCBI GI	g421980
BLAST score	543
E value	1.0e-55
Match length	127
% identity	80
NCBI Description	transforming protein (myb3) - barley >gi_19059_emb_CAA50223_ (X70878) MybHv33 [Hordeum vulgare]

Seq. No.	281928
Contig ID	120184_1.R1011
5'-most EST	uC-zmrob73079d09b1

Seq. No.	281929
Contig ID	120191_1.R1011
5'-most EST	cjh700197123.h1

Seq. No.	281930

Contig ID	120208_1.R1011
5'-most EST	uC-zmrob73079f11b1
Method	BLASTX
NCBI GI	g3080391
BLAST score	277
E value	2.0e-24
Match length	106
% identity	50
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	281931
Contig ID	120214_1.R1011
5'-most EST	uC-zmrob73079g05b1

Seq. No.	281932
Contig ID	120216_1.R1011
5'-most EST	uC-zmrob73079g07b1

Seq. No.	281933
Contig ID	120241_1.R1011
5'-most EST	uC-zmrob73080a08b1

Seq. No.	281934
Contig ID	120246_1.R1011
5'-most EST	wty700169968.h1
Method	BLASTX
NCBI GI	g2275204
BLAST score	272
E value	8.0e-24
Match length	80
% identity	62
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	281935
Contig ID	120252_1.R1011
5'-most EST	xdb700340726.h1

Seq. No.	281936
Contig ID	120262_1.R1011
5'-most EST	uC-zmrob73080c07b1
Method	BLASTX
NCBI GI	g2117619
BLAST score	249
E value	3.0e-21
Match length	81
% identity	58
NCBI Description	peroxidase (EC 1.11.1.7) 4 precursor - wheat >gi_732976_emb_CAA59487_ (X85230) peroxidase [Triticum aestivum]

Seq. No.	281937
Contig ID	120266_1.R1011
5'-most EST	uC-zmrob73080c11b1

Seq. No.	281938
Contig ID	120275_1.R1011

5'-most EST	qmh700030582.f1
Method	BLASTX
NCBI GI	g2780192
BLAST score	414
E value	2.0e-40
Match length	95
% identity	72
NCBI Description	(AJ222713) unnamed protein product [Arabidopsis thaliana]

Seq. No.	281939
Contig ID	120281_1.R1011
5'-most EST	uC-zmrob73080e02b1
Method	BLASTX
NCBI GI	g3080435
BLAST score	332
E value	6.0e-31
Match length	103
% identity	58
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	281940
Contig ID	120289_1.R1011
5'-most EST	uC-zmrob73080e10b1

Seq. No.	281941
Contig ID	120294_1.R1011
5'-most EST	qmh700026941.f1
Method	BLASTX
NCBI GI	g4490309
BLAST score	391
E value	1.0e-38
Match length	161
% identity	53
NCBI Description	(AL035678) peroxidase ATP17a-like protein [Arabidopsis thaliana]

Seq. No.	281942
Contig ID	120302_1.R1011
5'-most EST	wyr700237230.h1
Method	BLASTX
NCBI GI	g2129670
BLAST score	336
E value	3.0e-31
Match length	176
% identity	35
NCBI Description	phosphoinositide-specific phospholipase C - Arabidopsis thaliana >gi_857374_dbj_BAA09432_ (D50804) phosphoinositide specific phospholipase C [Arabidopsis thaliana]

Seq. No.	281943
Contig ID	120314_1.R1011
5'-most EST	uC-zmrob73080g12b1

Seq. No.	281944
Contig ID	120321_1.R1011
5'-most EST	mwy700441960.h1

Seq. No.	281945
Contig ID	120328_1.R1011
5'-most EST	yyf700351762.h1
Method	BLASTX
NCBI GI	g544076
BLAST score	770
E value	3.0e-82
Match length	170
% identity	75
NCBI Description	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi_298097_emb_CAA49900_ (X70476) subunit of coatomer complex [Homo sapiens]

Seq. No.	281946
Contig ID	120336_1.R1011
5'-most EST	uC-zmflMo17002a10b1
Method	BLASTX
NCBI GI	g3461814
BLAST score	436
E value	4.0e-43
Match length	125
% identity	63
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281947
Contig ID	120348_1.R1011
5'-most EST	uC-zmflMo17002c01b1

Seq. No.	281948
Contig ID	120351_1.R1011
5'-most EST	uC-zmflmo17076b02b1

Seq. No.	281949
Contig ID	120356_1.R1011
5'-most EST	wyr700240823.h1
Method	BLASTX
NCBI GI	g1246823
BLAST score	543
E value	2.0e-55
Match length	153
% identity	66
NCBI Description	(X89865) unknown [Phoenix dactylifera]

Seq. No.	281950
Contig ID	120358_1.R1011
5'-most EST	uC-zmflMo17002c12b1

Seq. No.	281951
Contig ID	120363_1.R1011
5'-most EST	uC-zmflMo17002d06b1

Seq. No.	281952
Contig ID	120391_1.R1011
5'-most EST	wty700164732.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	34

E value	3.0e-09
Match length	34
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	281953
Contig ID	120400_1.R1011
5'-most EST	uC-zmflmo17057e09b1

Seq. No.	281954
Contig ID	120416_1.R1011
5'-most EST	tzu700205796.h1
Method	BLASTX
NCBI GI	g3790575
BLAST score	151
E value	3.0e-10
Match length	95
% identity	49
NCBI Description	(AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]

Seq. No.	281955
Contig ID	120425_1.R1011
5'-most EST	uC-zmflMo17003b05b1

Seq. No.	281956
Contig ID	120433_1.R1011
5'-most EST	uC-zmflMo17003c01b1

Seq. No.	281957
Contig ID	120435_1.R1011
5'-most EST	uC-zmflMo17003c04b1

Seq. No.	281958
Contig ID	120443_2.R1011
5'-most EST	wty700168887.h1

Seq. No.	281959
Contig ID	120448_1.R1011
5'-most EST	uC-zmflm017018d06b1

Seq. No.	281960
Contig ID	120449_1.R1011
5'-most EST	uC-zmflmo17136h04b1
Method	BLASTX
NCBI GI	g4432866
BLAST score	406
E value	3.0e-39
Match length	306
% identity	32
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	281961
Contig ID	120453_1.R1011
5'-most EST	zuv700355666.h1

Seq. No.	281962
Contig ID	120455_1.R1011
5'-most EST	uC-zmflMo17003d12b1

Seq. No.	281963
Contig ID	120533_1.R1011
5'-most EST	uC-zmflMo17004d04b1
Method	BLASTX
NCBI GI	g2673917
BLAST score	1120
E value	1.0e-123
Match length	278
% identity	41
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	281964
Contig ID	120546_1.R1011
5'-most EST	uC-zmflMo17004e07b1
Method	BLASTX
NCBI GI	g3643597
BLAST score	183
E value	3.0e-13
Match length	102
% identity	45
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281965
Contig ID	120551_1.R1011
5'-most EST	fdz701164171.h1

Seq. No.	281966
Contig ID	120581_1.R1011
5'-most EST	uC-zmflb73234f12b2

Seq. No.	281967
Contig ID	120585_1.R1011
5'-most EST	uC-zmflmo17283b02b1

Seq. No.	281968
Contig ID	120595_1.R1011
5'-most EST	uC-zmflMo17065a08b1
Method	BLASTN
NCBI GI	g1841354
BLAST score	37
E value	7.0e-11
Match length	85
% identity	86
NCBI Description	Oryza sativa mitochondrial DNA for cytochrome c oxidase subunit Vb precursor, complete cds

Seq. No.	281969
Contig ID	120595_2.R1011
5'-most EST	uC-zmflMo17005a12b1

Seq. No.	281970
Contig ID	120608_1.R1011

5'-most EST	uC-zmflMo17005c04b1
Method	BLASTX
NCBI GI	g4220522
BLAST score	164
E value	4.0e-11
Match length	195
% identity	27
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	281971
Contig ID	120612_1.R1011
5'-most EST	hbs701186059.h1

Seq. No.	281972
Contig ID	120620_1.R1011
5'-most EST	uC-zmflMo17005d07b1

Seq. No.	281973
Contig ID	120630_1.R1011
5'-most EST	uC-zmflMo17005e05b1
Method	BLASTX
NCBI GI	g3643088
BLAST score	585
E value	2.0e-60
Match length	214
% identity	51
NCBI Description	(AF075581) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	281974
Contig ID	120645_1.R1011
5'-most EST	uC-zmflmo17127a11b1

Seq. No.	281975
Contig ID	120646_1.R1011
5'-most EST	uC-zmflmo17113g02b1

Seq. No.	281976
Contig ID	120654_1.R1011
5'-most EST	uC-zmflMo17005g07b1
Method	BLASTX
NCBI GI	g3402684
BLAST score	559
E value	2.0e-57
Match length	151
% identity	68
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	281977
Contig ID	120661_1.R1011
5'-most EST	uC-zmroteosinte083c01b1
Method	BLASTX
NCBI GI	g1915960
BLAST score	630
E value	8.0e-66
Match length	166
% identity	72

NCBI Description	(Y07636) peptidylprolyl isomerase [Triticum aestivum]
Seq. No.	281978
Contig ID	120664_1.R1011
5'-most EST	uC-zmflMo17005h06b1
Seq. No.	281979
Contig ID	120690_1.R1011
5'-most EST	yyf700348761.h1
Seq. No.	281980
Contig ID	120691_1.R1011
5'-most EST	uC-zmflMo17006b10b1
Method	BLASTX
NCBI GI	g1723643
BLAST score	205
E value	3.0e-16
Match length	121
% identity	40
NCBI Description	HYPOTHETICAL 44.9 KD PROTEIN IN SEC9-MSB2 INTERGENIC REGION >gi_2132582_pir__S64299 probable membrane protein YGR010w - yeast (Saccharomyces cerevisiae) >gi_1322971_emb_CAA96993_ (Z72795) ORF YGR010w [Saccharomyces cerevisiae]
Seq. No.	281981
Contig ID	120696_1.R1011
5'-most EST	yyf700348167.h1
Seq. No.	281982
Contig ID	120697_1.R1011
5'-most EST	uwc700154036.h1
Seq. No.	281983
Contig ID	120715_1.R1011
5'-most EST	uC-zmflMo17006f01b1
Method	BLASTX
NCBI GI	g4589961
BLAST score	148
E value	4.0e-09
Match length	122
% identity	30
NCBI Description	(AC007169) unknown protein [Arabidopsis thaliana]
Seq. No.	281984
Contig ID	120724_1.R1011
5'-most EST	uC-zmflMo17006e11b1
Seq. No.	281985
Contig ID	120742_1.R1011
5'-most EST	yyf700347405.h1
Method	BLASTX
NCBI GI	g3335366
BLAST score	635
E value	5.0e-66
Match length	203
% identity	58
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 281986
Contig ID 120764_1.R1011
5'-most EST uC-zmflMo17007a08b1

Seq. No. 281987
Contig ID 120769_1.R1011
5'-most EST uC-zmflMo17007b01b1

Seq. No. 281988
Contig ID 120785_1.R1011
5'-most EST uC-zmflmo17222b12b1

Seq. No. 281989
Contig ID 120787_1.R1011
5'-most EST uC-zmflMo17007c08b1
Method BLASTX
NCBI GI g2191187
BLAST score 357
E value 1.0e-33
Match length 236
% identity 39
NCBI Description (AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]

Seq. No. 281990
Contig ID 120792_1.R1011
5'-most EST dyk700104472.h1
Method BLASTX
NCBI GI g4510339
BLAST score 674
E value 6.0e-71
Match length 185
% identity 42
NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No. 281991
Contig ID 120812_1.R1011
5'-most EST hvj700622677.h1

Seq. No. 281992
Contig ID 120812_2.R1011
5'-most EST uC-zmflMo17007e09b1

Seq. No. 281993
Contig ID 120837_1.R1011
5'-most EST zuv700352854.h1
Method BLASTX
NCBI GI g4454464
BLAST score 358
E value 8.0e-34
Match length 139
% identity 50
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 281994

Contig ID	120849_1.R1011
5'-most EST	uC-zmflMo17007h12b1
Method	BLASTX
NCBI GI	g473874
BLAST score	587
E value	1.0e-60
Match length	215
% identity	20
NCBI Description	(U08285) a membrane-associated salt-inducible protein [Nicotiana tabacum]

Seq. No.	281995
Contig ID	120862_1.R1011
5'-most EST	xmt700259581.h1

Seq. No.	281996
Contig ID	120867_1.R1011
5'-most EST	uC-zmflm017205g09b1

Seq. No.	281997
Contig ID	120886_1.R1011
5'-most EST	uC-zmflmo17008d04a1

Seq. No.	281998
Contig ID	120890_1.R1011
5'-most EST	uC-zmflMo17008d09b1
Method	BLASTX
NCBI GI	g4220522
BLAST score	149
E value	4.0e-09
Match length	141
% identity	33
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	281999
Contig ID	120892_1.R1011
5'-most EST	uC-zmflMo17008e02b1

Seq. No.	282000
Contig ID	120914_1.R1011
5'-most EST	uC-zmflb73122f08b2

Seq. No.	282001
Contig ID	120917_1.R1011
5'-most EST	ymt700223117.h1

Seq. No.	282002
Contig ID	120923_1.R1011
5'-most EST	wyr700241137.h1
Method	BLASTX
NCBI GI	g4104929
BLAST score	616
E value	4.0e-64
Match length	178
% identity	66
NCBI Description	(AF042195) auxin response factor 7 [Arabidopsis thaliana]

Seq. No.	282003
Contig ID	120938_1.R1011
5'-most EST	uC-zmflMo17009a05b1

Seq. No.	282004
Contig ID	120950_1.R1011
5'-most EST	uC-zmflMo17009b04b1
Method	BLASTX
NCBI GI	g3063710
BLAST score	363
E value	2.0e-34
Match length	157
% identity	52
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	282005
Contig ID	120952_1.R1011
5'-most EST	uC-zmflMo17009b06b1
Method	BLASTN
NCBI GI	g1041422
BLAST score	81
E value	2.0e-37
Match length	369
% identity	85
NCBI Description	H.vulgare mRNA for aminolevulinate dehydratase

Seq. No.	282006
Contig ID	120957_1.R1011
5'-most EST	uC-zmflMo17009b11b1
Method	BLASTX
NCBI GI	g3249109
BLAST score	517
E value	1.0e-52
Match length	142
% identity	71
NCBI Description	(AC003114) Contains similarity to pre-mRNA splicing factor (SF2), P33 subunit gb_M72709 from Homo sapiens. ESTs gb_T42588 and gb_R65514 come from this gene. [Arabidopsis thaliana]

Seq. No.	282007
Contig ID	120957_2.R1011
5'-most EST	uC-zmflmo17116f07b1
Method	BLASTX
NCBI GI	g3249109
BLAST score	481
E value	2.0e-48
Match length	135
% identity	70
NCBI Description	(AC003114) Contains similarity to pre-mRNA splicing factor (SF2), P33 subunit gb_M72709 from Homo sapiens. ESTs gb_T42588 and gb_R65514 come from this gene. [Arabidopsis thaliana]

Seq. No.	282008
Contig ID	120973_1.R1011
5'-most EST	uC-zmflMo17009d06b1

Seq. No.	282009
Contig ID	120977_1.R1011
5'-most EST	uC-zmflMo17009d11b1
Method	BLASTX
NCBI GI	g3885341
BLAST score	251
E value	2.0e-21
Match length	161
% identity	34
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	282010
Contig ID	120981_1.R1011
5'-most EST	uC-zmflMo17009e05b1

Seq. No.	282011
Contig ID	120997_1.R1011
5'-most EST	uC-zmflMo17010e07b1

Seq. No.	282012
Contig ID	120998_2.R1011
5'-most EST	uC-zmflmo17281h01b1

Seq. No.	282013
Contig ID	121029_1.R1011
5'-most EST	uC-zmflmo17018d06a1

Seq. No.	282014
Contig ID	121036_1.R1011
5'-most EST	uC-zmflMo17010b02b1
Method	BLASTX
NCBI GI	g2244987
BLAST score	340
E value	1.0e-31
Match length	146
% identity	51
NCBI Description	(Z97340) similarity to protein kinase - slime mold (Dictyostelium) [Arabidopsis thaliana]

Seq. No.	282015
Contig ID	121057_1.R1011
5'-most EST	uC-zmflMo17010d02b1
Method	BLASTX
NCBI GI	g3334661
BLAST score	371
E value	2.0e-35
Match length	120
% identity	58
NCBI Description	(Y10490) putative cytochrome P450 [Glycine max]

Seq. No.	282016
Contig ID	121082_1.R1011
5'-most EST	ymt700222133.h1

Seq. No.	282017
Contig ID	121100_1.R1011

5'-most EST	uC-zmflMo17010h03b1
Seq. No.	282018
Contig ID	121102_1.R1011
5'-most EST	uC-zmflmo17262c06b1
Method	BLASTX
NCBI GI	g3355471
BLAST score	366
E value	8.0e-35
Match length	126
% identity	54
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]
Seq. No.	282019
Contig ID	121111_1.R1011
5'-most EST	uC-zmflmo17012a02b1
Seq. No.	282020
Contig ID	121113_1.R1011
5'-most EST	uC-zmflMo17012a04b1
Seq. No.	282021
Contig ID	121122_1.R1011
5'-most EST	uC-zmflmo17012b07b1
Seq. No.	282022
Contig ID	121128_1.R1011
5'-most EST	uC-zmflMo17012c01b1
Seq. No.	282023
Contig ID	121130_1.R1011
5'-most EST	uC-zmflmo17012c03b1
Method	BLASTX
NCBI GI	g3540208
BLAST score	261
E value	2.0e-24
Match length	115
% identity	50
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	282024
Contig ID	121146_1.R1011
5'-most EST	uC-zmflMo17012d09b1
Seq. No.	282025
Contig ID	121154_1.R1011
5'-most EST	uC-zmflmo17012e07b1
Seq. No.	282026
Contig ID	121158_1.R1011
5'-most EST	uC-zmflmo17023f12b1
Method	BLASTX
NCBI GI	g2191187
BLAST score	163
E value	7.0e-11
Match length	106

% identity	37
NCBI Description	(AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]

Seq. No.	282027
Contig ID	121161_1.R1011
5'-most EST	uC-zmflmo17012f03b1

Seq. No.	282028
Contig ID	121166_1.R1011
5'-most EST	uC-zmflMo17012f08b1

Seq. No.	282029
Contig ID	121177_1.R1011
5'-most EST	uC-zmflmo17012g08b1
Method	BLASTX
NCBI GI	g2924792
BLAST score	338
E value	1.0e-31
Match length	131
% identity	50
NCBI Description	(AC002334) similar to synaptobrevin [Arabidopsis thaliana]

Seq. No.	282030
Contig ID	121181_1.R1011
5'-most EST	ntr700077325.h1
Method	BLASTX
NCBI GI	g1946373
BLAST score	230
E value	9.0e-19
Match length	99
% identity	47
NCBI Description	(U93215) leader peptidase I isolog [Arabidopsis thaliana]

Seq. No.	282031
Contig ID	121183_1.R1011
5'-most EST	uC-zmflmo17012h02b1
Method	BLASTX
NCBI GI	g3445201
BLAST score	363
E value	2.0e-34
Match length	109
% identity	61
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	282032
Contig ID	121188_1.R1011
5'-most EST	qmh700030607.f1

Seq. No.	282033
Contig ID	121198_1.R1011
5'-most EST	uC-zmflmo17013a08b1

Seq. No.	282034
Contig ID	121208_1.R1011
5'-most EST	uC-zmflMo17013b09b1

Seq. No.	282035
Contig ID	121216_1.R1011
5'-most EST	uC-zmflMo17013c05b1

Seq. No.	282036
Contig ID	121221_1.R1011
5'-most EST	uC-zmflMo17013c10b1
Method	BLASTX
NCBI GI	g2842496
BLAST score	276
E value	2.0e-24
Match length	83
% identity	69
NCBI Description	(AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	282037
Contig ID	121222_1.R1011
5'-most EST	uC-zmroteosinte066d05b1
Method	BLASTX
NCBI GI	g4056467
BLAST score	332
E value	7.0e-31
Match length	96
% identity	62
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256 come from this gene. [Arabidopsis thaliana]

Seq. No.	282038
Contig ID	121229_1.R1011
5'-most EST	uC-zmflmo17013d07b1
Method	BLASTX
NCBI GI	g3892204
BLAST score	518
E value	5.0e-57
Match length	141
% identity	79
NCBI Description	(AF078105) site-1 protease of sterol regulatory element binding proteins [Cricetulus griseus]

Seq. No.	282039
Contig ID	121231_1.R1011
5'-most EST	uC-zmflMo17013d09b1

Seq. No.	282040
Contig ID	121233_1.R1011
5'-most EST	uC-zmflMo17013d11b1

Seq. No.	282041
Contig ID	121237_1.R1011
5'-most EST	uC-zmflmo17013e03b1

Seq. No.	282042
Contig ID	121243_1.R1011
5'-most EST	uC-zmflMo17013e10b1
Method	BLASTX

NCBI GI	g2367431
BLAST score	163
E value	4.0e-11
Match length	126
% identity	33
NCBI Description	(AF000403) putative cytochrome P450 [Lotus japonicus]

Seq. No.	282043
Contig ID	121248_1.R1011
5'-most EST	uC-zmflmo17013f04b1

Seq. No.	282044
Contig ID	121250_1.R1011
5'-most EST	uC-zmflMo17013f06b1

Seq. No.	282045
Contig ID	121253_1.R1011
5'-most EST	xsy700210576.h1
Method	BLASTX
NCBI GI	g3335347
BLAST score	760
E value	6.0e-81
Match length	200
% identity	68
NCBI Description	(AC004512) Contains similarity to ARI, RING finger protein gb_X98309 from Drosophila melanogaster. ESTs gb_T44383, gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and gb_AA042359 come from this gene. [Arabidopsis thaliana]

Seq. No.	282046
Contig ID	121264_1.R1011
5'-most EST	uC-zmflmo17013g09b1
Method	BLASTX
NCBI GI	g2088648
BLAST score	194
E value	1.0e-19
Match length	74
% identity	66
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282047
Contig ID	121266_1.R1011
5'-most EST	uC-zmflmo17013g12b1
Method	BLASTX
NCBI GI	g2316024
BLAST score	878
E value	1.0e-94
Match length	194
% identity	86
NCBI Description	(U96400) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	282048
Contig ID	121275_1.R1011
5'-most EST	uC-zmflMo17013h10b1
Method	BLASTX
NCBI GI	g4038044
BLAST score	173

E value	3.0e-12
Match length	54
% identity	56
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana] >gi_4406788_gb_AAD20098_ (AC006532) unknown protein [Arabidopsis thaliana]

Seq. No.	282049
Contig ID	121279_1.R1011
5'-most EST	uC-zmflMo17014a02b1

Seq. No.	282050
Contig ID	121293_1.R1011
5'-most EST	dyk700104760.h1
Method	BLASTN
NCBI GI	g4589418
BLAST score	35
E value	8.0e-10
Match length	131
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	282051
Contig ID	121297_1.R1011
5'-most EST	uC-zmflmo17174b09b1

Seq. No.	282052
Contig ID	121315_1.R1011
5'-most EST	uC-zmflb73251a09b3
Method	BLASTX
NCBI GI	g3219151
BLAST score	417
E value	1.0e-44
Match length	128
% identity	75
NCBI Description	(AB015181) cdc2 related [Mesembryanthemum crystallinum]

Seq. No.	282053
Contig ID	121326_1.R1011
5'-most EST	uC-zmflmo17044f06b1

Seq. No.	282054
Contig ID	121329_1.R1011
5'-most EST	uC-zmflMo17014e10b1
Method	BLASTX
NCBI GI	g1899188
BLAST score	397
E value	2.0e-38
Match length	119
% identity	63
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	282055
Contig ID	121341_1.R1011
5'-most EST	uC-zmflmo17048b07b1
Method	BLASTX

NCBI GI	g1888357
BLAST score	756
E value	2.0e-80
Match length	198
% identity	70
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	282056
Contig ID	121345_1.R1011
5'-most EST	ceu700429973.h1
Method	BLASTX
NCBI GI	g3892057
BLAST score	413
E value	9.0e-46
Match length	116
% identity	48
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282057
Contig ID	121346_1.R1011
5'-most EST	uwc700153676.h1
Method	BLASTX
NCBI GI	g3928086
BLAST score	202
E value	4.0e-29
Match length	176
% identity	47
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	282058
Contig ID	121348_1.R1011
5'-most EST	uC-zmflmo17240e04b1

Seq. No.	282059
Contig ID	121349_1.R1011
5'-most EST	uC-zmflMo17014g07b1

Seq. No.	282060
Contig ID	121366_1.R1011
5'-most EST	uC-zmflMo17015a01b1
Method	BLASTX
NCBI GI	g3269297
BLAST score	149
E value	2.0e-09
Match length	114
% identity	33
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	282061
Contig ID	121369_1.R1011
5'-most EST	uC-zmflMo17015a04b1

Seq. No.	282062
Contig ID	121376_1.R1011
5'-most EST	uC-zmflmo17015a11b1

Seq. No.	282063
Contig ID	121382_1.R1011
5'-most EST	uC-zmflmo17161f09b1

Seq. No.	282064
Contig ID	121383_1.R1011
5'-most EST	uC-zmflMo17015b06b1
Method	BLASTX
NCBI GI	g585053
BLAST score	260
E value	2.0e-22
Match length	140
% identity	42
NCBI Description	MITOTIC CONTROL PROTEIN DIS3 >gi_283075_pir__A41944 mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe) >gi_173381 (M74094) mitotic control protein [Schizosaccharomyces pombe] >gi_3650393_emb_CAA21102_ (AL031743) mitotic control protein dis3. [Schizosaccharomyces pombe]

Seq. No.	282065
Contig ID	121388_1.R1011
5'-most EST	uC-zmflmo17015b11b1

Seq. No.	282066
Contig ID	121388_2.R1011
5'-most EST	uC-zmflmo17262a02b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	34
E value	6.0e-10
Match length	38
% identity	97
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	282067
Contig ID	121389_1.R1011
5'-most EST	uC-zmflmo17015b12b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	368
E value	2.0e-35
Match length	110
% identity	65
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	282068
Contig ID	121403_1.R1011
5'-most EST	uC-zmflMo17015d02b1

Seq. No.	282069
Contig ID	121412_1.R1011
5'-most EST	uC-zmflmo17015e06b1

Seq. No. 282070

Contig ID	121423_1.R1011
5'-most EST	uC-zmroteosinte045b01b2

Seq. No.	282071
Contig ID	121426_1.R1011
5'-most EST	uC-zmflmo17015f09b1
Method	BLASTX
NCBI GI	g4337187
BLAST score	524
E value	1.0e-60
Match length	167
% identity	66
NCBI Description	(AC006403) putative prolylcarboxypeptidase, 5' partial [Arabidopsis thaliana]

Seq. No.	282072
Contig ID	121443_1.R1011
5'-most EST	uC-zmflMo17015h03b1

Seq. No.	282073
Contig ID	121446_1.R1011
5'-most EST	uC-zmflMo17015h07b1
Method	BLASTX
NCBI GI	g125201
BLAST score	211
E value	1.0e-16
Match length	153
% identity	34
NCBI Description	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN >gi_279515_pir__OKRT2R protein kinase (EC 2.7.1.37), cAMP-dependent, type II-alpha regulatory chain - rat (fragment) >gi_206150 (J02934) protein kinase type II regulatory subunit (, EC 2.7.1.37) [Rattus norvegicus]

Seq. No.	282074
Contig ID	121454_1.R1011
5'-most EST	uC-zmflMo17016a03b1

Seq. No.	282075
Contig ID	121468_1.R1011
5'-most EST	uC-zmflm017016b06b1

Seq. No.	282076
Contig ID	121471_1.R1011
5'-most EST	uC-zmflm017016b09b1

Seq. No.	282077
Contig ID	121478_1.R1011
5'-most EST	uC-zmflMo17016c07b1

Seq. No.	282078
Contig ID	121489_1.R1011
5'-most EST	uC-zmflMo17016d08b1

Seq. No.	282079
Contig ID	121491_1.R1011
5'-most EST	uC-zmflMo17016d10b1

Method	BLASTX
NCBI GI	g2129559
BLAST score	251
E value	2.0e-21
Match length	115
% identity	48
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	282080
Contig ID	121493_1.R1011
5'-most EST	uC-zmflMo17016d12b1
Method	BLASTX
NCBI GI	g4416303
BLAST score	415
E value	1.0e-40
Match length	101
% identity	83
NCBI Description	(AF105716) gag protein [Zea mays]

Seq. No.	282081
Contig ID	121504_1.R1011
5'-most EST	uC-zmflMo17016e12b1
Method	BLASTX
NCBI GI	g4210449
BLAST score	325
E value	5.0e-30
Match length	89
% identity	71
NCBI Description	(AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No.	282082
Contig ID	121506_1.R1011
5'-most EST	uC-zmflMo17016f02b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	48
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	282083
Contig ID	121525_1.R1011
5'-most EST	mwy700442646.h1

Seq. No.	282084
Contig ID	121526_1.R1011
5'-most EST	uC-zmflm017016h01b1

Seq. No.	282085
Contig ID	121534_1.R1011
5'-most EST	uC-zmflMo17016h09b1

Seq. No.	282086
Contig ID	121541_1.R1011
5'-most EST	rvt700549452.h1
Method	BLASTX
NCBI GI	g4588012
BLAST score	499
E value	2.0e-50
Match length	155
% identity	65
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	282087
Contig ID	121542_1.R1011
5'-most EST	uC-zmflm017018a05b1

Seq. No.	282088
Contig ID	121544_1.R1011
5'-most EST	uC-zmflm017018a07b1

Seq. No.	282089
Contig ID	121545_1.R1011
5'-most EST	uC-zmflm017018a08b1
Method	BLASTX
NCBI GI	g4544451
BLAST score	146
E value	4.0e-09
Match length	72
% identity	47
NCBI Description	(AC006592) unknown protein [Arabidopsis thaliana]

Seq. No.	282090
Contig ID	121547_1.R1011
5'-most EST	uC-zmflm017018a10b1

Seq. No.	282091
Contig ID	121553_1.R1011
5'-most EST	uC-zmflm017018b05b1
Method	BLASTX
NCBI GI	g4101564
BLAST score	266
E value	4.0e-23
Match length	95
% identity	57
NCBI Description	(AF004556) IFA-binding protein [Arabidopsis thaliana]

Seq. No.	282092
Contig ID	121565_1.R1011
5'-most EST	uC-zmflm017018c05b1

Seq. No.	282093
Contig ID	121567_1.R1011
5'-most EST	uC-zmflm017018c07b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36

E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	282094
Contig ID	121571_1.R1011
5'-most EST	uC-zmflm017018c11b1

Seq. No.	282095
Contig ID	121576_1.R1011
5'-most EST	uC-zmflm017018d04b1
Method	BLASTX
NCBI GI	g585536
BLAST score	154
E value	5.0e-10
Match length	56
% identity	57
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	282096
Contig ID	121577_1.R1011
5'-most EST	uC-zmflm017018d05b1
Method	BLASTX
NCBI GI	g3337389
BLAST score	245
E value	2.0e-20
Match length	246
% identity	38
NCBI Description	(AC004682) pre-mRNA splicing factor (PRP16)(KIAA0224) [Homo sapiens]

Seq. No.	282097
Contig ID	121583_1.R1011
5'-most EST	uC-zmflm017018d11b1

Seq. No.	282098
Contig ID	121585_1.R1011
5'-most EST	uC-zmflm017018e02b1

Seq. No.	282099
Contig ID	121590_1.R1011
5'-most EST	uC-zmflm017018e07b1
Method	BLASTX
NCBI GI	g2809246
BLAST score	144
E value	6.0e-09
Match length	76
% identity	38
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	282100
Contig ID	121591_1.R1011

09054050 - 4050

5'-most EST	uC-zmflMo17018e08b1
Seq. No.	282101
Contig ID	121601_1.R1011
5'-most EST	uC-zmflm017018f07b1
Seq. No.	282102
Contig ID	121603_1.R1011
5'-most EST	uC-zmflm017018f09b1
Seq. No.	282103
Contig ID	121615_1.R1011
5'-most EST	wyr700241145.h1
Method	BLASTX
NCBI GI	g4415912
BLAST score	279
E value	2.0e-24
Match length	109
% identity	48
NCBI Description	(AC006282) putative protease [Arabidopsis thaliana]
Seq. No.	282104
Contig ID	121627_1.R1011
5'-most EST	uC-zmflm017018h11b1
Seq. No.	282105
Contig ID	121634_1.R1011
5'-most EST	uC-zmflmo17282f05b1
Seq. No.	282106
Contig ID	121652_1.R1011
5'-most EST	uC-zmflmo17055b02b1
Seq. No.	282107
Contig ID	121653_1.R1011
5'-most EST	uC-zmflb73118b08b1
Method	BLASTN
NCBI GI	g342661
BLAST score	99
E value	6.0e-48
Match length	111
% identity	98
NCBI Description	Maize mitochondrial 26S rRNA gene and flanks
Seq. No.	282108
Contig ID	121659_1.R1011
5'-most EST	uC-zmflMo17019c08b1
Seq. No.	282109
Contig ID	121663_1.R1011
5'-most EST	uC-zmflmo17215b08b1
Method	BLASTX
NCBI GI	g3875707
BLAST score	243
E value	7.0e-20
Match length	261
% identity	26

NCBI Description	(Z35598) similarity with the yeast hypothetical 251.0 KD protein YCR32W (Swiss-Prot accession number P25356); cDNA EST EMBL:D34073 comes from this gene; cDNA EST EMBL:D32376 comes from this gene; cDNA EST EMBL:D37092 comes from... >gi_3876725_emb_CAA86337_ (Z46242) similarity with the yeast hypothetical 251.0 KD protein YCR32W (Swiss-Prot accession number P25356); cDNA EST EMBL:D34073 comes from this gene; cDNA EST EMBL:D32376 comes from this gene; cDNA EST EMBL:D37092 comes from

Seq. No.	282110
Contig ID	121675_1.R1011
5'-most EST	uC-zmflMo17019e02b1

Seq. No.	282111
Contig ID	121685_1.R1011
5'-most EST	uC-zmflmo17f02b1
Method	BLASTX
NCBI GI	g3850129
BLAST score	402
E value	7.0e-39
Match length	184
% identity	41
NCBI Description	(AL033391) conserved hypothetical protein [Candida albicans]

Seq. No.	282112
Contig ID	121691_1.R1011
5'-most EST	uC-zmflb73246b02b3
Method	BLASTX
NCBI GI	g3785997
BLAST score	154
E value	7.0e-10
Match length	91
% identity	40
NCBI Description	(AC005499) putative annexin [Arabidopsis thaliana]

Seq. No.	282113
Contig ID	121699_1.R1011
5'-most EST	uC-zmflmo17011h08b1
Method	BLASTX
NCBI GI	g4512659
BLAST score	553
E value	1.0e-56
Match length	180
% identity	64
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	282114
Contig ID	121699_2.R1011
5'-most EST	fC-zmle700578571f1
Method	BLASTX
NCBI GI	g4512659
BLAST score	494
E value	5.0e-50

Match length	132
% identity	77
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	282115
Contig ID	121699_3.R1011
5'-most EST	uC-zmflmo17126a12b1
Method	BLASTX
NCBI GI	g3482919
BLAST score	382
E value	9.0e-39
Match length	95
% identity	87
NCBI Description	(AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	282116
Contig ID	121731_1.R1011
5'-most EST	uC-zmflMo17062b03b1

Seq. No.	282117
Contig ID	121739_1.R1011
5'-most EST	wyr700238167.h1
Method	BLASTX
NCBI GI	g2244899
BLAST score	395
E value	5.0e-38
Match length	169
% identity	52
NCBI Description	(Z97338) similar to UFD1 protein [Arabidopsis thaliana]

Seq. No.	282118
Contig ID	121746_1.R1011
5'-most EST	uC-zmflMo17062c07b1

Seq. No.	282119
Contig ID	121776_1.R1011
5'-most EST	clt700044750.f1

Seq. No.	282120
Contig ID	121782_1.R1011
5'-most EST	uC-zmflmo17216e01a1

Seq. No.	282121
Contig ID	121784_1.R1011
5'-most EST	uer700579014.h1

Seq. No.	282122
Contig ID	121797_1.R1011
5'-most EST	gct701173532.h1

Seq. No.	282123
Contig ID	121816_1.R1011
5'-most EST	uC-zmflMo17063b07b1

Seq. No.	282124

Contig ID	121822_1.R1011
5'-most EST	nbm700475812.h1
Method	BLASTX
NCBI GI	g4455338
BLAST score	525
E value	4.0e-53
Match length	379
% identity	36
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	282125
Contig ID	121841_1.R1011
5'-most EST	uC-zmflMo17063c11b1
Method	BLASTX
NCBI GI	g1711543
BLAST score	270
E value	2.0e-23
Match length	156
% identity	42
NCBI Description	SERINE/THREONINE-PROTEIN KINASE SSP1 >gi_2130468_pir__S58666 protein kinase ssp1 - fission yeast (Schizosaccharomyces pombe) >gi_1041185_dbj_BAA08301_ (D45882) protein kinase [Schizosaccharomyces pombe] >gi_4584701_emb_CAB40783.1_ (AL049609) serine/threonine-protein kinase ssp1 [Schizosaccharomyces pombe]

Seq. No.	282126
Contig ID	121846_1.R1011
5'-most EST	uC-zmflmo17035c03b1

Seq. No.	282127
Contig ID	121847_1.R1011
5'-most EST	uC-zmflMo17063d05b1

Seq. No.	282128
Contig ID	121866_1.R1011
5'-most EST	uC-zmflMo17063f05b1
Method	BLASTX
NCBI GI	g1771158
BLAST score	166
E value	2.0e-11
Match length	109
% identity	32
NCBI Description	(Y07861) MFP1 protein [Lycopersicon esculentum]

Seq. No.	282129
Contig ID	121927_1.R1011
5'-most EST	uC-zmflMo17064c10b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	33
E value	5.0e-09
Match length	33
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	282130
Contig ID	121942_1.R1011
5'-most EST	uC-zmflmo17065f02b1
Method	BLASTN
NCBI GI	g22371
BLAST score	468
E value	0.0e+00
Match length	629
% identity	57
NCBI Description	Maize Mu4 transposable element DNA

Seq. No.	282131
Contig ID	121966_1.R1011
5'-most EST	ntr700071706.h1

Seq. No.	282132
Contig ID	121968_1.R1011
5'-most EST	uC-zmflMo17064g05b1
Method	BLASTX
NCBI GI	g3063449
BLAST score	507
E value	2.0e-51
Match length	148
% identity	66
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	282133
Contig ID	122019_1.R1011
5'-most EST	uC-zmflmo17065d04b1
Method	BLASTX
NCBI GI	g3249098
BLAST score	167
E value	8.0e-12
Match length	44
% identity	75
NCBI Description	(AC003114) ESTs gb_T04610, gb_N38459, gb_T45174, gb_R30481 and gb_N64971 come from this gene. [Arabidopsis thaliana]

Seq. No.	282134
Contig ID	122022_1.R1011
5'-most EST	uC-zmflmo17065d07b1

Seq. No.	282135
Contig ID	122035_1.R1011
5'-most EST	uC-zmflmo17269b04b1

Seq. No.	282136
Contig ID	122038_1.R1011
5'-most EST	uC-zmflMo17065e11b1
Method	BLASTX
NCBI GI	g4519936
BLAST score	370
E value	3.0e-35
Match length	135
% identity	55
NCBI Description	(AB019186) RPR1 [Oryza sativa]

Seq. No.	282137
Contig ID	122052_1.R1011
5'-most EST	uC-zmflMo17065g03b1

Seq. No.	282138
Contig ID	122067_1.R1011
5'-most EST	uC-zmflmo17065h08b1
Method	BLASTN
NCBI GI	g666088
BLAST score	80
E value	5.0e-37
Match length	135
% identity	90
NCBI Description	S.bicolor mRNA for p-(S)-hydroxymandelonitrile lyase

Seq. No.	282139
Contig ID	122069_1.R1011
5'-most EST	uC-zmflmo17065h10b1

Seq. No.	282140
Contig ID	122071_1.R1011
5'-most EST	uC-zmflmo17067a01b1

Seq. No.	282141
Contig ID	122083_1.R1011
5'-most EST	uC-zmflmo17067b07b1

Seq. No.	282142
Contig ID	122084_1.R1011
5'-most EST	uC-zmflmo17067b08b1
Method	BLASTX
NCBI GI	g3876895
BLAST score	145
E value	4.0e-15
Match length	84
% identity	52
NCBI Description	(Z77660) predicted using Genefinder; Similarity to Human serine/threonine protein phosphatase P2AB (SW:P2AB_HUMAN); cDNA EST EMBL:D74346 comes from this gene; cDNA EST EMBL:D74151 comes from this gene; cDNA EST EMBL:D74424 come

Seq. No.	282143
Contig ID	122095_1.R1011
5'-most EST	uC-zmflmo17067c10b1
Method	BLASTX
NCBI GI	g2827711
BLAST score	646
E value	9.0e-68
Match length	152
% identity	78
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	282144
Contig ID	122096_1.R1011
5'-most EST	uC-zmflmo17067c11b1
Method	BLASTX

NCBI GI	g4371296
BLAST score	155
E value	4.0e-10
Match length	73
% identity	40
NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	282145
Contig ID	122097_1.R1011
5'-most EST	xjt700092315.h1

Seq. No.	282146
Contig ID	122098_1.R1011
5'-most EST	uC-zmflmo17067d01b1

Seq. No.	282147
Contig ID	122100_1.R1011
5'-most EST	uC-zmflmo17067d03b1

Seq. No.	282148
Contig ID	122153_1.R1011
5'-most EST	uC-zmflmo17068a05b2
Method	BLASTX
NCBI GI	g1418331
BLAST score	235
E value	7.0e-20
Match length	97
% identity	49
NCBI Description	(X95909) receptor like protein kinase [Arabidopsis thaliana]

Seq. No.	282149
Contig ID	122164_1.R1011
5'-most EST	uC-zmflmo17068b08b2

Seq. No.	282150
Contig ID	122173_1.R1011
5'-most EST	uC-zmflmo17245a05b1

Seq. No.	282151
Contig ID	122173_2.R1011
5'-most EST	uC-zmflmo17077e01b1

Seq. No.	282152
Contig ID	122180_1.R1011
5'-most EST	uC-zmflmo17068e07b2

Seq. No.	282153
Contig ID	122183_1.R1011
5'-most EST	uC-zmflmo17068f01b2
Method	BLASTX
NCBI GI	g2947070
BLAST score	221
E value	5.0e-18
Match length	83
% identity	47

NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	282154
Contig ID	122199_1.R1011
5'-most EST	uC-zmflm017082b06b1
Method	BLASTX
NCBI GI	g4454051
BLAST score	452
E value	9.0e-50
Match length	180
% identity	54
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	282155
Contig ID	122199_2.R1011
5'-most EST	uC-zmflMo17082b06b1

Seq. No.	282156
Contig ID	122207_1.R1011
5'-most EST	zuv700354922.h1
Method	BLASTX
NCBI GI	g4572668
BLAST score	273
E value	4.0e-24
Match length	122
% identity	49
NCBI Description	(AC006954) putative retrotransposon polyprotein [Arabidopsis thaliana]

Seq. No.	282157
Contig ID	122212_1.R1011
5'-most EST	uC-zmflmo17341b08b1
Method	BLASTX
NCBI GI	g2887500
BLAST score	547
E value	5.0e-56
Match length	182
% identity	62
NCBI Description	(AC002339) putative AP2 domain-containing protein [Arabidopsis thaliana]

Seq. No.	282158
Contig ID	122212_2.R1011
5'-most EST	uC-zmflm017082c08b1
Method	BLASTN
NCBI GI	g6598350
BLAST score	36
E value	1.0e-10
Match length	92
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	282159
Contig ID	122215_1.R1011

5'-most EST	uC-zmflMo17082c11b1
Seq. No.	282160
Contig ID	122221_1.R1011
5'-most EST	ceu700430990.h1
Seq. No.	282161
Contig ID	122222_1.R1011
5'-most EST	uC-zmflm017082d07b1
Seq. No.	282162
Contig ID	122224_1.R1011
5'-most EST	uC-zmflm017082d09b1
Seq. No.	282163
Contig ID	122224_2.R1011
5'-most EST	fdz701164147.h1
Seq. No.	282164
Contig ID	122230_1.R1011
5'-most EST	fwa700097934.h1
Seq. No.	282165
Contig ID	122235_1.R1011
5'-most EST	dyk700106626.h1
Method	BLASTX
NCBI GI	g2832658
BLAST score	427
E value	5.0e-42
Match length	117
% identity	63
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]
Seq. No.	282166
Contig ID	122249_1.R1011
5'-most EST	uC-zmflm017082h01b1
Seq. No.	282167
Contig ID	122250_1.R1011
5'-most EST	uC-zmflm017082f12b1
Seq. No.	282168
Contig ID	122265_1.R1011
5'-most EST	gwl700614938.h1
Seq. No.	282169
Contig ID	122266_1.R1011
5'-most EST	uC-zmflm017082h05b1
Seq. No.	282170
Contig ID	122284_1.R1011
5'-most EST	tzu700205916.h1
Method	BLASTX
NCBI GI	g3242789
BLAST score	456
E value	2.0e-45
Match length	177

% identity	58
NCBI Description	(AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]
Seq. No.	282171
Contig ID	122309_1.R1011
5'-most EST	uC-zmflmo17295d01b1
Method	BLASTX
NCBI GI	g2809246
BLAST score	892
E value	6.0e-96
Match length	311
% identity	55
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]
Seq. No.	282172
Contig ID	122327_1.R1011
5'-most EST	uC-zmflm017084a03b1
Seq. No.	282173
Contig ID	122333_1.R1011
5'-most EST	uC-zmflMo17084a10b1
Seq. No.	282174
Contig ID	122336_1.R1011
5'-most EST	uC-zmflm017084b01b1
Seq. No.	282175
Contig ID	122338_1.R1011
5'-most EST	uC-zmflmo17269a09b1
Seq. No.	282176
Contig ID	122350_1.R1011
5'-most EST	uC-zmflm017084c05b1
Seq. No.	282177
Contig ID	122361_1.R1011
5'-most EST	uC-zmflm017084d04b1
Seq. No.	282178
Contig ID	122369_1.R1011
5'-most EST	uC-zmflMo17084e02b1
Seq. No.	282179
Contig ID	122383_1.R1011
5'-most EST	cat700019286.r1
Seq. No.	282180
Contig ID	122399_1.R1011
5'-most EST	uC-zmflMo17084g08b1
Seq. No.	282181
Contig ID	122401_1.R1011
5'-most EST	uC-zmflm017084g10b1
Method	BLASTN
NCBI GI	g2832242
BLAST score	243

E value	1.0e-134
Match length	442
% identity	89
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	282182
Contig ID	122414_1.R1011
5'-most EST	tzu700206769.h1
Method	BLASTX
NCBI GI	g2764806
BLAST score	367
E value	5.0e-35
Match length	115
% identity	57
NCBI Description	(X78548) epoxide hydrolase [Glycine max]

Seq. No.	282183
Contig ID	122427_1.R1011
5'-most EST	yyf700349505.h1

Seq. No.	282184
Contig ID	122442_1.R1011
5'-most EST	uC-zmflmo17184g03b1

Seq. No.	282185
Contig ID	122443_1.R1011
5'-most EST	uC-zmflMo17085d05b1

Seq. No.	282186
Contig ID	122448_1.R1011
5'-most EST	xmt700263310.h1

Seq. No.	282187
Contig ID	122454_1.R1011
5'-most EST	uC-zmflMo17085e04b1
Method	BLASTX
NCBI GI	g4580395
BLAST score	609
E value	2.0e-63
Match length	149
% identity	76
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	282188
Contig ID	122464_1.R1011
5'-most EST	uC-zmflmo17077a05b1
Method	BLASTX
NCBI GI	g799369
BLAST score	190
E value	3.0e-14
Match length	57
% identity	70
NCBI Description	(U25111) metalloendopeptidase [Pisum sativum]

Seq. No.	282189
Contig ID	122473_1.R1011

5'-most EST	xyt700345765.h1
Seq. No.	282190
Contig ID	122485_1.R1011
5'-most EST	uC-zmflMo17085h06b1
Method	BLASTX
NCBI GI	g4544431
BLAST score	322
E value	1.0e-59
Match length	169
% identity	75
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.	282191
Contig ID	122492_1.R1011
5'-most EST	uC-zmflMo17091b02b1
Seq. No.	282192
Contig ID	122497_1.R1011
5'-most EST	uC-zmflMo17086a09b1
Seq. No.	282193
Contig ID	122518_1.R1011
5'-most EST	uC-zmflb73122c02b2
Seq. No.	282194
Contig ID	122533_2.R1011
5'-most EST	uC-zmflMo17086d11b1
Seq. No.	282195
Contig ID	122535_1.R1011
5'-most EST	uC-zmflMo17086e01b1
Seq. No.	282196
Contig ID	122542_1.R1011
5'-most EST	uC-zmflMo17086e08b1
Method	BLASTX
NCBI GI	g4240305
BLAST score	197
E value	5.0e-15
Match length	116
% identity	37
NCBI Description	(AB020715) KIAA0908 protein [Homo sapiens]
Seq. No.	282197
Contig ID	122545_1.R1011
5'-most EST	uC-zmflm017086e11b1
Seq. No.	282198
Contig ID	122551_1.R1011
5'-most EST	vux700160217.h1
Seq. No.	282199
Contig ID	122561_1.R1011
5'-most EST	uC-zmflMo17086g05b1
Seq. No.	282200

Contig ID	122563_1.R1011
5'-most EST	uC-zmflMo17086g07b1
Method	BLASTN
NCBI GI	g3452290
BLAST score	147
E value	5.0e-77
Match length	331
% identity	87
NCBI Description	Zea mays retrotransposon Huck-1 5' LTR, partial sequence

Seq. No.	282201
Contig ID	122565_1.R1011
5'-most EST	uC-zmflMo17086g09b1
Method	BLASTN
NCBI GI	g3452300
BLAST score	88
E value	9.0e-42
Match length	242
% identity	86
NCBI Description	Zea mays retrotransposon Ji-6 5' LTR, partial sequence

Seq. No.	282202
Contig ID	122569_1.R1011
5'-most EST	uC-zmflMo17086h01b1
Method	BLASTN
NCBI GI	g2668739
BLAST score	94
E value	2.0e-45
Match length	158
% identity	91
NCBI Description	Zea mays translation initiation factor GOS2 (TIF) mRNA, complete cds

Seq. No.	282203
Contig ID	122570_1.R1011
5'-most EST	uC-zmflm017086h05b1
Method	BLASTX
NCBI GI	g2765817
BLAST score	273
E value	3.0e-42
Match length	134
% identity	61
NCBI Description	(Z95352) AtMlo-h1 [Arabidopsis thaliana] >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No.	282204
Contig ID	122611_1.R1011
5'-most EST	uC-zmflmo17330e04b1
Method	BLASTX
NCBI GI	g461812
BLAST score	351
E value	7.0e-54
Match length	222
% identity	47
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)

Cytochrome P-450 protein [Catharanthus roseus]
>gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	282205
Contig ID	122617_1.R1011
5'-most EST	uC-zmflb73131b04b2

Seq. No.	282206
Contig ID	122624_1.R1011
5'-most EST	dyk700104559.h1
Method	BLASTX
NCBI GI	g4539335
BLAST score	644
E value	3.0e-67
Match length	229
% identity	55
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	282207
Contig ID	122640_1.R1011
5'-most EST	gct701175050.h1

Seq. No.	282208
Contig ID	122646_1.R1011
5'-most EST	uC-zmflMo17089a10b1

Seq. No.	282209
Contig ID	122650_1.R1011
5'-most EST	uC-zmflm017089b02b1
Method	BLASTX
NCBI GI	g2286200
BLAST score	423
E value	1.0e-41
Match length	105
% identity	77
NCBI Description	(AF010578) polynucleotide phosphorylase [Pisum sativum]

Seq. No.	282210
Contig ID	122650_2.R1011
5'-most EST	xjt700092427.h1
Method	BLASTX
NCBI GI	g2286200
BLAST score	695
E value	2.0e-73
Match length	169
% identity	78
NCBI Description	(AF010578) polynucleotide phosphorylase [Pisum sativum]

Seq. No.	282211
Contig ID	122650_4.R1011
5'-most EST	pmx700087250.h1
Method	BLASTX
NCBI GI	g2286200
BLAST score	311
E value	7.0e-29
Match length	94

% identity 65
NCBI Description (AF010578) polynucleotide phosphorylase [Pisum sativum]

Seq. No. 282212
Contig ID 122655_1.R1011
5'-most EST uC-zmflm017089b07b1

Seq. No. 282213
Contig ID 122662_1.R1011
5'-most EST uC-zmflMo17089c02b1

Seq. No. 282214
Contig ID 122663_1.R1011
5'-most EST uC-zmflm017089c03b1

Seq. No. 282215
Contig ID 122665_1.R1011
5'-most EST uC-zmflm017089c05b1

Seq. No. 282216
Contig ID 122667_1.R1011
5'-most EST uC-zmflmo17118d08b1
Method BLASTX
NCBI GI g2827536
BLAST score 223
E value 6.0e-18
Match length 123
% identity 40
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 282217
Contig ID 122676_1.R1011
5'-most EST wyr700237160.h1

Seq. No. 282218
Contig ID 122690_1.R1011
5'-most EST uC-zmflm017089e10b1

Seq. No. 282219
Contig ID 122692_1.R1011
5'-most EST uC-zmflm017089e12b1
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 282220
Contig ID 122693_1.R1011
5'-most EST uC-zmflm017089f01b1

Seq. No. 282221
Contig ID 122695_1.R1011
5'-most EST uC-zmflMo17089f03b1
Method BLASTX

NCBI GI g2191187
BLAST score 175
E value 2.0e-12
Match length 137
% identity 18
NCBI Description (AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]

Seq. No. 282222
Contig ID 122696_1.R1011
5'-most EST uC-zmflm017089f04b1

Seq. No. 282223
Contig ID 122699_1.R1011
5'-most EST uC-zmflm017089f08b1
Method BLASTX
NCBI GI g3402719
BLAST score 259
E value 7.0e-25
Match length 131
% identity 47
NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No. 282224
Contig ID 122713_2.R1011
5'-most EST wyr700239554.h1
Method BLASTN
NCBI GI g717080
BLAST score 135
E value 1.0e-69
Match length 365
% identity 85
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (GapC4) gene, promoter region

Seq. No. 282225
Contig ID 122713_3.R1011
5'-most EST uC-zmflmo17263h03b1

Seq. No. 282226
Contig ID 122713_5.R1011
5'-most EST uC-zmflb73109a03a1

Seq. No. 282227
Contig ID 122716_1.R1011
5'-most EST uC-zmflMo17093e10b1
Method BLASTX
NCBI GI g4581203
BLAST score 267
E value 4.0e-23
Match length 100
% identity 49
NCBI Description (Y17912) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No. 282228
Contig ID 122720_1.R1011

5'-most EST	uC-zmflm017089h09b1
Seq. No.	282229
Contig ID	122727_1.R1011
5'-most EST	uC-zmflmo17329f01a1
Seq. No.	282230
Contig ID	122732_1.R1011
5'-most EST	uC-zmflMo17091b01b1
Method	BLASTX
NCBI GI	g1869901
BLAST score	275
E value	4.0e-24
Match length	126
% identity	34
NCBI Description	(X99699) XIAP associated factor-1 (ZAP-1) [Homo sapiens]
Seq. No.	282231
Contig ID	122739_1.R1011
5'-most EST	uC-zmflMo17091b10b1
Method	BLASTX
NCBI GI	g2117303
BLAST score	524
E value	2.0e-53
Match length	169
% identity	56
NCBI Description	(Z95620) n-acetylglucosaminyl-phosphatidylinositol [Schizosaccharomyces pombe]
Seq. No.	282232
Contig ID	122744_1.R1011
5'-most EST	wyr700241792.h1
Method	BLASTX
NCBI GI	g2443887
BLAST score	192
E value	8.0e-31
Match length	145
% identity	47
NCBI Description	(AC002294) Similar to transcription factor gb_Z46606_1658307 and others [Arabidopsis thaliana]
Seq. No.	282233
Contig ID	122745_1.R1011
5'-most EST	uC-zmflMo17091c08b1
Method	BLASTX
NCBI GI	g4038037
BLAST score	310
E value	1.0e-29
Match length	112
% identity	61
NCBI Description	(AC005936) hypothetical protein [Arabidopsis thaliana]
Seq. No.	282234
Contig ID	122749_1.R1011
5'-most EST	uC-zmflMo17091d01b1
Method	BLASTX
NCBI GI	g3004549

BLAST score 154
E value 3.0e-10
Match length 79
% identity 44
NCBI Description (AC003673) unknown protein [Arabidopsis thaliana] >gi_4185152 (AC005724) unknown protein [Arabidopsis thaliana]

Seq. No. 282235
Contig ID 122760_1.R1011
5'-most EST ymt700223453.h1

Seq. No. 282236
Contig ID 122795_1.R1011
5'-most EST uC-zmflm017092b04b1
Method BLASTX
NCBI GI g2342683
BLAST score 419
E value 4.0e-41
Match length 147
% identity 56
NCBI Description (AC000106) Contains similarity to Bos beta-mannosidase (gb_U46067). [Arabidopsis thaliana]

Seq. No. 282237
Contig ID 122800_1.R1011
5'-most EST uC-zmflMo17092b09b1

Seq. No. 282238
Contig ID 122802_1.R1011
5'-most EST uC-zmflMo17092b12b1

Seq. No. 282239
Contig ID 122811_1.R1011
5'-most EST uC-zmflMo17092c09b1

Seq. No. 282240
Contig ID 122817_1.R1011
5'-most EST uC-zmflm017092d10b1

Seq. No. 282241
Contig ID 122817_2.R1011
5'-most EST uC-zmflmo17158d10a1

Seq. No. 282242
Contig ID 122828_1.R1011
5'-most EST clt700045759.f1

Seq. No. 282243
Contig ID 122837_1.R1011
5'-most EST uC-zmflMo17092f04b1

Seq. No. 282244
Contig ID 122838_1.R1011
5'-most EST uC-zmflMo17092f05b1

Seq. No. 282245

Contig ID 122840_1.R1011
5'-most EST uC-zmflm017092f08b1

Seq. No. 282246
Contig ID 122845_1.R1011
5'-most EST uC-zmflMo17092g04b1

Seq. No. 282247
Contig ID 122853_1.R1011
5'-most EST uC-zmflMo17092h04b1
Method BLASTX
NCBI GI g2832642
BLAST score 559
E value 5.0e-57
Match length 314
% identity 42
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 282248
Contig ID 122857_1.R1011
5'-most EST uC-zmflMo17092h10b1

Seq. No. 282249
Contig ID 122868_1.R1011
5'-most EST uC-zmflMo17093a10b1

Seq. No. 282250
Contig ID 122869_1.R1011
5'-most EST uC-zmflMo17093a11b1

Seq. No. 282251
Contig ID 122873_1.R1011
5'-most EST uC-zmflMo17093b03b1

Seq. No. 282252
Contig ID 122876_1.R1011
5'-most EST uC-zmflMo17093b06b1
Method BLASTX
NCBI GI g4559372
BLAST score 145
E value 2.0e-11
Match length 77
% identity 51
NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana] >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No. 282253
Contig ID 122883_1.R1011
5'-most EST uC-zmflm017093c02b1

Seq. No. 282254
Contig ID 122891_1.R1011
5'-most EST uC-zmflmo17022e01b1

Seq. No. 282255
Contig ID 122894_1.R1011

5'-most EST	uC-zmflMo17093d04b1
Seq. No.	282256
Contig ID	122903_1.R1011
5'-most EST	uC-zmflMo17093e03b1
Seq. No.	282257
Contig ID	122908_1.R1011
5'-most EST	dyk700102512.h1
Method	BLASTX
NCBI GI	g4008008
BLAST score	174
E value	3.0e-12
Match length	49
% identity	67
NCBI Description	(AF084035) receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	282258
Contig ID	122911_1.R1011
5'-most EST	uC-zmflm017093f01b1
Seq. No.	282259
Contig ID	122912_1.R1011
5'-most EST	uC-zmflMo17093f02b1
Method	BLASTX
NCBI GI	g3249077
BLAST score	298
E value	3.0e-32
Match length	123
% identity	56
NCBI Description	(AC004473) Similar to prunasin hydrolase precursor gb_U50201 from Prunus serotina. ESTs gb_T21225 and gb_AA586305 come from this gene. [Arabidopsis thaliana]
Seq. No.	282260
Contig ID	122916_1.R1011
5'-most EST	uC-zmflMo17093f06b1
Method	BLASTX
NCBI GI	g2108252
BLAST score	451
E value	7.0e-45
Match length	105
% identity	81
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.	282261
Contig ID	122917_1.R1011
5'-most EST	uC-zmflMo17093f07b1
Method	BLASTX
NCBI GI	g3043694
BLAST score	383
E value	8.0e-37
Match length	163

% identity	48
NCBI Description	(AB011157) KIAA0585 protein [Homo sapiens]

Seq. No.	282262
Contig ID	122924_1.R1011
5'-most EST	uC-zmflMo17093g05b1

Seq. No.	282263
Contig ID	122936_1.R1011
5'-most EST	uC-zmflMo17093h05b1
Method	BLASTX
NCBI GI	g4033735
BLAST score	147
E value	4.0e-09
Match length	127
% identity	35
NCBI Description	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No.	282264
Contig ID	123109_1.R1011
5'-most EST	uC-zmflmo17181c07b1

Seq. No.	282265
Contig ID	123117_1.R1011
5'-most EST	uC-zmflm017025a11b1
Method	BLASTX
NCBI GI	g3785975
BLAST score	452
E value	6.0e-45
Match length	166
% identity	60
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282266
Contig ID	123131_1.R1011
5'-most EST	uC-zmflm017025c02b1
Method	BLASTX
NCBI GI	g3219786
BLAST score	235
E value	2.0e-19
Match length	149
% identity	38
NCBI Description	PEPTIDYLPROLYL ISOMERASE CYP-1 (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_984562 (L37292) peptidylprolyl isomerase [Brugia malayi] >gi_1583559_prf__2121248A cyclophilin [Brugia malayi]

Seq. No.	282267
Contig ID	123144_1.R1011
5'-most EST	uC-zmflm017025d05b1

Seq. No.	282268
Contig ID	123152_1.R1011
5'-most EST	uC-zmflm017025e02b1
Method	BLASTX
NCBI GI	g2589164
BLAST score	701

E value	3.0e-74
Match length	163
% identity	83
NCBI Description	(D88452) aldehyde oxidase-2 [Zea mays]

Seq. No.	282269
Contig ID	123153_1.R1011
5'-most EST	uC-zmflmo17027e03a1
Method	BLASTX
NCBI GI	g3395431
BLAST score	520
E value	1.0e-52
Match length	249
% identity	47
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	282270
Contig ID	123155_1.R1011
5'-most EST	uC-zmflm017025e05b1

Seq. No.	282271
Contig ID	123156_1.R1011
5'-most EST	uC-zmflm017025e06b1

Seq. No.	282272
Contig ID	123162_1.R1011
5'-most EST	uC-zmflm017025e12b1

Seq. No.	282273
Contig ID	123166_1.R1011
5'-most EST	uC-zmflm017025f04b1

Seq. No.	282274
Contig ID	123168_1.R1011
5'-most EST	uC-zmflm017025f06b1

Seq. No.	282275
Contig ID	123175_1.R1011
5'-most EST	ntr700076883.h1

Seq. No.	282276
Contig ID	123189_1.R1011
5'-most EST	uC-zmflmo17041e10b1
Method	BLASTX
NCBI GI	g2632254
BLAST score	149
E value	3.0e-09
Match length	111
% identity	31
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	282277
Contig ID	123216_1.R1011
5'-most EST	uC-zmroteosinte094e08b2
Method	BLASTX
NCBI GI	g3850569
BLAST score	271

E value	1.0e-23
Match length	98
% identity	50
NCBI Description	(AC005278) ESTs gb_T21276, gb_T45403, and gb_AA586113 come from this gene. [Arabidopsis thaliana]

Seq. No.	282278
Contig ID	123217_1.R1011
5'-most EST	uC-zmflm017026c03b1
Method	BLASTX
NCBI GI	g4102600
BLAST score	716
E value	6.0e-76
Match length	160
% identity	85
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	282279
Contig ID	123238_1.R1011
5'-most EST	uC-zmflm017026e03b1

Seq. No.	282280
Contig ID	123246_1.R1011
5'-most EST	uC-zmflm017026e12b1

Seq. No.	282281
Contig ID	123250_1.R1011
5'-most EST	xmt700258289.h1

Seq. No.	282282
Contig ID	123260_1.R1011
5'-most EST	uC-zmflb73280g01b2

Seq. No.	282283
Contig ID	123365_1.R1011
5'-most EST	uC-zmflmo17045g08b1
Method	BLASTN
NCBI GI	g22332
BLAST score	329
E value	0.0e+00
Match length	415
% identity	95
NCBI Description	Z.mays HRGP gene

Seq. No.	282284
Contig ID	123653_1.R1011
5'-most EST	uC-zmflm017092e07b1
Method	BLASTX
NCBI GI	g3549654
BLAST score	307
E value	8.0e-28
Match length	107
% identity	62
NCBI Description	(AL031394) metal-transporting P-type ATPase (fragment) [Arabidopsis thaliana]

Seq. No. 282285

Contig ID	123680_1.R1011
5'-most EST	vux700161622.h1
Seq. No.	282286
Contig ID	123789_1.R1011
5'-most EST	uC-zmflm017205d01b1
Seq. No.	282287
Contig ID	123801_1.R1011
5'-most EST	uC-zmflm017205e02b1
Seq. No.	282288
Contig ID	123801_2.R1011
5'-most EST	uC-zmflb73004c03a1
Seq. No.	282289
Contig ID	123828_1.R1011
5'-most EST	uC-zmflmo17050b08b2
Method	BLASTN
NCBI GI	g3821780
BLAST score	34
E value	4.0e-09
Match length	34
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	282290
Contig ID	123837_1.R1011
5'-most EST	uC-zmflm017205h05b1
Method	BLASTX
NCBI GI	g2623246
BLAST score	282
E value	3.0e-25
Match length	65
% identity	88
NCBI Description	(AF030709) poly(A) polymerase [Pisum sativum]
Seq. No.	282291
Contig ID	123839_1.R1011
5'-most EST	uC-zmflmo17097c05b1
Seq. No.	282292
Contig ID	123843_1.R1011
5'-most EST	uC-zmflm017205h11b1
Method	BLASTX
NCBI GI	g2746079
BLAST score	1028
E value	1.0e-112
Match length	305
% identity	68
NCBI Description	(AF015310) BTH1 [Brassica napus]
Seq. No.	282293
Contig ID	123843_2.R1011
5'-most EST	pmx700081919.h1
Method	BLASTX
NCBI GI	g2746079

BLAST score	480
E value	2.0e-48
Match length	154
% identity	60
NCBI Description	(AF015310) BTH1 [Brassica napus]

Seq. No.	282294
Contig ID	123865_1.R1011
5'-most EST	uC-zmflm017207b11b1
Method	BLASTX
NCBI GI	g2262107
BLAST score	856
E value	3.0e-92
Match length	194
% identity	81
NCBI Description	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	282295
Contig ID	123869_1.R1011
5'-most EST	uC-zmflm017207c03b1

Seq. No.	282296
Contig ID	123884_1.R1011
5'-most EST	uC-zmflm017207d07b1
Method	BLASTX
NCBI GI	g1553133
BLAST score	174
E value	2.0e-12
Match length	158
% identity	14
NCBI Description	(U64722) actin-fragmin kinase [Physarum polycephalum]

Seq. No.	282297
Contig ID	123885_1.R1011
5'-most EST	afb700380835.h1
Method	BLASTX
NCBI GI	g2997684
BLAST score	216
E value	4.0e-17
Match length	83
% identity	49
NCBI Description	(AF053302) putative transcriptional co-activator [Arabidopsis thaliana]

Seq. No.	282298
Contig ID	123891_1.R1011
5'-most EST	uC-zmflm017207e02b1
Method	BLASTX
NCBI GI	g4325282
BLAST score	551
E value	2.0e-56
Match length	180
% identity	59
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	282299
Contig ID	123899_1.R1011
5'-most EST	uC-zmflm017207e10b1

Seq. No.	282300
Contig ID	123901_1.R1011
5'-most EST	cyk700049193.f1
Method	BLASTX
NCBI GI	g2708749
BLAST score	220
E value	1.0e-17
Match length	107
% identity	49
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No.	282301
Contig ID	123901_2.R1011
5'-most EST	uC-zmflmo17078c08b1
Method	BLASTX
NCBI GI	g2708749
BLAST score	197
E value	5.0e-15
Match length	127
% identity	41
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No.	282302
Contig ID	123901_3.R1011
5'-most EST	xdb700340816.h1
Method	BLASTX
NCBI GI	g2708749
BLAST score	143
E value	4.0e-09
Match length	91
% identity	45
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No.	282303
Contig ID	123929_1.R1011
5'-most EST	uC-zmflm017207h07b1
Method	BLASTX
NCBI GI	g4567265
BLAST score	167
E value	2.0e-11
Match length	77
% identity	45
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	282304
Contig ID	123930_1.R1011
5'-most EST	uC-zmflb73127h04b2

Seq. No.	282305

Contig ID	123939_1.R1011
5'-most EST	uC-zmflmo17163a02b1
Seq. No.	282306
Contig ID	123956_1.R1011
5'-most EST	uC-zmflb73154a01b2
Method	BLASTX
NCBI GI	g4539404
BLAST score	199
E value	6.0e-17
Match length	119
% identity	43
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]
Seq. No.	282307
Contig ID	123969_1.R1011
5'-most EST	xmt700258204.h1
Seq. No.	282308
Contig ID	123995_1.R1011
5'-most EST	uC-zmflm017209f05b1
Seq. No.	282309
Contig ID	123999_1.R1011
5'-most EST	uC-zmflmo17019h09a1
Seq. No.	282310
Contig ID	124019_1.R1011
5'-most EST	uC-zmflmo17179b03a1
Seq. No.	282311
Contig ID	124019_2.R1011
5'-most EST	uC-zmflm017209h06b1
Seq. No.	282312
Contig ID	124034_1.R1011
5'-most EST	uC-zmflm017211a11b1
Seq. No.	282313
Contig ID	124039_1.R1011
5'-most EST	uC-zmflm017211b04b1
Seq. No.	282314
Contig ID	124049_1.R1011
5'-most EST	uC-zmflm017211c03b1
Seq. No.	282315
Contig ID	124052_1.R1011
5'-most EST	uC-zmflm017211c06b1
Seq. No.	282316
Contig ID	124062_1.R1011
5'-most EST	uC-zmflm017211d06b1
Seq. No.	282317
Contig ID	124069_1.R1011
5'-most EST	uC-zmflm017211e01b1

Seq. No.	282318
Contig ID	124071_1.R1011
5'-most EST	ntr700074292.h1

Seq. No.	282319
Contig ID	124094_1.R1011
5'-most EST	uC-zmflb73276d03a1
Method	BLASTX
NCBI GI	g3335359
BLAST score	164
E value	2.0e-11
Match length	63
% identity	51
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	282320
Contig ID	124095_1.R1011
5'-most EST	uC-zmflm017211g03b1
Method	BLASTX
NCBI GI	g2947063
BLAST score	219
E value	5.0e-30
Match length	180
% identity	42
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	282321
Contig ID	124111_1.R1011
5'-most EST	nbm700476079.h1
Method	BLASTX
NCBI GI	g3342382
BLAST score	297
E value	7.0e-27
Match length	130
% identity	52
NCBI Description	(AF059678) VIP-receptor-gene repressor protein [Rattus norvegicus]

Seq. No.	282322
Contig ID	124112_1.R1011
5'-most EST	uC-zmflm017211h11b1

Seq. No.	282323
Contig ID	124124_1.R1011
5'-most EST	uC-zmflm017212a11b1

Seq. No.	282324
Contig ID	124125_1.R1011
5'-most EST	uC-zmflm017212a12b1

Seq. No.	282325
Contig ID	124130_1.R1011
5'-most EST	uC-zmflm017212b06b1

Seq. No. 282326

Contig ID	124169_1.R1011
5'-most EST	xyt700347304.h1
Seq. No.	282327
Contig ID	124187_1.R1011
5'-most EST	xsy700210761.h1
Method	BLASTX
NCBI GI	g1617268
BLAST score	322
E value	3.0e-35
Match length	118
% identity	58
NCBI Description	(Z72153) acyl CoA synthetase [Brassica napus]
Seq. No.	282328
Contig ID	124202_1.R1011
5'-most EST	uC-zmflb73297f05a1
Seq. No.	282329
Contig ID	124202_2.R1011
5'-most EST	uC-zmflm017214a04b1
Seq. No.	282330
Contig ID	124220_1.R1011
5'-most EST	uC-zmflm017214c02b1
Method	BLASTX
NCBI GI	g2660669
BLAST score	326
E value	2.0e-37
Match length	169
% identity	56
NCBI Description	(AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]
Seq. No.	282331
Contig ID	124232_1.R1011
5'-most EST	uC-zmflmo17267b02b1
Seq. No.	282332
Contig ID	124242_1.R1011
5'-most EST	uC-zmflm017214e04b1
Seq. No.	282333
Contig ID	124254_1.R1011
5'-most EST	uC-zmflm017214f05b1
Method	BLASTX
NCBI GI	g4506043
BLAST score	323
E value	1.0e-32
Match length	154
% identity	48
NCBI Description	prolyl endopeptidase >gi_1346769_sp_P48147_PPCE_HUMAN PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase [Homo sapiens]

Seq. No.	282334
Contig ID	124256_1.R1011
5'-most EST	uC-zmflm017214f07b1

Seq. No.	282335
Contig ID	124296_1.R1011
5'-most EST	uC-zmflm017233b03b1

Seq. No.	282336
Contig ID	124299_1.R1011
5'-most EST	uC-zmroteosinte105d09b1
Method	BLASTX
NCBI GI	g2829894
BLAST score	195
E value	9.0e-15
Match length	121
% identity	53
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	282337
Contig ID	124305_1.R1011
5'-most EST	xay700053548.r1
Method	BLASTN
NCBI GI	g168436
BLAST score	55
E value	6.0e-22
Match length	188
% identity	87
NCBI Description	Zea mays catalase (Cat3) gene, complete cds

Seq. No.	282338
Contig ID	124325_1.R1011
5'-most EST	uC-zmflm017233d09b1

Seq. No.	282339
Contig ID	124330_1.R1011
5'-most EST	uC-zmroteosinte028b01b1
Method	BLASTX
NCBI GI	g3914212
BLAST score	877
E value	2.0e-94
Match length	281
% identity	61
NCBI Description	5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE) >gi_1732065 (U70825) 5-oxo-L-prolinase [Rattus norvegicus]

Seq. No.	282340
Contig ID	124331_1.R1011
5'-most EST	uC-zmflm017233e04b1
Method	BLASTX
NCBI GI	g465737
BLAST score	160
E value	3.0e-10
Match length	113
% identity	31
NCBI Description	HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III

>gi_630510_pir__S44606 C02F5.4 protein - Caenorhabditis elegans >gi_289611 (L14745) coded for by C. elegans cDNA GenBank:CEL16D4 (M89109); putative [Caenorhabditis elegans]

Seq. No.	282341
Contig ID	124342_1.R1011
5'-most EST	uC-zmflmo17266h05b1

Seq. No.	282342
Contig ID	124372_1.R1011
5'-most EST	uC-zmflm017233h12b1

Seq. No.	282343
Contig ID	124404_1.R1011
5'-most EST	fwa700097845.h1
Method	BLASTX
NCBI GI	g4309969
BLAST score	254
E value	1.0e-21
Match length	124
% identity	43
NCBI Description	(AC002983) putative phosphoglyceride transfer protein [Arabidopsis thaliana]

Seq. No.	282344
Contig ID	124456_1.R1011
5'-most EST	uC-zmflmo17001h01b1
Method	BLASTX
NCBI GI	g4210504
BLAST score	496
E value	4.0e-50
Match length	165
% identity	57
NCBI Description	(AC002392) putative cadmium-transporting ATPase [Arabidopsis thaliana]

Seq. No.	282345
Contig ID	124487_1.R1011
5'-most EST	ceu700426913.h1
Method	BLASTX
NCBI GI	g4587577
BLAST score	258
E value	3.0e-22
Match length	141
% identity	39
NCBI Description	(AC006550) F10O3.17 [Arabidopsis thaliana]

Seq. No.	282346
Contig ID	124498_1.R1011
5'-most EST	vux700158274.h1

Seq. No.	282347
Contig ID	124500_1.R1011
5'-most EST	uC-zmflmo170112d07b1

Seq. No.	282348
Contig ID	124502_1.R1011

5'-most EST	uC-zmflb73213g10b1
Seq. No.	282349
Contig ID	124507_1.R1011
5'-most EST	uC-zmflmo170112e03b1
Method	BLASTX
NCBI GI	g2961371
BLAST score	196
E value	5.0e-15
Match length	139
% identity	38
NCBI Description	(AL022141) hypothetical protein (fragment) [Arabidopsis thaliana]
Seq. No.	282350
Contig ID	124522_1.R1011
5'-most EST	uC-zmflb73029d09a1
Method	BLASTX
NCBI GI	g4455300
BLAST score	1290
E value	1.0e-143
Match length	273
% identity	83
NCBI Description	(AL035528) putative pectate lyase A11 (fragment) [Arabidopsis thaliana]
Seq. No.	282351
Contig ID	124540_1.R1011
5'-most EST	rvl700457619.h1
Method	BLASTX
NCBI GI	g2231149
BLAST score	789
E value	2.0e-84
Match length	169
% identity	91
NCBI Description	(L81152) integral membrane protein [Oryza sativa]
Seq. No.	282352
Contig ID	124557_1.R1011
5'-most EST	uC-zmflmo17113b05b1
Seq. No.	282353
Contig ID	124570_1.R1011
5'-most EST	uC-zmflmo17113c10b1
Method	BLASTX
NCBI GI	g3647182
BLAST score	268
E value	8.0e-23
Match length	155
% identity	37
NCBI Description	(AL031178) dJ341E18.2.1 (novel PUTATIVE protein) (isoform 1) [Homo sapiens]
Seq. No.	282354
Contig ID	124570_2.R1011
5'-most EST	uC-zmflmo17336g07b1

Seq. No.	282355
Contig ID	124576_1.R1011
5'-most EST	uC-zmflb73301d12b2

Seq. No.	282356
Contig ID	124578_1.R1011
5'-most EST	uC-zmflmo17292e05b1

Seq. No.	282357
Contig ID	124580_1.R1011
5'-most EST	uC-zmflmo17113d12b1

Seq. No.	282358
Contig ID	124588_1.R1011
5'-most EST	uC-zmflmo17113e12b1

Seq. No.	282359
Contig ID	124603_1.R1011
5'-most EST	uC-zmflmo17113g11b1
Method	BLASTX
NCBI GI	g4580462
BLAST score	442
E value	1.0e-43
Match length	212
% identity	43
NCBI Description	(AC006081) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282360
Contig ID	124605_1.R1011
5'-most EST	uC-zmflmo17113h04b1
Method	BLASTX
NCBI GI	g4097547
BLAST score	155
E value	4.0e-10
Match length	68
% identity	47
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	282361
Contig ID	124606_1.R1011
5'-most EST	uC-zmflmo17113h05b1

Seq. No.	282362
Contig ID	124608_1.R1011
5'-most EST	uC-zmflmo17113h08b1

Seq. No.	282363
Contig ID	124637_1.R1011
5'-most EST	uC-zmflmo170114c05b1

Seq. No.	282364
Contig ID	124679_1.R1011
5'-most EST	gct701170926.h1
Method	BLASTX
NCBI GI	g2245131
BLAST score	417
E value	9.0e-41

Match length	210
% identity	44
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282365
Contig ID	124694_1.R1011
5'-most EST	uC-zmflmo17011a04b1

Seq. No.	282366
Contig ID	124703_1.R1011
5'-most EST	uC-zmflmo17011b01b1

Seq. No.	282367
Contig ID	124717_1.R1011
5'-most EST	uC-zmflb73172g05b2

Seq. No.	282368
Contig ID	124745_1.R1011
5'-most EST	uC-zmflmo17011f01b1

Seq. No.	282369
Contig ID	124768_2.R1011
5'-most EST	nbm700473014.h1

Seq. No.	282370
Contig ID	124773_1.R1011
5'-most EST	ntr700073101.h1

Seq. No.	282371
Contig ID	124774_1.R1011
5'-most EST	uC-zmflmo17023g11b1
Method	BLASTX
NCBI GI	g2104949
BLAST score	389
E value	1.0e-37
Match length	90
% identity	82
NCBI Description	(U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	282372
Contig ID	125055_1.R1011
5'-most EST	xjt700094942.h1

Seq. No.	282373
Contig ID	125062_1.R1011
5'-most EST	xsy700208863.h1
Method	BLASTX
NCBI GI	g3876622
BLAST score	241
E value	5.0e-20
Match length	96
% identity	45
NCBI Description	(Z81523) Similarity to Yeast SOH-1 protein (SW:P38633) [Caenorhabditis elegans]

Seq. No.	282374
Contig ID	125100_1.R1011

5'-most EST	uC-zmflmo17017f11b1
Seq. No.	282375
Contig ID	125120_1.R1011
5'-most EST	uC-zmflmo17017h08b1
Method	BLASTX
NCBI GI	g2961387
BLAST score	216
E value	3.0e-18
Match length	108
% identity	51
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]
Seq. No.	282376
Contig ID	125142_1.R1011
5'-most EST	wty700171549.h1
Seq. No.	282377
Contig ID	125146_1.R1011
5'-most EST	uC-zmflmo17020c03b1
Seq. No.	282378
Contig ID	125152_1.R1011
5'-most EST	uC-zmflmo17020c09b1
Seq. No.	282379
Contig ID	125152_2.R1011
5'-most EST	fdz701161342.h1
Seq. No.	282380
Contig ID	125164_1.R1011
5'-most EST	uC-zmflmo17155a05b1
Seq. No.	282381
Contig ID	125172_1.R1011
5'-most EST	lhp700053367.r1
Seq. No.	282382
Contig ID	125175_1.R1011
5'-most EST	uC-zmflmo17020e11b1
Method	BLASTX
NCBI GI	g2191168
BLAST score	387
E value	4.0e-37
Match length	170
% identity	46
NCBI Description	(AF007270) contains similarity to myosin heavy chain [Arabidopsis thaliana]
Seq. No.	282383
Contig ID	125188_1.R1011
5'-most EST	uC-zmflmo17199c06b1
Seq. No.	282384
Contig ID	125191_1.R1011
5'-most EST	hbs701182828.h1

Seq. No.	282385
Contig ID	125205_1.R1011
5'-most EST	dyk700106040.h1
Method	BLASTX
NCBI GI	g3913808
BLAST score	616
E value	3.0e-64
Match length	137
% identity	87
NCBI Description	FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120) ferrochelatase [Oryza sativa]

Seq. No.	282386
Contig ID	125218_1.R1011
5'-most EST	uC-zmflmo17021a12b1

Seq. No.	282387
Contig ID	125230_1.R1011
5'-most EST	uC-zmflmo17021c04b1

Seq. No.	282388
Contig ID	125231_1.R1011
5'-most EST	uC-zmflmo17021c05b1
Method	BLASTX
NCBI GI	g4586260
BLAST score	171
E value	7.0e-12
Match length	93
% identity	44
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	282389
Contig ID	125234_1.R1011
5'-most EST	uC-zmflmo17021c08b1

Seq. No.	282390
Contig ID	125235_1.R1011
5'-most EST	uC-zmflmo17021c09b1

Seq. No.	282391
Contig ID	125240_2.R1011
5'-most EST	xmt700262806.h1
Method	BLASTX
NCBI GI	g1084415
BLAST score	154
E value	3.0e-10
Match length	52
% identity	58
NCBI Description	RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_ (D26182) RNA-binding glycine rich protein (RGP-2) [Nicotiana sylvestris]

Seq. No.	282392
Contig ID	125249_1.R1011
5'-most EST	uC-zmflmo17021e01b1
Method	BLASTX

NCBI GI	g4510395
BLAST score	713
E value	3.0e-75
Match length	196
% identity	63
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	282393
Contig ID	125259_1.R1011
5'-most EST	pmx700088564.h1
Method	BLASTX
NCBI GI	g3157932
BLAST score	301
E value	3.0e-27
Match length	86
% identity	63
NCBI Description	(AC002131) Similar to hypothetical protein HYP1 gb_Z97338 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	282394
Contig ID	125307_1.R1011
5'-most EST	uC-zmflmo17037e05a1
Method	BLASTX
NCBI GI	g4455227
BLAST score	386
E value	5.0e-37
Match length	100
% identity	74
NCBI Description	(AL035440) SNF8 like protein [Arabidopsis thaliana]

Seq. No.	282395
Contig ID	125314_1.R1011
5'-most EST	uC-zmflmo17161e07b1
Method	BLASTX
NCBI GI	g2443881
BLAST score	522
E value	5.0e-53
Match length	139
% identity	43
NCBI Description	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]

Seq. No.	282396
Contig ID	125316_1.R1011
5'-most EST	uC-zmflmo17022b12b1
Method	BLASTN
NCBI GI	g1864000
BLAST score	189
E value	1.0e-102
Match length	197
% identity	99
NCBI Description	Maize DNA for Fd III, complete cds

Seq. No.	282397
Contig ID	125320_1.R1011
5'-most EST	uC-zmflmo17022c04b1

Method	BLASTX
NCBI GI	g3122070
BLAST score	145
E value	6.0e-09
Match length	76
% identity	42
NCBI Description	ELONGATION FACTOR 1-ALPHA 2 (EF-1-ALPHA-2) >gi_886061 (U26267) translation elongation factor EF-1alpha [Euplotes crassus]

Seq. No.	282398
Contig ID	125343_1.R1011
5'-most EST	uC-zmflmo17022e06b1

Seq. No.	282399
Contig ID	125344_1.R1011
5'-most EST	ymt700223836.h1
Method	BLASTX
NCBI GI	g4587572
BLAST score	809
E value	3.0e-86
Match length	251
% identity	60
NCBI Description	(AC006550) Similar to gb_U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF_00400 WD40, G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from this gene. [Arabidopsis thaliana]

Seq. No.	282400
Contig ID	125351_1.R1011
5'-most EST	uC-zmflmo17022f02b1
Method	BLASTX
NCBI GI	g1946361
BLAST score	195
E value	6.0e-15
Match length	88
% identity	51
NCBI Description	(U93215) C3HC4 zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	282401
Contig ID	125356_1.R1011
5'-most EST	uC-zmflmo17022f08b1
Method	BLASTX
NCBI GI	g3882018
BLAST score	305
E value	1.0e-27
Match length	137
% identity	46
NCBI Description	(Y18377) cytokinin oxidase [Zea mays]

Seq. No.	282402
Contig ID	125362_1.R1011
5'-most EST	fdz701158817.h1
Method	BLASTX
NCBI GI	g2589162
BLAST score	694

E value	3.0e-73
Match length	199
% identity	68
NCBI Description	(D88451) aldehyde oxidase [Zea mays]

Seq. No.	282403
Contig ID	125372_1.R1011
5'-most EST	yyf700350903.h1

Seq. No.	282404
Contig ID	125376_1.R1011
5'-most EST	uC-zmflmo17022h08b1
Method	BLASTX
NCBI GI	g2266985
BLAST score	835
E value	1.0e-89
Match length	187
% identity	82
NCBI Description	(Y13943) MEtRS [Arabidopsis thaliana]

Seq. No.	282405
Contig ID	125410_1.R1011
5'-most EST	uC-zmflmo17023c08b1

Seq. No.	282406
Contig ID	125412_1.R1011
5'-most EST	uC-zmflmo17023c10b1
Method	BLASTX
NCBI GI	g78787
BLAST score	148
E value	2.0e-09
Match length	50
% identity	54
NCBI Description	proteinase II (EC 3.4.21.-) - Escherichia coli >gi_216624_dbj_BAA01750_ (D10976) protease II [Escherichia coli]

Seq. No.	282407
Contig ID	125422_1.R1011
5'-most EST	uC-zmflmo17023d08b1
Method	BLASTX
NCBI GI	g4176546
BLAST score	180
E value	9.0e-13
Match length	236
% identity	20
NCBI Description	(AL035259) possible RanBP7-importin-beta-Cse1p superfamily [Schizosaccharomyces pombe]

Seq. No.	282408
Contig ID	125448_1.R1011
5'-most EST	uC-zmflmo17023f10b1

Seq. No.	282409
Contig ID	125449_1.R1011
5'-most EST	uC-zmflmo17023f11b1

Seq. No.	282410
Contig ID	125452_1.R1011
5'-most EST	uC-zmroteosinte115g10b1
Method	BLASTX
NCBI GI	g3600036
BLAST score	242
E value	3.0e-20
Match length	134
% identity	46
NCBI Description	(AF080119) contains similarity to protein kinase domains (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]

Seq. No.	282411
Contig ID	125472_1.R1011
5'-most EST	clt700044888.f1
Method	BLASTN
NCBI GI	g3212102
BLAST score	46
E value	1.0e-16
Match length	150
% identity	83
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	282412
Contig ID	125476_1.R1011
5'-most EST	uC-zmflmo17029a07b1

Seq. No.	282413
Contig ID	125482_1.R1011
5'-most EST	uC-zmflmo17029b02b1
Method	BLASTX
NCBI GI	g1657621
BLAST score	291
E value	4.0e-26
Match length	80
% identity	68
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	282414
Contig ID	125493_1.R1011
5'-most EST	ymt700219647.h1
Method	BLASTX
NCBI GI	g4584527
BLAST score	180
E value	6.0e-13
Match length	195
% identity	29
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	282415
Contig ID	125528_1.R1011
5'-most EST	uC-zmflmo17164b04b1
Method	BLASTX
NCBI GI	g2244940
BLAST score	585

E value	3.0e-60
Match length	250
% identity	51
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282416
Contig ID	125533_1.R1011
5'-most EST	uC-zmflmo17029g06b1

Seq. No.	282417
Contig ID	125541_1.R1011
5'-most EST	xmt700261314.h1

Seq. No.	282418
Contig ID	125558_1.R1011
5'-most EST	uC-zmflmo17030b01b1
Method	BLASTX
NCBI GI	g3157945
BLAST score	254
E value	1.0e-21
Match length	96
% identity	59
NCBI Description	(AC002131) Contains similarity to axi 1 gene gb_X80301 from Nicotiana tabacum. [Arabidopsis thaliana]

Seq. No.	282419
Contig ID	125563_1.R1011
5'-most EST	uC-zmflmo17030b06b1
Method	BLASTX
NCBI GI	g4581123
BLAST score	432
E value	2.0e-42
Match length	215
% identity	48
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	282420
Contig ID	125572_1.R1011
5'-most EST	uC-zmflmo17030c03b1
Method	BLASTX
NCBI GI	g2244785
BLAST score	464
E value	3.0e-46
Match length	134
% identity	66
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282421
Contig ID	125584_1.R1011
5'-most EST	uC-zmflmo17030d04b1
Method	BLASTX
NCBI GI	g3493131
BLAST score	353
E value	2.0e-33
Match length	87
% identity	78
NCBI Description	(AF081570) thymidylate kinase [Arabidopsis thaliana]

Seq. No.	282422
Contig ID	125584_2.R1011
5'-most EST	xjt700094451.h1
Seq. No.	282423
Contig ID	125586_1.R1011
5'-most EST	nbm700475822.h1
Seq. No.	282424
Contig ID	125590_1.R1011
5'-most EST	gct701179827.h1
Method	BLASTX
NCBI GI	g2827992
BLAST score	346
E value	2.0e-32
Match length	113
% identity	54
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]
Seq. No.	282425
Contig ID	125610_1.R1011
5'-most EST	uC-zmflb73252g10b3
Method	BLASTX
NCBI GI	g3152568
BLAST score	403
E value	4.0e-39
Match length	201
% identity	48
NCBI Description	(AC002986) Similar to hypothetical protein product gb_Z97337 from A. thaliana. EST gb_H76597 comes from this gene. [Arabidopsis thaliana]
Seq. No.	282426
Contig ID	125646_1.R1011
5'-most EST	uC-zmflmo17031a12b1
Seq. No.	282427
Contig ID	125682_1.R1011
5'-most EST	cyk700052124.f1
Seq. No.	282428
Contig ID	125683_1.R1011
5'-most EST	uC-zmflmo17031e02b1
Method	BLASTX
NCBI GI	g3913366
BLAST score	282
E value	1.0e-24
Match length	244
% identity	30
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >gi_1597723 (U67422) CRINKLY4 precursor [Zea mays]
Seq. No.	282429
Contig ID	125706_1.R1011
5'-most EST	uC-zmflmo17031g03b1

Seq. No.	282430
Contig ID	125754_1.R1011
5'-most EST	uC-zmflmo17126e10b1

Seq. No.	282431
Contig ID	125770_1.R1011
5'-most EST	uC-zmflmo17035a06b1
Method	BLASTX
NCBI GI	g3193294
BLAST score	176
E value	9.0e-13
Match length	108
% identity	34
NCBI Description	(AF069298) similar to reverse transcriptases (Pfam: rvt.hmm, score: 53.76) [Arabidopsis thaliana]

Seq. No.	282432
Contig ID	125773_1.R1011
5'-most EST	xsy700209059.h1

Seq. No.	282433
Contig ID	125780_1.R1011
5'-most EST	uC-zmflmo17116f12b1
Method	BLASTX
NCBI GI	g3702691
BLAST score	608
E value	2.0e-63
Match length	137
% identity	39
NCBI Description	(AB005902) AtPIP5K1 [Arabidopsis thaliana]

Seq. No.	282434
Contig ID	125783_1.R1011
5'-most EST	yyf700350780.h1

Seq. No.	282435
Contig ID	125794_1.R1011
5'-most EST	uC-zmflb73161g05b2

Seq. No.	282436
Contig ID	125799_1.R1011
5'-most EST	uC-zmflmo17312e04b1

Seq. No.	282437
Contig ID	125800_1.R1011
5'-most EST	uC-zmflmo17035d01b1

Seq. No.	282438
Contig ID	125805_1.R1011
5'-most EST	pmx700088524.h1

Seq. No.	282439
Contig ID	125822_1.R1011
5'-most EST	uC-zmflmo17035f04b1
Method	BLASTX
NCBI GI	g4512703
BLAST score	537

E value 7.0e-55
Match length 151
% identity 71
NCBI Description (AC006569) unknown protein [Arabidopsis thaliana]

Seq. No. 282440
Contig ID 125832_1.R1011
5'-most EST uC-zmflmo17054c03b1
Method BLASTX
NCBI GI g3237273
BLAST score 398
E value 1.0e-38
Match length 126
% identity 66
NCBI Description (U59489) sucrose-phosphate synthase [Musa acuminata]

Seq. No. 282441
Contig ID 125851_1.R1011
5'-most EST fC-zmst700624311f1

Seq. No. 282442
Contig ID 125875_1.R1011
5'-most EST uC-zmflmo17036c05b2

Seq. No. 282443
Contig ID 125887_1.R1011
5'-most EST uC-zmflmo17136g06b1

Seq. No. 282444
Contig ID 125888_1.R1011
5'-most EST uC-zmflmo17036d10b2

Seq. No. 282445
Contig ID 125889_1.R1011
5'-most EST uC-zmflmo17036d11b2

Seq. No. 282446
Contig ID 125927_1.R1011
5'-most EST uC-zmflmo17036h04b2

Seq. No. 282447
Contig ID 125951_1.R1011
5'-most EST tfd700574730.h1
Method BLASTX
NCBI GI g4558673
BLAST score 225
E value 4.0e-20
Match length 85
% identity 56
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 282448
Contig ID 125975_1.R1011
5'-most EST uwc700152456.h1

Seq. No. 282449
Contig ID 125977_1.R1011

5'-most EST	uC-zmflmo17039c07b1
Seq. No.	282450
Contig ID	125986_1.R1011
5'-most EST	uC-zmflmo17037e05b1
Method	BLASTX
NCBI GI	g1065506
BLAST score	281
E value	7.0e-25
Match length	106
% identity	50
NCBI Description	(U40419) nearly identical to C. elegans predicted protein F17C8.5 (GB:Z35719) [Caenorhabditis elegans]
Seq. No.	282451
Contig ID	125995_1.R1011
5'-most EST	uC-zmflmo17344b02b1
Method	BLASTX
NCBI GI	g4218535
BLAST score	200
E value	3.0e-20
Match length	68
% identity	72
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]
Seq. No.	282452
Contig ID	126006_1.R1011
5'-most EST	uC-zmflmo17048g12b1
Seq. No.	282453
Contig ID	126010_1.R1011
5'-most EST	uC-zmflmo17037g07b1
Method	BLASTX
NCBI GI	g1076755
BLAST score	473
E value	1.0e-59
Match length	129
% identity	82
NCBI Description	protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]
Seq. No.	282454
Contig ID	126024_1.R1011
5'-most EST	uC-zmflmo17037h10b1
Seq. No.	282455
Contig ID	126026_1.R1011
5'-most EST	fC-zmle700431965a3
Seq. No.	282456
Contig ID	126063_1.R1011
5'-most EST	dyk700104622.h1
Method	BLASTX
NCBI GI	g4204759
BLAST score	298
E value	6.0e-27
Match length	99

% identity	60
NCBI Description	(U51191) peroxidase precursor [Glycine max]

Seq. No.	282457
Contig ID	126064_1.R1011
5'-most EST	uC-zmroteosinte069c11b1
Method	BLASTX
NCBI GI	g1363484
BLAST score	371
E value	4.0e-35
Match length	155
% identity	54
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415) IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	282458
Contig ID	126080_1.R1011
5'-most EST	uC-zmflmo17038e11b1
Method	BLASTX
NCBI GI	g1707412
BLAST score	463
E value	3.0e-46
Match length	130
% identity	64
NCBI Description	(X95906) Cleavage and Polyadenylation Specifity Factor protein [Bos taurus]

Seq. No.	282459
Contig ID	126094_1.R1011
5'-most EST	uC-zmflmo17038g01b1
Method	BLASTX
NCBI GI	g4115922
BLAST score	237
E value	9.0e-20
Match length	148
% identity	37
NCBI Description	(AF118222) contains similarity to ubiquitin carboxyl-terminal hydrolase family 2 (Pfam:PF00443, score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0 E=5.2e-08, N=1) [Arabidopsis thaliana]

Seq. No.	282460
Contig ID	126095_1.R1011
5'-most EST	gct701180513.h1

Seq. No.	282461
Contig ID	126113_1.R1011
5'-most EST	uC-zmflmo17038h08b1

Seq. No.	282462
Contig ID	126148_1.R1011
5'-most EST	nbm700468133.h1
Method	BLASTX
NCBI GI	g3643611
BLAST score	832
E value	2.0e-89

Match length	174
% identity	84
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	282463
Contig ID	126162_1.R1011
5'-most EST	xsy700212371.h1

Seq. No.	282464
Contig ID	126166_1.R1011
5'-most EST	uC-zmflmo17039e09b1
Method	BLASTX
NCBI GI	g2335097
BLAST score	715
E value	1.0e-75
Match length	261
% identity	14
NCBI Description	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	282465
Contig ID	126187_1.R1011
5'-most EST	uC-zmflmo17039g10b1

Seq. No.	282466
Contig ID	126195_1.R1011
5'-most EST	uC-zmflmo17039h07b1

Seq. No.	282467
Contig ID	126202_1.R1011
5'-most EST	uC-zmflmo17040a03b1
Method	BLASTX
NCBI GI	g1402916
BLAST score	451
E value	1.0e-44
Match length	218
% identity	49
NCBI Description	(X98319) peroxidase [Arabidopsis thaliana] >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a [Arabidopsis thaliana]

Seq. No.	282468
Contig ID	126211_1.R1011
5'-most EST	uC-zmflmo17040a12b1

Seq. No.	282469
Contig ID	126232_1.R1011
5'-most EST	uC-zmflmo17040c09b1

Seq. No.	282470
Contig ID	126245_1.R1011
5'-most EST	ymt700224632.h1

Seq. No.	282471
Contig ID	126247_1.R1011
5'-most EST	uC-zmflmo17040e02b1
Method	BLASTX

NCBI GI	g2462760
BLAST score	247
E value	1.0e-20
Match length	173
% identity	38
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	282472
Contig ID	126267_1.R1011
5'-most EST	cyk700049240.f1
Method	BLASTX
NCBI GI	g1314711
BLAST score	810
E value	1.0e-86
Match length	227
% identity	72
NCBI Description	(U54615) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_3068712 (AF049236) calcium dependent protein kinase [Arabidopsis thaliana]

Seq. No.	282473
Contig ID	126273_1.R1011
5'-most EST	uC-zmflb73272f07b1
Method	BLASTX
NCBI GI	g2190576
BLAST score	168
E value	1.0e-11
Match length	134
% identity	36
NCBI Description	(U75363) putative 2-hydroxycyclohexanecarboxyl-CoA dehyrogenase [Rhodopseudomonas palustris]

Seq. No.	282474
Contig ID	126275_1.R1011
5'-most EST	uC-zmflmo17040h01a1

Seq. No.	282475
Contig ID	126313_1.R1011
5'-most EST	uC-zmflmo17129g08b1
Method	BLASTX
NCBI GI	g465008
BLAST score	878
E value	8.0e-95
Match length	203
% identity	79
NCBI Description	UREASE (UREA AMIDOHYDROLASE) >gi_418642_pir__URJB urease (EC 3.5.1.5) - jack bean

Seq. No.	282476
Contig ID	126316_1.R1011
5'-most EST	uC-zmflmo17341e12a1

Seq. No.	282477
Contig ID	126319_1.R1011
5'-most EST	uC-zmflmo17041c11b1

Seq. No.	282478

Contig ID	126321_1.R1011
5'-most EST	ymt700222542.h1
Method	BLASTX
NCBI GI	g3337366
BLAST score	269
E value	2.0e-23
Match length	177
% identity	36
NCBI Description	(AC004481) unknown protein [Arabidopsis thaliana]

Seq. No.	282479
Contig ID	126419_1.R1011
5'-most EST	ceu700429626.h1

Seq. No.	282480
Contig ID	126430_1.R1011
5'-most EST	qmh700029643.f1

Seq. No.	282481
Contig ID	126456_1.R1011
5'-most EST	uC-zmflmo17042h08b1
Method	BLASTX
NCBI GI	g3063447
BLAST score	264
E value	7.0e-23
Match length	165
% identity	8
NCBI Description	(AC003981) F22O13.9 [Arabidopsis thaliana]

Seq. No.	282482
Contig ID	126475_1.R1011
5'-most EST	uC-zmflmo17043c11a1

Seq. No.	282483
Contig ID	126500_1.R1011
5'-most EST	uC-zmflmo17043g02b1
Method	BLASTX
NCBI GI	g416873
BLAST score	380
E value	2.0e-36
Match length	132
% identity	56
NCBI Description	3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH) >gi_111295_pir__A32867 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) precursor - rat (fragment) >gi_556389 (J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus norvegicus]

Seq. No.	282484
Contig ID	126504_1.R1011
5'-most EST	uwc700154837.h1
Method	BLASTX
NCBI GI	g2558664
BLAST score	147
E value	4.0e-09
Match length	50
% identity	54

NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]
Seq. No.	282485
Contig ID	126522_1.R1011
5'-most EST	uC-zmflmo17044a09b1
Method	BLASTX
NCBI GI	g2618691
BLAST score	342
E value	6.0e-32
Match length	179
% identity	42
NCBI Description	(AC002510) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.	282486
Contig ID	126526_1.R1011
5'-most EST	uC-zmflb73095a08a1
Method	BLASTX
NCBI GI	g1707642
BLAST score	280
E value	9.0e-25
Match length	59
% identity	90
NCBI Description	(Y07748) TMK [Oryza sativa]
Seq. No.	282487
Contig ID	126526_2.R1011
5'-most EST	kem700611212.h1
Seq. No.	282488
Contig ID	126540_1.R1011
5'-most EST	uC-zmflmo17201g12b1
Seq. No.	282489
Contig ID	126541_1.R1011
5'-most EST	uC-zmflmo17044c04b1
Seq. No.	282490
Contig ID	126561_1.R1011
5'-most EST	uC-zmflmo17044d12b1
Method	BLASTX
NCBI GI	g4454480
BLAST score	284
E value	5.0e-25
Match length	127
% identity	41
NCBI Description	(AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]
Seq. No.	282491
Contig ID	126562_1.R1011
5'-most EST	uC-zmflmo17312d02b1
Method	BLASTX
NCBI GI	g3355473
BLAST score	199
E value	7.0e-15
Match length	237

% identity	31
NCBI Description	(AC004218) hypothetical protein [Arabidopsis thaliana]
Seq. No.	282492
Contig ID	126565_1.R1011
5'-most EST	uC-zmflmo17156g06b1
Seq. No.	282493
Contig ID	126583_1.R1011
5'-most EST	tfd700572341.h1
Method	BLASTX
NCBI GI	g3298474
BLAST score	950
E value	1.0e-103
Match length	192
% identity	97
NCBI Description	(AB012765) ovp1 [Oryza sativa]
Seq. No.	282494
Contig ID	126583_2.R1011
5'-most EST	ymt700220713.h1
Method	BLASTX
NCBI GI	g3298474
BLAST score	416
E value	6.0e-41
Match length	81
% identity	98
NCBI Description	(AB012765) ovp1 [Oryza sativa]
Seq. No.	282495
Contig ID	126596_1.R1011
5'-most EST	uC-zmflb73258e02b3
Method	BLASTX
NCBI GI	g133443
BLAST score	1050
E value	1.0e-115
Match length	241
% identity	88
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA" CHAIN >gi_66987_pir__RNZMB2 DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - maize chloroplast >gi_12482_emb_CAA35197_ (X17318) RNA polymerase beta-2 subunit (AA 1-1527) [Zea mays] >gi_902214_emb_CAA60278_ (X86563) RNA polymerase beta' subunit-2 [Zea mays]
Seq. No.	282496
Contig ID	126603_1.R1011
5'-most EST	fdz701164876.h1
Seq. No.	282497
Contig ID	126604_1.R1011
5'-most EST	uC-zmflmo17044h10b1
Method	BLASTX
NCBI GI	g4530126
BLAST score	370
E value	3.0e-35
Match length	186

% identity	44
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]
Seq. No.	282498
Contig ID	126610_1.R1011
5'-most EST	uC-zmflmo17099g08b1
Seq. No.	282499
Contig ID	126628_1.R1011
5'-most EST	uC-zmflmo17045c03b1
Seq. No.	282500
Contig ID	126631_1.R1011
5'-most EST	nbm700466983.h1
Seq. No.	282501
Contig ID	126638_2.R1011
5'-most EST	ceu700422144.h1
Seq. No.	282502
Contig ID	126649_1.R1011
5'-most EST	gct701168479.h1
Seq. No.	282503
Contig ID	126667_1.R1011
5'-most EST	uC-zmflmo17045f09b1
Seq. No.	282504
Contig ID	126689_1.R1011
5'-most EST	ymt700219714.h1
Method	BLASTX
NCBI GI	g4415933
BLAST score	426
E value	9.0e-42
Match length	220
% identity	40
NCBI Description	(AC006418) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana]
Seq. No.	282505
Contig ID	126693_1.R1011
5'-most EST	clt700044581.f1
Seq. No.	282506
Contig ID	126701_1.R1011
5'-most EST	uC-zmflmo17046b08b1
Method	BLASTX
NCBI GI	g1931640
BLAST score	367
E value	6.0e-35
Match length	111
% identity	62
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis

thaliana]

Seq. No.	282507
Contig ID	126706_1.R1011
5'-most EST	uC-zmflb73148c09a1

Seq. No.	282508
Contig ID	126713_1.R1011
5'-most EST	uC-zmflmo17046c08b1
Method	BLASTX
NCBI GI	g2335106
BLAST score	169
E value	9.0e-12
Match length	86
% identity	41
NCBI Description	(AC002339) salt inducible protein-like [Arabidopsis thaliana]

Seq. No.	282509
Contig ID	126720_1.R1011
5'-most EST	uC-zmflmo17046d03a1

Seq. No.	282510
Contig ID	126740_1.R1011
5'-most EST	dyk700105315.h1
Method	BLASTX
NCBI GI	g3953595
BLAST score	325
E value	9.0e-30
Match length	138
% identity	53
NCBI Description	(AB008486) response regulator 3 [Arabidopsis thaliana]

Seq. No.	282511
Contig ID	126750_1.R1011
5'-most EST	uC-zmflb73163f05b2
Method	BLASTX
NCBI GI	g1684913
BLAST score	613
E value	3.0e-66
Match length	282
% identity	50
NCBI Description	(U77888) receptor-like protein kinase [Ipomoea nil]

Seq. No.	282512
Contig ID	126752_1.R1011
5'-most EST	uC-zmflmo17046f12b1

Seq. No.	282513
Contig ID	126755_1.R1011
5'-most EST	uC-zmflmo17046g03b1

Seq. No.	282514
Contig ID	126782_1.R1011
5'-most EST	uC-zmroteosinte016f01b1
Method	BLASTX
NCBI GI	g4508069

BLAST score	315
E value	1.0e-28
Match length	77
% identity	77
NCBI Description	(AC005882) 12246 [Arabidopsis thaliana]

Seq. No.	282515
Contig ID	126826_1.R1011
5'-most EST	uC-zmflmo17048e07b1
Method	BLASTX
NCBI GI	g4006851
BLAST score	217
E value	9.0e-20
Match length	114
% identity	44
NCBI Description	(Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	282516
Contig ID	126834_1.R1011
5'-most EST	uC-zmflb73163a01b2

Seq. No.	282517
Contig ID	126834_2.R1011
5'-most EST	uC-zmflmo17057a04b1

Seq. No.	282518
Contig ID	126836_1.R1011
5'-most EST	wyr700240862.h1
Method	BLASTX
NCBI GI	g2809251
BLAST score	454
E value	1.0e-90
Match length	292
% identity	55
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No.	282519
Contig ID	126846_1.R1011
5'-most EST	wty700163848.h1
Method	BLASTX
NCBI GI	g1495366
BLAST score	161
E value	4.0e-11
Match length	42
% identity	67
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	282520
Contig ID	126861_1.R1011
5'-most EST	uC-zmflmo17050a04b2

Seq. No.	282521
Contig ID	126868_1.R1011
5'-most EST	uC-zmflmo17050a11b2
Method	BLASTX
NCBI GI	g3413700

BLAST score	797
E value	2.0e-85
Match length	191
% identity	82
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	282522
Contig ID	126916_1.R1011
5'-most EST	uC-zmflmo17176g04b1
Method	BLASTX
NCBI GI	g3805846
BLAST score	181
E value	3.0e-13
Match length	38
% identity	92
NCBI Description	(AL031986) DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain [Arabidopsis thaliana]

Seq. No.	282523
Contig ID	126921_1.R1011
5'-most EST	uC-zmflmo17050g01b2

Seq. No.	282524
Contig ID	126939_1.R1011
5'-most EST	uC-zmflmo17051a02b1
Method	BLASTX
NCBI GI	g2385410
BLAST score	283
E value	5.0e-25
Match length	185
% identity	30
NCBI Description	(AB001372) TFIID subunit taf72p [Schizosaccharomyces pombe] >gi_3859081_emb_CAA21958_ (AL033406) tfiid subunit taf72p. [Schizosaccharomyces pombe]

Seq. No.	282525
Contig ID	126949_1.R1011
5'-most EST	uC-zmflmo17051b01b1

Seq. No.	282526
Contig ID	126949_2.R1011
5'-most EST	uC-zmflb73248h01b3

Seq. No.	282527
Contig ID	126955_1.R1011
5'-most EST	uC-zmflmo17051b08b1

Seq. No.	282528
Contig ID	126976_1.R1011
5'-most EST	uC-zmflmo17238b10b1

Seq. No.	282529
Contig ID	126994_1.R1011
5'-most EST	uC-zmflmo17051e11b1

Seq. No.	282530
Contig ID	127000_1.R1011

5'-most EST	wty700162924.h1
Seq. No.	282531
Contig ID	127005_1.R1011
5'-most EST	nbm700475682.h1
Method	BLASTX
NCBI GI	g4335722
BLAST score	200
E value	5.0e-17
Match length	126
% identity	44
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]
Seq. No.	282532
Contig ID	127006_1.R1011
5'-most EST	uC-zmflmo17051f12b1
Method	BLASTX
NCBI GI	g4522009
BLAST score	212
E value	8.0e-17
Match length	89
% identity	52
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]
Seq. No.	282533
Contig ID	127016_1.R1011
5'-most EST	uC-zmflmo17051g10b1
Seq. No.	282534
Contig ID	127028_1.R1011
5'-most EST	uC-zmflmo17051h12b1
Method	BLASTX
NCBI GI	g2924509
BLAST score	198
E value	3.0e-32
Match length	123
% identity	59
NCBI Description	(AL022023) subtilisin proteinase - like [Arabidopsis thaliana]
Seq. No.	282535
Contig ID	127032_1.R1011
5'-most EST	uC-zmflmo17052a07b1
Seq. No.	282536
Contig ID	127037_1.R1011
5'-most EST	ltv700479654.h1
Method	BLASTX
NCBI GI	g3242705
BLAST score	469
E value	1.0e-48
Match length	137
% identity	78
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]
Seq. No.	282537

Contig ID	127068_1.R1011
5'-most EST	fwa700098323.h1
Seq. No.	282538
Contig ID	127086_1.R1011
5'-most EST	ypc700800345.h1
Method	BLASTX
NCBI GI	g2914700
BLAST score	238
E value	4.0e-20
Match length	67
% identity	76
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]
Seq. No.	282539
Contig ID	127092_1.R1011
5'-most EST	uC-zmflmo17052g04b1
Seq. No.	282540
Contig ID	127108_1.R1011
5'-most EST	uC-zmflmo17052h08b1
Method	BLASTX
NCBI GI	g1297187
BLAST score	153
E value	3.0e-23
Match length	115
% identity	56
NCBI Description	(U53501) similar to protein encoded by GenBank Accession Number U41815, nucleoporin 98 [Arabidopsis thaliana]
Seq. No.	282541
Contig ID	127114_1.R1011
5'-most EST	ceu700423988.h1
Seq. No.	282542
Contig ID	127136_1.R1011
5'-most EST	uC-zmflmo17053c06b1
Seq. No.	282543
Contig ID	127145_1.R1011
5'-most EST	fwa700098005.h1
Seq. No.	282544
Contig ID	127170_1.R1011
5'-most EST	uC-zmflmo17215b09b1
Seq. No.	282545
Contig ID	127174_1.R1011
5'-most EST	uC-zmflmo17258b03b1
Seq. No.	282546
Contig ID	127175_1.R1011
5'-most EST	uC-zmflmo17053g09a1
Seq. No.	282547
Contig ID	127176_1.R1011

5'-most EST	uC-zmflmo17053g04b1
Method	BLASTX
NCBI GI	g4115937
BLAST score	339
E value	1.0e-31
Match length	125
% identity	56
NCBI Description	(AF118223) contains similarity to human PCF11p homolog (GB:AF046935) [Arabidopsis thaliana]

Seq. No.	282548
Contig ID	127184_1.R1011
5'-most EST	uC-zmflmo17053g12b1

Seq. No.	282549
Contig ID	127209_1.R1011
5'-most EST	uC-zmflmo17054b05b1

Seq. No.	282550
Contig ID	127214_1.R1011
5'-most EST	ymt700219868.h1
Method	BLASTX
NCBI GI	g627469
BLAST score	210
E value	3.0e-16
Match length	256
% identity	12
NCBI Description	hypothetical protein 2 - human (fragment)

Seq. No.	282551
Contig ID	127249_1.R1011
5'-most EST	uC-zmflmo17054e12b1

Seq. No.	282552
Contig ID	127282_1.R1011
5'-most EST	uC-zmflmo17055a02b1

Seq. No.	282553
Contig ID	127291_1.R1011
5'-most EST	uC-zmflmo17055a11b1

Seq. No.	282554
Contig ID	127292_1.R1011
5'-most EST	uC-zmflmo17055b11b1
Method	BLASTN
NCBI GI	g168462
BLAST score	88
E value	1.0e-41
Match length	193
% identity	87
NCBI Description	Zea mays defective suppressor-mutator from the brittle-1-mutable allele

Seq. No.	282555
Contig ID	127298_1.R1011
5'-most EST	cjh700195654.h1

Seq. No.	282556
Contig ID	127298_2.R1011
5'-most EST	uC-zmflmo17036b09a1

Seq. No.	282557
Contig ID	127301_1.R1011
5'-most EST	uC-zmflmo17055b10b1

Seq. No.	282558
Contig ID	127321_1.R1011
5'-most EST	pmx700086232.h1
Method	BLASTX
NCBI GI	g3882183
BLAST score	201
E value	2.0e-15
Match length	105
% identity	40
NCBI Description	(AB018274) KIAA0731 protein [Homo sapiens]

Seq. No.	282559
Contig ID	127325_1.R1011
5'-most EST	uC-zmflmo17055d12b1

Seq. No.	282560
Contig ID	127344_1.R1011
5'-most EST	afb700381948.h1

Seq. No.	282561
Contig ID	127385_1.R1011
5'-most EST	uC-zmflmo17057b11b1
Method	BLASTX
NCBI GI	g4455293
BLAST score	227
E value	2.0e-18
Match length	56
% identity	79
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	282562
Contig ID	127390_1.R1011
5'-most EST	uC-zmflmo17261c04b1

Seq. No.	282563
Contig ID	127426_1.R1011
5'-most EST	uC-zmflmo17222e02b1

Seq. No.	282564
Contig ID	127437_1.R1011
5'-most EST	uC-zmflmo17057g06b1
Method	BLASTX
NCBI GI	g3892057
BLAST score	471
E value	4.0e-47
Match length	169
% identity	55
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282565
Contig ID	127499_1.R1011
5'-most EST	pmx700084995.h1
Method	BLASTX
NCBI GI	g4512703
BLAST score	419
E value	7.0e-41
Match length	247
% identity	40
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	282566
Contig ID	127505_1.R1011
5'-most EST	nbm700467061.h1

Seq. No.	282567
Contig ID	127512_1.R1011
5'-most EST	uC-zmflmo17058f11a1

Seq. No.	282568
Contig ID	127544_1.R1011
5'-most EST	uC-zmflmo17059a08b1

Seq. No.	282569
Contig ID	127545_1.R1011
5'-most EST	uC-zmflmo17059a09b1

Seq. No.	282570
Contig ID	127548_1.R1011
5'-most EST	uC-zmflmo17059a12b1

Seq. No.	282571
Contig ID	127573_1.R1011
5'-most EST	uC-zmflb73063f07a1

Seq. No.	282572
Contig ID	127575_1.R1011
5'-most EST	uC-zmflmo17059d05b1

Seq. No.	282573
Contig ID	127584_1.R1011
5'-most EST	uC-zmflmo17059e02a1

Seq. No.	282574
Contig ID	127592_1.R1011
5'-most EST	uC-zmflmo17222g08b1
Method	BLASTX
NCBI GI	g4006894
BLAST score	294
E value	4.0e-26
Match length	83
% identity	69
NCBI Description	(Z99708) homeodomain protein [Arabidopsis thaliana]

Seq. No.	282575
Contig ID	127605_1.R1011
5'-most EST	uC-zmflmo17344c11b1

Seq. No.	282576
Contig ID	127617_1.R1011
5'-most EST	gct701172828.h2

Seq. No.	282577
Contig ID	127626_1.R1011
5'-most EST	uC-zmflmo17190h07b1

Seq. No.	282578
Contig ID	127670_1.R1011
5'-most EST	uwc700151622.h1
Method	BLASTX
NCBI GI	g2252830
BLAST score	358
E value	1.0e-33
Match length	130
% identity	55
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	282579
Contig ID	127675_1.R1011
5'-most EST	uC-zmflmo17060e05b1

Seq. No.	282580
Contig ID	127682_1.R1011
5'-most EST	uC-zmflmo17060e12b1
Method	BLASTX
NCBI GI	g3912929
BLAST score	496
E value	4.0e-50
Match length	140
% identity	59
NCBI Description	(AF001308) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	282581
Contig ID	127699_1.R1011
5'-most EST	xsy700210017.h1
Method	BLASTX
NCBI GI	g1546694
BLAST score	259
E value	3.0e-22
Match length	85
% identity	64
NCBI Description	(X98806) peroxidase ATP20a [Arabidopsis thaliana]

Seq. No.	282582
Contig ID	127722_1.R1011
5'-most EST	uC-zmflmo17061a07b1

Seq. No.	282583
Contig ID	127769_1.R1011
5'-most EST	uC-zmflmo17061e10b1

Seq. No.	282584

Contig ID	127771_2.R1011
5'-most EST	uC-zmflb73157a01a1

Seq. No.	282585
Contig ID	127797_1.R1011
5'-most EST	uC-zmflb73185h04a1
Method	BLASTX
NCBI GI	g3123161
BLAST score	201
E value	3.0e-15
Match length	208
% identity	28
NCBI Description	HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F35G12.4 IN CHROMOSOME III >gi_3876723_emb_CAA86335_ (Z46242) similar to beta-transducin; cDNA EST EMBL:Z14703 comes from this gene; cDNA EST EMBL:D67532 comes from this gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST EMBL:D64515 comes from this gene; cDNA EST EMBL:D655

Seq. No.	282586
Contig ID	127799_1.R1011
5'-most EST	uC-zmroteosinte063h06b1
Method	BLASTX
NCBI GI	g2497818
BLAST score	398
E value	5.0e-48
Match length	160
% identity	62
NCBI Description	DNA REPLICATION LICENSING FACTOR MCM2 (X.MCM2) >gi_2134113_pir__JC5085 minichromosome maintenance protein 2 - African clawed frog >gi_1753193_dbj_BAA09948_ (D63919) xMCM2 [Xenopus laevis]

Seq. No.	282587
Contig ID	127804_1.R1011
5'-most EST	hbs701186260.h1
Method	BLASTX
NCBI GI	g3395428
BLAST score	154
E value	8.0e-10
Match length	62
% identity	55
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	282588
Contig ID	127913_1.R1011
5'-most EST	uC-zmflmo17066c02b1
Method	BLASTX
NCBI GI	g3702327
BLAST score	150
E value	1.0e-09
Match length	83
% identity	42
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	282589
Contig ID	127914_1.R1011

5'-most EST	uC-zmflmo17066c04b1
Seq. No.	282590
Contig ID	127922_1.R1011
5'-most EST	uC-zmflmo17066d04b1
Method	BLASTX
NCBI GI	g729094
BLAST score	237
E value	8.0e-20
Match length	124
% identity	40
NCBI Description	CCAAT DISPLACEMENT PROTEIN (CDP) >gi_300300_bbs_131514 CCAAT displacement protein, CDP [human, Peptide, 1505 aa]
Seq. No.	282591
Contig ID	127925_1.R1011
5'-most EST	uC-zmflmo17344a01b1
Seq. No.	282592
Contig ID	127926_1.R1011
5'-most EST	uC-zmflmo17066d07b1
Method	BLASTX
NCBI GI	g4115920
BLAST score	347
E value	1.0e-32
Match length	132
% identity	51
NCBI Description	(AF118222) similar to the subtilase family of serine proteases (Pfam: PF00082, score; 45.8, E=1.1e-11, n=2) [Arabidopsis thaliana]
Seq. No.	282593
Contig ID	127935_1.R1011
5'-most EST	uC-zmflmo17066e05b1
Method	BLASTN
NCBI GI	g22118
BLAST score	40
E value	1.0e-12
Match length	68
% identity	90
NCBI Description	Z.mays DNA for Adh1-Cm allele
Seq. No.	282594
Contig ID	127936_1.R1011
5'-most EST	uC-zmflmo17066e06b1
Method	BLASTX
NCBI GI	g1857447
BLAST score	225
E value	2.0e-18
Match length	117
% identity	46
NCBI Description	(U82367) UDP-glucose glucosyltransferase [Solanum tuberosum]
Seq. No.	282595
Contig ID	127990_1.R1011
5'-most EST	ntr700075885.h1

Seq. No.	282596
Contig ID	128056_1.R1011
5'-most EST	uC-zmflmo17068a01b2
Seq. No.	282597
Contig ID	128061_1.R1011
5'-most EST	uC-zmflmo17068a06b2
Seq. No.	282598
Contig ID	128082_1.R1011
5'-most EST	uC-zmflmo17068c06b2
Method	BLASTX
NCBI GI	g4006926
BLAST score	560
E value	2.0e-57
Match length	222
% identity	55
NCBI Description	(Z99708) putative protein (fragment) [Arabidopsis thaliana]
Seq. No.	282599
Contig ID	128086_1.R1011
5'-most EST	uC-zmflmo17068c10b2
Seq. No.	282600
Contig ID	128179_1.R1011
5'-most EST	uC-zmflmo17069e01b1
Seq. No.	282601
Contig ID	128191_1.R1011
5'-most EST	uC-zmflb73223e06b2
Seq. No.	282602
Contig ID	128249_1.R1011
5'-most EST	uC-zmflmo17070c09b1
Method	BLASTN
NCBI GI	g902200
BLAST score	700
E value	0.0e+00
Match length	892
% identity	94
NCBI Description	Z.mays complete chloroplast genome
Seq. No.	282603
Contig ID	128268_1.R1011
5'-most EST	uC-zmflmo17070e06b1
Seq. No.	282604
Contig ID	128270_1.R1011
5'-most EST	uC-zmflmo17070e08b1
Seq. No.	282605
Contig ID	128280_1.R1011
5'-most EST	uC-zmflmo17070f06b1
Seq. No.	282606
Contig ID	128319_1.R1011

5'-most EST	uC-zmflmo17071b02b1
Method	BLASTX
NCBI GI	g3355480
BLAST score	166
E value	2.0e-11
Match length	68
% identity	43
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	282607
Contig ID	128319_2.R1011
5'-most EST	xsy700208719.h1

Seq. No.	282608
Contig ID	128320_1.R1011
5'-most EST	clt700042840.f1

Seq. No.	282609
Contig ID	128333_1.R1011
5'-most EST	uC-zmflmo17071c05b1
Method	BLASTX
NCBI GI	g1418331
BLAST score	508
E value	1.0e-51
Match length	127
% identity	74
NCBI Description	(X95909) receptor like protein kinase [Arabidopsis thaliana]

Seq. No.	282610
Contig ID	128350_1.R1011
5'-most EST	uC-zmflmo17071d11b1

Seq. No.	282611
Contig ID	128367_1.R1011
5'-most EST	uC-zmflmo17071f06b1

Seq. No.	282612
Contig ID	128368_1.R1011
5'-most EST	uC-zmflmo17071f07b1
Method	BLASTX
NCBI GI	g3135493
BLAST score	221
E value	6.0e-18
Match length	110
% identity	45
NCBI Description	(AF060248) unknown [Arabidopsis thaliana]

Seq. No.	282613
Contig ID	128371_1.R1011
5'-most EST	wty700172794.h1

Seq. No.	282614
Contig ID	128393_2.R1011
5'-most EST	pmx700090936.h1

Seq. No.	282615
Contig ID	128467_1.R1011
5'-most EST	uwc700155645.h1
Seq. No.	282616
Contig ID	128472_1.R1011
5'-most EST	uC-zmflmo17163a10b1
Seq. No.	282617
Contig ID	128473_1.R1011
5'-most EST	uC-zmflmo17301e03b1
Method	BLASTX
NCBI GI	g2352492
BLAST score	547
E value	4.0e-56
Match length	155
% identity	65
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]
Seq. No.	282618
Contig ID	128498_1.R1011
5'-most EST	uC-zmflmo17073d09b1
Seq. No.	282619
Contig ID	128500_1.R1011
5'-most EST	uC-zmflmo17073d11b1
Seq. No.	282620
Contig ID	128501_1.R1011
5'-most EST	xjt700093807.h1
Method	BLASTX
NCBI GI	g4468817
BLAST score	244
E value	1.0e-20
Match length	93
% identity	53
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]
Seq. No.	282621
Contig ID	128510_1.R1011
5'-most EST	uC-zmflmo17073e12b1
Method	BLASTX
NCBI GI	g2781347
BLAST score	402
E value	3.0e-39
Match length	109
% identity	70
NCBI Description	(AC003113) F24O1.3 [Arabidopsis thaliana]
Seq. No.	282622
Contig ID	128516_1.R1011
5'-most EST	uC-zmflmo17161b12b1
Method	BLASTX
NCBI GI	g4455198
BLAST score	440

E value	1.0e-43
Match length	113
% identity	77
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	282623
Contig ID	128530_1.R1011
5'-most EST	uC-zmflmo17073g08b1
Method	BLASTX
NCBI GI	g4490302
BLAST score	142
E value	8.0e-09
Match length	84
% identity	43
NCBI Description	(AL035678) Tic22-like protein [Arabidopsis thaliana]

Seq. No.	282624
Contig ID	128534_1.R1011
5'-most EST	uC-zmflmo17073g12b1

Seq. No.	282625
Contig ID	128537_1.R1011
5'-most EST	fC-zmle700432990r3
Method	BLASTX
NCBI GI	g3980406
BLAST score	211
E value	6.0e-20
Match length	77
% identity	64
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	282626
Contig ID	128557_1.R1011
5'-most EST	uC-zmflmo17074b08b1
Method	BLASTX
NCBI GI	g3292817
BLAST score	331
E value	8.0e-31
Match length	78
% identity	78
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282627
Contig ID	128560_1.R1011
5'-most EST	uC-zmflmo17076c04b1

Seq. No.	282628
Contig ID	128562_1.R1011
5'-most EST	uC-zmflmo17074c02b1

Seq. No.	282629
Contig ID	128562_2.R1011
5'-most EST	cat700017756.r1

Seq. No.	282630
Contig ID	128566_1.R1011

5'-most EST	rvl700456433.h1
Method	BLASTN
NCBI GI	g4007864
BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Zea mays HRGP gene, AC1503 line

Seq. No.	282631
Contig ID	128566_2.R1011
5'-most EST	hvj700622887.h1

Seq. No.	282632
Contig ID	128572_1.R1011
5'-most EST	uC-zmflmo17074d02b1

Seq. No.	282633
Contig ID	128578_1.R1011
5'-most EST	uC-zmflmo17074d09b1

Seq. No.	282634
Contig ID	128630_1.R1011
5'-most EST	uC-zmflmo17075a08b2

Seq. No.	282635
Contig ID	128640_1.R1011
5'-most EST	uC-zmflmo17075c03b2

Seq. No.	282636
Contig ID	128647_1.R1011
5'-most EST	uC-zmflmo17075d04b2

Seq. No.	282637
Contig ID	128657_1.R1011
5'-most EST	uC-zmflmo17075e07b2

Seq. No.	282638
Contig ID	128705_2.R1011
5'-most EST	uC-zmflb73244f11b2

Seq. No.	282639
Contig ID	128710_1.R1011
5'-most EST	xmt700267464.h1

Seq. No.	282640
Contig ID	128715_1.R1011
5'-most EST	uC-zmflmo17076b11b1

Seq. No.	282641
Contig ID	128731_1.R1011
5'-most EST	uC-zmflmo17248c06a1
Method	BLASTX
NCBI GI	g2982455
BLAST score	157
E value	2.0e-10
Match length	33

% identity	88
NCBI Description	(AL022223) putative uracil phosphoribosyl transferase [Arabidopsis thaliana]

Seq. No.	282642
Contig ID	128732_1.R1011
5'-most EST	uC-zmflmo17076d08b1

Seq. No.	282643
Contig ID	128732_2.R1011
5'-most EST	uC-zmroteosinte099f02b2
Method	BLASTX
NCBI GI	g2499987
BLAST score	151
E value	1.0e-09
Match length	82
% identity	38
NCBI Description	PEPTIDYL-TRNA HYDROLASE (PTH) >gi_1870014_emb_CAB06865_ (Z92539) pth [Mycobacterium tuberculosis]

Seq. No.	282644
Contig ID	128757_1.R1011
5'-most EST	xsy700210533.h1
Method	BLASTX
NCBI GI	g3643085
BLAST score	321
E value	5.0e-30
Match length	95
% identity	68
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	282645
Contig ID	128762_1.R1011
5'-most EST	fC-zmle700427768f2

Seq. No.	282646
Contig ID	128763_1.R1011
5'-most EST	uC-zmflmo17076g08b1

Seq. No.	282647
Contig ID	128767_1.R1011
5'-most EST	uC-zmflmo17076h02b1

Seq. No.	282648
Contig ID	128793_1.R1011
5'-most EST	uC-zmflb73219e12b2

Seq. No.	282649
Contig ID	128811_1.R1011
5'-most EST	pmx700083068.h1
Method	BLASTX
NCBI GI	g4314370
BLAST score	231
E value	6.0e-19
Match length	87
% identity	59

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 282650
Contig ID 128811_2.R1011
5'-most EST rvl700457230.h1

Seq. No. 282651
Contig ID 128818_1.R1011
5'-most EST dyk700103585.h1

Seq. No. 282652
Contig ID 128824_1.R1011
5'-most EST uC-zmflmo17077f01b1

Seq. No. 282653
Contig ID 128827_1.R1011
5'-most EST gct701167287.h1
Method BLASTX
NCBI GI g2979549
BLAST score 287
E value 3.0e-29
Match length 191
% identity 42
NCBI Description (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No. 282654
Contig ID 128828_1.R1011
5'-most EST uC-zmflmo17077f06b1

Seq. No. 282655
Contig ID 128836_1.R1011
5'-most EST uC-zmflmo17077g06b1
Method BLASTX
NCBI GI g4138647
BLAST score 411
E value 5.0e-40
Match length 150
% identity 53
NCBI Description (AJ011939) peroxidase [Trifolium repens]

Seq. No. 282656
Contig ID 128844_1.R1011
5'-most EST uC-zmflmo17077h02b1

Seq. No. 282657
Contig ID 128845_1.R1011
5'-most EST uC-zmflmo17077h03b1

Seq. No. 282658
Contig ID 128859_1.R1011
5'-most EST uC-zmflmo17078a09b1

Seq. No. 282659
Contig ID 128897_1.R1011
5'-most EST rvt700549369.h1
Method BLASTX

NCBI GI	g4467123
BLAST score	178
E value	9.0e-13
Match length	187
% identity	24
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282660
Contig ID	128902_1.R1011
5'-most EST	uC-zmflmo17078e06b1

Seq. No.	282661
Contig ID	128902_2.R1011
5'-most EST	nbm700471071.h1

Seq. No.	282662
Contig ID	128958_1.R1011
5'-most EST	uC-zmflmo17079c02b1
Method	BLASTX
NCBI GI	g1652280
BLAST score	252
E value	2.0e-21
Match length	154
% identity	38
NCBI Description	(D90904) ribonuclease II [Synechocystis sp.]

Seq. No.	282663
Contig ID	129008_1.R1011
5'-most EST	wyr700241247.h1
Method	BLASTX
NCBI GI	g3540182
BLAST score	207
E value	6.0e-16
Match length	160
% identity	28
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	282664
Contig ID	129012_1.R1011
5'-most EST	uC-zmflmo17095a05b3
Method	BLASTX
NCBI GI	g1532171
BLAST score	287
E value	6.0e-26
Match length	95
% identity	57
NCBI Description	(U63815) AT.I.24-9 gene product [Arabidopsis thaliana]

Seq. No.	282665
Contig ID	129016_1.R1011
5'-most EST	uC-zmflmo17095a08b2

Seq. No.	282666
Contig ID	129022_1.R1011
5'-most EST	uC-zmflmo17118a01b1

Seq. No. 282667

Contig ID	129039_1.R1011
5'-most EST	qmh700027653.f1
Seq. No.	282668
Contig ID	129040_1.R1011
5'-most EST	uC-zmflmo17095c10b3
Seq. No.	282669
Contig ID	129044_1.R1011
5'-most EST	uC-zmflmo17118c01b1
Seq. No.	282670
Contig ID	129047_1.R1011
5'-most EST	uC-zmflmo17095d07b2
Seq. No.	282671
Contig ID	129060_1.R1011
5'-most EST	uC-zmflmo17095e08b2
Method	BLASTX
NCBI GI	g2245120
BLAST score	479
E value	3.0e-53
Match length	140
% identity	71
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	282672
Contig ID	129066_1.R1011
5'-most EST	uC-zmflmo17238d06b1
Seq. No.	282673
Contig ID	129102_1.R1011
5'-most EST	uC-zmflmo17097a04b1
Seq. No.	282674
Contig ID	129107_1.R1011
5'-most EST	uC-zmflmo17097a09b1
Method	BLASTX
NCBI GI	g2108252
BLAST score	591
E value	2.0e-61
Match length	143
% identity	42
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.	282675
Contig ID	129125_1.R1011
5'-most EST	uC-zmflmo17097c04b1
Seq. No.	282676
Contig ID	129137_1.R1011
5'-most EST	uC-zmflmo17097d06b1
Method	BLASTX
NCBI GI	g505100

BLAST score	176
E value	3.0e-12
Match length	142
% identity	33
NCBI Description	(D31886) KIAA0066 [Homo sapiens]

Seq. No.	282677
Contig ID	129170_1.R1011
5'-most EST	uC-zmflmo17097g04b1

Seq. No.	282678
Contig ID	129176_1.R1011
5'-most EST	ntr700077239.h1

Seq. No.	282679
Contig ID	129183_1.R1011
5'-most EST	uC-zmflmo17097h06b1

Seq. No.	282680
Contig ID	129187_1.R1011
5'-most EST	uC-zmflmo17097h11b1
Method	BLASTX
NCBI GI	g2648032
BLAST score	497
E value	3.0e-50
Match length	133
% identity	74
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	282681
Contig ID	129196_1.R1011
5'-most EST	uC-zmflmo17099b07b1

Seq. No.	282682
Contig ID	129237_1.R1011
5'-most EST	uC-zmflmo17099e05b1

Seq. No.	282683
Contig ID	129265_1.R1011
5'-most EST	uC-zmflmo17099h02b1
Method	BLASTX
NCBI GI	g3540184
BLAST score	516
E value	2.0e-52
Match length	147
% identity	65
NCBI Description	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No.	282684
Contig ID	129275_2.R1011
5'-most EST	ceu700426017.h1

Seq. No.	282685
Contig ID	129295_1.R1011
5'-most EST	vqh700053142.r1

Seq. No.	282686

Contig ID	129313_1.R1011
5'-most EST	uC-zmflmo17340f05b1
Method	BLASTX
NCBI GI	g3292821
BLAST score	170
E value	2.0e-11
Match length	140
% identity	36
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	282687
Contig ID	129337_1.R1011
5'-most EST	uC-zmflmo17309a04b1

Seq. No.	282688
Contig ID	129347_1.R1011
5'-most EST	uC-zmflmo17100g10b1

Seq. No.	282689
Contig ID	129349_1.R1011
5'-most EST	uC-zmflmo17100g12b1

Seq. No.	282690
Contig ID	129359_1.R1011
5'-most EST	xmt700264190.h1

Seq. No.	282691
Contig ID	129364_1.R1011
5'-most EST	uC-zmflmo17101a04b1
Method	BLASTX
NCBI GI	g2134979
BLAST score	179
E value	6.0e-13
Match length	148
% identity	34
NCBI Description	damage-specific DNA binding protein 2 - human

Seq. No.	282692
Contig ID	129370_1.R1011
5'-most EST	uC-zmflmo17101a10b1

Seq. No.	282693
Contig ID	129379_1.R1011
5'-most EST	uC-zmflmo17101b07b1

Seq. No.	282694
Contig ID	129388_1.R1011
5'-most EST	mwy700439129.h1
Method	BLASTX
NCBI GI	g1707032
BLAST score	351
E value	6.0e-34
Match length	193
% identity	40
NCBI Description	(U80445) coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for

by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8

Seq. No.	282695
Contig ID	129390_1.R1011
5'-most EST	ypc700807174.h1
Method	BLASTX
NCBI GI	g2914700
BLAST score	436
E value	1.0e-67
Match length	235
% identity	65
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	282696
Contig ID	129421_1.R1011
5'-most EST	uC-zmflmo17101f04b1
Method	BLASTX
NCBI GI	g2224897
BLAST score	245
E value	1.0e-20
Match length	77
% identity	56
NCBI Description	(U67132) DNA-binding protein PcMYB1 [Petroselinum crispum]

Seq. No.	282697
Contig ID	129433_1.R1011
5'-most EST	uC-zmflmo17101g06b1

Seq. No.	282698
Contig ID	129439_1.R1011
5'-most EST	wyr700240574.h1

Seq. No.	282699
Contig ID	129442_1.R1011
5'-most EST	uC-zmflmo17156a09b1
Method	BLASTX
NCBI GI	g1408460
BLAST score	300
E value	4.0e-27
Match length	75
% identity	81
NCBI Description	(U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]

Seq. No.	282700
Contig ID	129455_1.R1011
5'-most EST	uC-zmflmo17103a04b1
Method	BLASTX
NCBI GI	g4490323
BLAST score	392
E value	6.0e-38
Match length	141
% identity	59
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	282701
Contig ID	129458_1.R1011
5'-most EST	uC-zmflmo17116h03b1
Method	BLASTX
NCBI GI	g3033401
BLAST score	997
E value	1.0e-108
Match length	281
% identity	67
NCBI Description	(AC004238) putative potassium transporter [Arabidopsis thaliana]

Seq. No.	282702
Contig ID	129535_1.R1011
5'-most EST	uC-zmflmo17192a07b1

Seq. No.	282703
Contig ID	129551_1.R1011
5'-most EST	dyk700102667.h1
Method	BLASTX
NCBI GI	g3445397
BLAST score	515
E value	2.0e-52
Match length	116
% identity	85
NCBI Description	(AJ010166) S-domain receptor-like protein kinase [Zea mays]

Seq. No.	282704
Contig ID	129568_1.R1011
5'-most EST	uC-zmflmo17105a05b1

Seq. No.	282705
Contig ID	129570_1.R1011
5'-most EST	clt700041759.f1
Method	BLASTX
NCBI GI	g1806140
BLAST score	344
E value	2.0e-32
Match length	117
% identity	58
NCBI Description	(X97314) cdc2MsC [Medicago sativa]

Seq. No.	282706
Contig ID	129577_1.R1011
5'-most EST	cat700017474.r1

Seq. No.	282707
Contig ID	129597_1.R1011
5'-most EST	uC-zmflmo17105d07b1
Method	BLASTX
NCBI GI	g3980380
BLAST score	333
E value	4.0e-31
Match length	127
% identity	54
NCBI Description	(AC004561) putative enolase [Arabidopsis thaliana]

Seq. No.	282708
Contig ID	129604_1.R1011
5'-most EST	uwc700149663.h1
Method	BLASTX
NCBI GI	g4544451
BLAST score	549
E value	2.0e-56
Match length	140
% identity	73
NCBI Description	(AC006592) unknown protein [Arabidopsis thaliana]

Seq. No.	282709
Contig ID	129614_1.R1011
5'-most EST	uC-zmflmo17105f02b1

Seq. No.	282710
Contig ID	129622_1.R1011
5'-most EST	uC-zmflmo17105g08b1
Method	BLASTX
NCBI GI	g3075389
BLAST score	184
E value	2.0e-13
Match length	88
% identity	52
NCBI Description	(AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282711
Contig ID	129626_1.R1011
5'-most EST	uC-zmflmo17105h02b1

Seq. No.	282712
Contig ID	129627_1.R1011
5'-most EST	ceu700433917.h2

Seq. No.	282713
Contig ID	129628_1.R1011
5'-most EST	wty700167486.h1

Seq. No.	282714
Contig ID	129645_1.R1011
5'-most EST	cat700017369.r1

Seq. No.	282715
Contig ID	129646_1.R1011
5'-most EST	uC-zmflmo17108b02b1

Seq. No.	282716
Contig ID	129690_1.R1011
5'-most EST	cyk700049882.f1
Method	BLASTX
NCBI GI	g3540181
BLAST score	190
E value	3.0e-14
Match length	64
% identity	55
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	282717
Contig ID	129690_2.R1011
5'-most EST	wyr700238343.h1
Seq. No.	282718
Contig ID	129705_1.R1011
5'-most EST	zuv700356478.h1
Seq. No.	282719
Contig ID	129765_1.R1011
5'-most EST	uC-zmflmo17109e07b1
Seq. No.	282720
Contig ID	129775_1.R1011
5'-most EST	uC-zmflmo17109f11b1
Method	BLASTX
NCBI GI	g3367788
BLAST score	221
E value	7.0e-18
Match length	60
% identity	67
NCBI Description	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	282721
Contig ID	129778_1.R1011
5'-most EST	pmx700083785.h1
Method	BLASTX
NCBI GI	g2842424
BLAST score	325
E value	3.0e-30
Match length	120
% identity	52
NCBI Description	(AJ223948) RNA helicase [Homo sapiens]
Seq. No.	282722
Contig ID	129783_1.R1011
5'-most EST	uC-zmflmo17109g07b1
Seq. No.	282723
Contig ID	129793_1.R1011
5'-most EST	pwr700450241.h1
Method	BLASTX
NCBI GI	g1871176
BLAST score	197
E value	4.0e-15
Match length	121
% identity	40
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]
Seq. No.	282724
Contig ID	129913_1.R1011
5'-most EST	uC-zmflmo17294h10b1
Seq. No.	282725
Contig ID	129915_1.R1011
5'-most EST	uC-zmflmo17201f07b1

US09540460-20040906

Seq. No.	282726
Contig ID	129916_1.R1011
5'-most EST	uC-zmflmo17116d09b1
Seq. No.	282727
Contig ID	129924_1.R1011
5'-most EST	uC-zmflmo17116e06b1
Method	BLASTX
NCBI GI	g4455330
BLAST score	209
E value	2.0e-16
Match length	113
% identity	40
NCBI Description	(AL035525) contains EST gb:T44002 [Arabidopsis thaliana]
Seq. No.	282728
Contig ID	129939_1.R1011
5'-most EST	xjt700092846.h1
Seq. No.	282729
Contig ID	129945_1.R1011
5'-most EST	xsy700210566.h1
Seq. No.	282730
Contig ID	129946_1.R1011
5'-most EST	uC-zmflmo17116g09b1
Seq. No.	282731
Contig ID	129948_1.R1011
5'-most EST	uC-zmflmo17116h01b1
Method	BLASTX
NCBI GI	g3241944
BLAST score	473
E value	1.0e-49
Match length	162
% identity	60
NCBI Description	(AC004625) DNA-(apurinic or apyrimidinic site) lyase, ARP [Arabidopsis thaliana]
Seq. No.	282732
Contig ID	129980_1.R1011
5'-most EST	uC-zmflmo17242c01b1
Seq. No.	282733
Contig ID	130004_1.R1011
5'-most EST	uC-zmflmo17122e05b1
Seq. No.	282734
Contig ID	130010_1.R1011
5'-most EST	uC-zmflmo17117e10b1
Seq. No.	282735
Contig ID	130017_1.R1011
5'-most EST	uC-zmflmo17117f04b1
Seq. No.	282736
Contig ID	130022_1.R1011

5'-most EST	uC-zmflmo17117f11b1
Method	BLASTX
NCBI GI	g4206209
BLAST score	773
E value	2.0e-99
Match length	222
% identity	81
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No.	282737
Contig ID	130076_1.R1011
5'-most EST	uC-zmflmo17118c10b1

Seq. No.	282738
Contig ID	130078_1.R1011
5'-most EST	pmx700087363.h1
Method	BLASTX
NCBI GI	g4585884
BLAST score	314
E value	1.0e-28
Match length	151
% identity	45
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	282739
Contig ID	130084_1.R1011
5'-most EST	uC-zmflmo17118d07b1

Seq. No.	282740
Contig ID	130104_1.R1011
5'-most EST	xyt700346245.h1

Seq. No.	282741
Contig ID	130124_1.R1011
5'-most EST	uC-zmflmo17118h06b1

Seq. No.	282742
Contig ID	130151_1.R1011
5'-most EST	uC-zmflmo17122b10b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	282743
Contig ID	130155_1.R1011
5'-most EST	nwy700446744.h1

Seq. No.	282744
Contig ID	130189_1.R1011
5'-most EST	uC-zmflmo17161e04b1

Seq. No.	282745
Contig ID	130190_1.R1011
5'-most EST	hbs701183177.h1

Seq. No.	282746
Contig ID	130192_1.R1011
5'-most EST	afb700381963.h1
Method	BLASTX
NCBI GI	g1399305
BLAST score	420
E value	7.0e-41
Match length	291
% identity	55
NCBI Description	(U41474) phosphoinositide-specific phospholipase C P13 [Glycine max]

Seq. No.	282747
Contig ID	130201_1.R1011
5'-most EST	pmx700087292.h1

Seq. No.	282748
Contig ID	130204_1.R1011
5'-most EST	uC-zmflmo17122g06b1
Method	BLASTX
NCBI GI	g4490331
BLAST score	359
E value	4.0e-34
Match length	88
% identity	77
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282749
Contig ID	130212_1.R1011
5'-most EST	uC-zmflmo17122h04b1
Method	BLASTX
NCBI GI	g4510401
BLAST score	183
E value	3.0e-13
Match length	41
% identity	73
NCBI Description	(AC006587) putative general negative regulator of transcription [Arabidopsis thaliana]

Seq. No.	282750
Contig ID	130213_1.R1011
5'-most EST	uC-zmflmo17300f03b1

Seq. No.	282751
Contig ID	130214_1.R1011
5'-most EST	uC-zmflmo17265c10a2

Seq. No.	282752
Contig ID	130227_1.R1011
5'-most EST	uC-zmflmo17165f02b1

Seq. No.	282753
Contig ID	130330_1.R1011

5'-most EST	pmx700085092.h1
Seq. No.	282754
Contig ID	130344_1.R1011
5'-most EST	uC-zmflmo17126d05b1
Seq. No.	282755
Contig ID	130346_1.R1011
5'-most EST	uC-zmflmo17126d07b1
Seq. No.	282756
Contig ID	130358_1.R1011
5'-most EST	uC-zmflmo17126e08b1
Seq. No.	282757
Contig ID	130361_1.R1011
5'-most EST	uC-zmflb73255b08b1
Method	BLASTX
NCBI GI	g4220524
BLAST score	209
E value	2.0e-16
Match length	54
% identity	70
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	282758
Contig ID	130389_1.R1011
5'-most EST	uC-zmflmo17126h05b1
Seq. No.	282759
Contig ID	130409_1.R1011
5'-most EST	uC-zmflmo17127b03b1
Seq. No.	282760
Contig ID	130419_1.R1011
5'-most EST	uC-zmflmo17127c02b1
Seq. No.	282761
Contig ID	130437_1.R1011
5'-most EST	uC-zmflmo17127d10b1
Method	BLASTX
NCBI GI	g1946355
BLAST score	330
E value	1.0e-30
Match length	163
% identity	38
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.	282762
Contig ID	130440_1.R1011
5'-most EST	uC-zmflmo17127e02b1
Method	BLASTX
NCBI GI	g3395439
BLAST score	163
E value	2.0e-20

Match length	144
% identity	40
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]
Seq. No.	282763
Contig ID	130448_1.R1011
5'-most EST	qmh700029180.f1
Seq. No.	282764
Contig ID	130456_1.R1011
5'-most EST	uC-zmflmo17127f07b1
Method	BLASTX
NCBI GI	g4587547
BLAST score	248
E value	6.0e-21
Match length	132
% identity	42
NCBI Description	(AC006577) Contains similarity to DNA-binding protein Gt-2 gb_X68261 from Oryza sativa. [Arabidopsis thaliana]
Seq. No.	282765
Contig ID	130457_1.R1011
5'-most EST	uC-zmflmo17327a03b1
Seq. No.	282766
Contig ID	130476_1.R1011
5'-most EST	uC-zmflmo17127h04b1
Seq. No.	282767
Contig ID	130485_1.R1011
5'-most EST	uC-zmflmo17128a01b1
Seq. No.	282768
Contig ID	130488_1.R1011
5'-most EST	wty700164755.h1
Method	BLASTX
NCBI GI	g2275199
BLAST score	206
E value	4.0e-16
Match length	104
% identity	45
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	282769
Contig ID	130505_1.R1011
5'-most EST	uC-zmflmo17128b12b1
Method	BLASTX
NCBI GI	g1805654
BLAST score	213
E value	6.0e-17
Match length	97
% identity	45
NCBI Description	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]
Seq. No.	282770
Contig ID	130508_1.R1011

5'-most EST	uC-zmflmo17128c03b1
Seq. No.	282771
Contig ID	130509_1.R1011
5'-most EST	uC-zmflmo17128c04b1
Method	BLASTX
NCBI GI	g130186
BLAST score	1054
E value	1.0e-115
Match length	215
% identity	94
NCBI Description	PHYTOCHROME A >gi_82715_pir__JQ0382 phytochrome A - maize
Seq. No.	282772
Contig ID	130522_1.R1011
5'-most EST	uC-zmflmo17128d06b1
Seq. No.	282773
Contig ID	130539_1.R1011
5'-most EST	nbm700477047.h1
Method	BLASTX
NCBI GI	g1084454
BLAST score	287
E value	4.0e-26
Match length	116
% identity	58
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice >gi_600765 (L29471) cyclophilin 1 [Oryza sativa]
Seq. No.	282774
Contig ID	130539_3.R1011
5'-most EST	wyr700243451.h1
Method	BLASTX
NCBI GI	g4049344
BLAST score	157
E value	1.0e-10
Match length	46
% identity	63
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	282775
Contig ID	130544_1.R1011
5'-most EST	uC-zmflmo17128f05b1
Seq. No.	282776
Contig ID	130545_1.R1011
5'-most EST	uC-zmflmo17128f06b1
Seq. No.	282777
Contig ID	130557_1.R1011
5'-most EST	uC-zmflmo17128g06b1
Seq. No.	282778
Contig ID	130563_1.R1011
5'-most EST	uC-zmflmo17128g12b1
Method	BLASTX
NCBI GI	g1360003

BLAST score	158
E value	2.0e-10
Match length	115
% identity	33
NCBI Description	(X97982) nuclear poly(C)-binding protein, splicevariant E [Mus musculus]

Seq. No.	282779
Contig ID	130572_1.R1011
5'-most EST	tzu700201134.h1
Method	BLASTX
NCBI GI	g4559292
BLAST score	566
E value	4.0e-58
Match length	185
% identity	56
NCBI Description	(AF124148) trehalase 1 GMTRE1 [Glycine max]

Seq. No.	282780
Contig ID	130595_1.R1011
5'-most EST	uC-zmroteosinte042g11b1

Seq. No.	282781
Contig ID	130607_1.R1011
5'-most EST	uC-zmflmo17129d01b1

Seq. No.	282782
Contig ID	130632_1.R1011
5'-most EST	uC-zmflmo17129f05b1

Seq. No.	282783
Contig ID	130636_1.R1011
5'-most EST	uC-zmflmo17129f09b1
Method	BLASTX
NCBI GI	g3024708
BLAST score	324
E value	5.0e-30
Match length	125
% identity	47
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID 20/15 KD SUBUNITS (TAFII-20/TAFII-15) (TAFII20/TAFII15) >gi_2135937_pir__JC4676 PolII transcription factor TFTIID chain TAFII20 - human >gi_791055_emb_CAA58826_ (X84002) PolII transcription factor TFTIID [Homo sapiens] >gi_1345404_dbj_BAA09112_ (D50544) TFIID subunit p22 [Homo sapiens] >gi_1373377 (U57693) TAF20 [Homo sapiens]

Seq. No.	282784
Contig ID	130649_1.R1011
5'-most EST	wyr700238115.h1

Seq. No.	282785
Contig ID	130661_1.R1011
5'-most EST	hbs701181832.h1
Method	BLASTX
NCBI GI	g1840425
BLAST score	875

E value	1.0e-108
Match length	370
% identity	52
NCBI Description	(U36586) alcohol dehydrogenase [Vitis vinifera]

Seq. No.	282786
Contig ID	130679_1.R1011
5'-most EST	uC-zmflb73362g09a2

Seq. No.	282787
Contig ID	130692_1.R1011
5'-most EST	uC-zmflmo17248h06b1
Method	BLASTX
NCBI GI	g2288985
BLAST score	329
E value	2.0e-30
Match length	120
% identity	51
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282788
Contig ID	130715_1.R1011
5'-most EST	uC-zmflmo17238e01b1
Method	BLASTX
NCBI GI	g1707007
BLAST score	250
E value	2.0e-25
Match length	138
% identity	18
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282789
Contig ID	130735_1.R1011
5'-most EST	yyf700350042.h1
Method	BLASTX
NCBI GI	g465535
BLAST score	280
E value	2.0e-24
Match length	148
% identity	41
NCBI Description	HYPOTHETICAL 32.7 KD PROTEIN IN NTH2-COQ1 INTERGENIC REGION >gi_626491_pir__S44561 hypothetical protein YBR002c - yeast (Saccharomyces cerevisiae) >gi_403317_emb_CAA81271_ (Z26494) unknown [Saccharomyces cerevisiae] >gi_536188_emb_CAA84938_ (Z35871) ORF YBR002c [Saccharomyces cerevisiae] >gi_4126457_dbj_BAA36577_ (AB013497) cis-prenyltransferase [Saccharomyces cerevisiae] >gi_1582565_prf__2118405F ORF YBR0107 [Saccharomyces cerevisiae]

Seq. No.	282790
Contig ID	130743_1.R1011
5'-most EST	uC-zmflmo17130h09b1

Seq. No.	282791
Contig ID	130784_1.R1011
5'-most EST	xmt700267069.h1

Seq. No.	282792
Contig ID	130788_2.R1011
5'-most EST	xtj700377836.h1
Method	BLASTX
NCBI GI	g4539404
BLAST score	376
E value	3.0e-36
Match length	108
% identity	58
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	282793
Contig ID	130795_1.R1011
5'-most EST	uC-zmflmo17131f01b1
Method	BLASTX
NCBI GI	g4416301
BLAST score	496
E value	2.0e-50
Match length	107
% identity	85
NCBI Description	(AF105716) gag protein [Zea mays]

Seq. No.	282794
Contig ID	130805_1.R1011
5'-most EST	uC-zmflmo17131g03b1

Seq. No.	282795
Contig ID	130843_1.R1011
5'-most EST	cjh700197649.h1
Method	BLASTX
NCBI GI	g2760839
BLAST score	223
E value	3.0e-18
Match length	121
% identity	45
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	282796
Contig ID	130849_1.R1011
5'-most EST	uC-zmflmo17288g02b1
Method	BLASTX
NCBI GI	g2809246
BLAST score	186
E value	9.0e-14
Match length	105
% identity	43
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	282797
Contig ID	130856_1.R1011
5'-most EST	uC-zmflb73162a02b2
Method	BLASTX
NCBI GI	g107350
BLAST score	151
E value	6.0e-12
Match length	170

% identity	34
NCBI Description	Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5 protein [Homo sapiens]

Seq. No.	282798
Contig ID	130867_1.R1011
5'-most EST	gct701171051.h1

Seq. No.	282799
Contig ID	130874_1.R1011
5'-most EST	uC-zmflmo17132f04b1
Method	BLASTN
NCBI GI	g2586128
BLAST score	131
E value	6.0e-68
Match length	131
% identity	100
NCBI Description	Zea mays b-keto acyl reductase (glossy8) mRNA, complete cds

Seq. No.	282800
Contig ID	130877_1.R1011
5'-most EST	uC-zmflmo17132f06b1

Seq. No.	282801
Contig ID	130880_1.R1011
5'-most EST	uC-zmflmo17132g03b1

Seq. No.	282802
Contig ID	130890_1.R1011
5'-most EST	uC-zmflmo17132h05b1

Seq. No.	282803
Contig ID	130896_1.R1011
5'-most EST	uC-zmflmo17241h04b1
Method	BLASTX
NCBI GI	g2642443
BLAST score	503
E value	1.0e-50
Match length	239
% identity	45
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	282804
Contig ID	130911_1.R1011
5'-most EST	uC-zmflmo17133b12b1
Method	BLASTX
NCBI GI	g1514643
BLAST score	206
E value	2.0e-26
Match length	122
% identity	44
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	282805
Contig ID	130979_1.R1011
5'-most EST	uC-zmflmo17134d12b1
Method	BLASTX

NCBI GI g4454012
BLAST score 379
E value 1.0e-36
Match length 88
% identity 72
NCBI Description (AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No. 282806
Contig ID 130989_1.R1011
5'-most EST xsy700210391.h1
Method BLASTX
NCBI GI g3157943
BLAST score 151
E value 8.0e-10
Match length 67
% identity 43
NCBI Description (AC002131) Contains similarity to BAP31 protein gb_X81816 from Mus musculus. [Arabidopsis thaliana]

Seq. No. 282807
Contig ID 130995_1.R1011
5'-most EST uC-zmflmo17134g03b1

Seq. No. 282808
Contig ID 131027_1.R1011
5'-most EST uC-zmroteosinte072b09b2
Method BLASTX
NCBI GI g2370253
BLAST score 359
E value 5.0e-34
Match length 102
% identity 67
NCBI Description (Y13273) putative protein kinase [Lycopersicon esculentum]

Seq. No. 282809
Contig ID 131035_1.R1011
5'-most EST uC-zmflmo17282b08b1

Seq. No. 282810
Contig ID 131042_1.R1011
5'-most EST uC-zmflmo17136d06b1

Seq. No. 282811
Contig ID 131045_1.R1011
5'-most EST ntr700076645.h1

Seq. No. 282812
Contig ID 131058_1.R1011
5'-most EST uC-zmflmo17136f06b1
Method BLASTX
NCBI GI g4538923
BLAST score 196
E value 4.0e-15
Match length 58
% identity 64
NCBI Description (AL049483) predicted protein destination factor

[Arabidopsis thaliana]

Seq. No.	282813
Contig ID	131058_2.R1011
5'-most EST	ceu700431722.h1
Method	BLASTX
NCBI GI	g4538923
BLAST score	178
E value	5.0e-13
Match length	53
% identity	64
NCBI Description	(AL049483) predicted protein destination factor [Arabidopsis thaliana]

Seq. No.	282814
Contig ID	131065_1.R1011
5'-most EST	gct701169207.h1

Seq. No.	282815
Contig ID	131071_1.R1011
5'-most EST	uC-zmflmo17136h02b1

Seq. No.	282816
Contig ID	131088_2.R1011
5'-most EST	uC-zmflmo17238e02b1

Seq. No.	282817
Contig ID	131102_1.R1011
5'-most EST	uC-zmflmo17137c03b1

Seq. No.	282818
Contig ID	131113_1.R1011
5'-most EST	qmh700026291.f1
Method	BLASTX
NCBI GI	g2735017
BLAST score	1504
E value	1.0e-168
Match length	272
% identity	99
NCBI Description	(U82481) KI domain interacting kinase 1 [Zea mays]

Seq. No.	282819
Contig ID	131114_1.R1011
5'-most EST	pmx700085587.h1
Method	BLASTX
NCBI GI	g2505870
BLAST score	312
E value	8.0e-29
Match length	90
% identity	73
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282820
Contig ID	131114_2.R1011
5'-most EST	uC-zmflmo17137d09b1
Method	BLASTX
NCBI GI	g2505870

BLAST score 527
E value 8.0e-54
Match length 151
% identity 68
NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 282821
Contig ID 131132_1.R1011
5'-most EST gwl700614715.h1
Method BLASTX
NCBI GI g3342913
BLAST score 559
E value 3.0e-57
Match length 174
% identity 61
NCBI Description (AF078916) oligopeptidase B [Trypanosoma brucei brucei]

Seq. No. 282822
Contig ID 131137_1.R1011
5'-most EST tzu700205016.h1

Seq. No. 282823
Contig ID 131144_1.R1011
5'-most EST uC-zmflmo17137g10b1
Method BLASTX
NCBI GI g2494116
BLAST score 217
E value 1.0e-17
Match length 47
% identity 74
NCBI Description (AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]

Seq. No. 282824
Contig ID 131160_1.R1011
5'-most EST uC-zmflmo17248d08b1
Method BLASTX
NCBI GI g1652856
BLAST score 490
E value 6.0e-49
Match length 246
% identity 43
NCBI Description (D90909) hypothetical protein [Synechocystis sp.]

Seq. No. 282825
Contig ID 131160_2.R1011
5'-most EST xmt700257446.h2
Method BLASTX
NCBI GI g3004556
BLAST score 233
E value 4.0e-19
Match length 59
% identity 80
NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No. 282826
Contig ID 131238_1.R1011

5'-most EST	fdz701161274.h1
Method	BLASTX
NCBI GI	g2618684
BLAST score	304
E value	2.0e-27
Match length	88
% identity	69
NCBI Description	(AC002510) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana] >gi_3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana]

Seq. No.	282827
Contig ID	131239_1.R1011
5'-most EST	fwa700100312.h1

Seq. No.	282828
Contig ID	131243_1.R1011
5'-most EST	uC-zmflb73359a03a2

Seq. No.	282829
Contig ID	131270_1.R1011
5'-most EST	uC-zmflmo17139d11b1

Seq. No.	282830
Contig ID	131275_1.R1011
5'-most EST	pmx700085118.h1
Method	BLASTX
NCBI GI	g3513727
BLAST score	331
E value	8.0e-31
Match length	125
% identity	60
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	282831
Contig ID	131278_1.R1011
5'-most EST	uC-zmflmo17139e08b1

Seq. No.	282832
Contig ID	131285_1.R1011
5'-most EST	vux700162158.h1

Seq. No.	282833
Contig ID	131308_1.R1011
5'-most EST	uC-zmflmo17150a03b1

Seq. No.	282834
Contig ID	131310_1.R1011
5'-most EST	uC-zmflmo17150a05a1

Seq. No.	282835
Contig ID	131323_1.R1011
5'-most EST	hbs701181596.h1

Seq. No.	282836
Contig ID	131324_1.R1011
5'-most EST	uC-zmroteosinte016d09b1

Seq. No.	282837
Contig ID	131325_1.R1011
5'-most EST	uC-zmflmo17150b09b1

Seq. No.	282838
Contig ID	131337_1.R1011
5'-most EST	uC-zmflmo17150c09b1

Seq. No.	282839
Contig ID	131339_1.R1011
5'-most EST	uC-zmflmo17150c12b1
Method	BLASTX
NCBI GI	g3786324
BLAST score	594
E value	2.0e-61
Match length	180
% identity	59
NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]

Seq. No.	282840
Contig ID	131346_1.R1011
5'-most EST	uC-zmflmo17150d07b1
Method	BLASTX
NCBI GI	g4581139
BLAST score	770
E value	7.0e-82
Match length	325
% identity	44
NCBI Description	(AC006919) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	282841
Contig ID	131346_3.R1011
5'-most EST	sem700930102.h1
Method	BLASTX
NCBI GI	g4510339
BLAST score	330
E value	8.0e-31
Match length	126
% identity	46
NCBI Description	(AC006921) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No.	282842
Contig ID	131360_1.R1011
5'-most EST	hbs701185452.h1
Method	BLASTX
NCBI GI	g1402878

BLAST score	562
E value	1.0e-57
Match length	215
% identity	48
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	282843
Contig ID	131391_1.R1011
5'-most EST	uC-zmflmo17150h09b1

Seq. No.	282844
Contig ID	131392_1.R1011
5'-most EST	uC-zmflmo17150h11b1

Seq. No.	282845
Contig ID	131392_2.R1011
5'-most EST	rvt700553401.h1

Seq. No.	282846
Contig ID	131416_1.R1011
5'-most EST	uC-zmflmo17357d07a1

Seq. No.	282847
Contig ID	131421_1.R1011
5'-most EST	uC-zmflmo17151c06b1

Seq. No.	282848
Contig ID	131430_1.R1011
5'-most EST	uC-zmflmo17151d04b1

Seq. No.	282849
Contig ID	131432_1.R1011
5'-most EST	uC-zmflmo17151d06b1

Seq. No.	282850
Contig ID	131455_1.R1011
5'-most EST	uC-zmflmo17151f08b1
Method	BLASTX
NCBI GI	g3080427
BLAST score	346
E value	1.0e-32
Match length	111
% identity	57
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	282851
Contig ID	131461_1.R1011
5'-most EST	uC-zmflmo17151g07b1

Seq. No.	282852
Contig ID	131462_1.R1011
5'-most EST	uC-zmflmo17151g08b1

Seq. No.	282853
Contig ID	131468_1.R1011
5'-most EST	uC-zmflmo17151g09b1

Seq. No.	282854
Contig ID	131469_1.R1011
5'-most EST	uC-zmflmo17151g10b1

Seq. No.	282855
Contig ID	131480_1.R1011
5'-most EST	pwr700453001.h1

Seq. No.	282856
Contig ID	131490_1.R1011
5'-most EST	uC-zmflmo17152a09b1
Method	BLASTX
NCBI GI	g2191191
BLAST score	228
E value	3.0e-21
Match length	73
% identity	75
NCBI Description	(AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]

Seq. No.	282857
Contig ID	131498_1.R1011
5'-most EST	ceu700433287.h1

Seq. No.	282858
Contig ID	131508_1.R1011
5'-most EST	uC-zmflmo17152c04b1

Seq. No.	282859
Contig ID	131525_1.R1011
5'-most EST	uC-zmflmo17152d09b1

Seq. No.	282860
Contig ID	131534_1.R1011
5'-most EST	uC-zmflmo17152e07b1
Method	BLASTX
NCBI GI	g4388731
BLAST score	223
E value	4.0e-18
Match length	87
% identity	57
NCBI Description	(AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282861
Contig ID	131535_1.R1011
5'-most EST	zla700379841.h1
Method	BLASTX
NCBI GI	g2462760
BLAST score	154
E value	1.0e-09
Match length	79
% identity	47
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	282862
Contig ID	131560_1.R1011
5'-most EST	xmt700264066.h1

Seq. No.	282863
Contig ID	131566_1.R1011
5'-most EST	uC-zmflmo17152h05b1
Method	BLASTX
NCBI GI	g4468984
BLAST score	494
E value	8.0e-50
Match length	183
% identity	54
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	282864
Contig ID	131580_1.R1011
5'-most EST	yyf700351160.h1
Method	BLASTX
NCBI GI	g4581111
BLAST score	169
E value	1.0e-11
Match length	150
% identity	33
NCBI Description	(AC005825) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	282865
Contig ID	131590_1.R1011
5'-most EST	uC-zmflmo17153b09b1

Seq. No.	282866
Contig ID	131602_1.R1011
5'-most EST	uC-zmflmo17153c11b1

Seq. No.	282867
Contig ID	131627_1.R1011
5'-most EST	uC-zmflmo17153f04b1

Seq. No.	282868
Contig ID	131645_1.R1011
5'-most EST	uC-zmflb73127e08b2

Seq. No.	282869
Contig ID	131652_1.R1011
5'-most EST	uC-zmflmo17153h07b1
Method	BLASTX
NCBI GI	g2352998
BLAST score	185
E value	2.0e-13
Match length	152
% identity	27
NCBI Description	(AF014461) EXO70 protein [Mus musculus]

Seq. No.	282870
Contig ID	131688_1.R1011
5'-most EST	uC-zmflmo17154c08b1
Method	BLASTX
NCBI GI	g4185310
BLAST score	574

E value	2.0e-74
Match length	163
% identity	82
NCBI Description	(AF090446) gag protein [Zea mays]

Seq. No.	282871
Contig ID	131692_1.R1011
5'-most EST	uC-zmflmo17154c12b1

Seq. No.	282872
Contig ID	131705_1.R1011
5'-most EST	uC-zmflmo17154e04b1
Method	BLASTX
NCBI GI	g4309760
BLAST score	196
E value	8.0e-15
Match length	155
% identity	46
NCBI Description	(AC006217) unknown protein [Arabidopsis thaliana]

Seq. No.	282873
Contig ID	131736_1.R1011
5'-most EST	wyr700237118.h1

Seq. No.	282874
Contig ID	131744_1.R1011
5'-most EST	uC-zmflmo17154h10b1

Seq. No.	282875
Contig ID	131749_1.R1011
5'-most EST	uC-zmflmo17267e12b1

Seq. No.	282876
Contig ID	131755_1.R1011
5'-most EST	uC-zmroteosinte058c07b2

Seq. No.	282877
Contig ID	131767_1.R1011
5'-most EST	uC-zmroteosinte015f11b1
Method	BLASTX
NCBI GI	g2739382
BLAST score	430
E value	3.0e-42
Match length	227
% identity	45
NCBI Description	(AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	282878
Contig ID	131773_1.R1011
5'-most EST	uC-zmflmo17155c05b1
Method	BLASTX
NCBI GI	g3915866
BLAST score	497
E value	5.0e-50
Match length	161
% identity	60

NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No.	282879
Contig ID	131785_1.R1011
5'-most EST	uC-zmflmo17155d06b1

Seq. No.	282880
Contig ID	131794_1.R1011
5'-most EST	afb700381222.h1
Method	BLASTX
NCBI GI	g3342249
BLAST score	409
E value	5.0e-42
Match length	185
% identity	50
NCBI Description	(AF047719) GA3 [Arabidopsis thaliana] >gi_3342251 (AF047720) GA3 [Arabidopsis thaliana]

Seq. No.	282881
Contig ID	131814_1.R1011
5'-most EST	uC-zmflmo17155f12b1

Seq. No.	282882
Contig ID	131831_1.R1011
5'-most EST	uC-zmflmo17155h06b1
Method	BLASTX
NCBI GI	g3320104
BLAST score	815
E value	1.0e-87
Match length	159
% identity	99
NCBI Description	(AJ007366) calcium-dependent protein kinase [Zea mays]

Seq. No.	282883
Contig ID	131846_1.R1011
5'-most EST	uC-zmflmo17156b04b1
Method	BLASTX
NCBI GI	g2984139
BLAST score	497
E value	5.0e-50
Match length	237
% identity	46
NCBI Description	(AE000760) aspartate-semialdehyde dehydrogenase [Aquifex aeolicus]

Seq. No.	282884
Contig ID	131847_1.R1011
5'-most EST	dyk700105015.h1
Method	BLASTX
NCBI GI	g2346978
BLAST score	164
E value	7.0e-20
Match length	83
% identity	67
NCBI Description	(AB006601) ZPT2-14 [Petunia x hybrida]

Seq. No.	282885
Contig ID	131871_1.R1011
5'-most EST	uC-zmflmo17156d10b1

Seq. No.	282886
Contig ID	131879_1.R1011
5'-most EST	uC-zmflmo17156e09b1
Method	BLASTX
NCBI GI	g2827653
BLAST score	424
E value	2.0e-41
Match length	209
% identity	39
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	282887
Contig ID	131891_1.R1011
5'-most EST	uC-zmflmo17172h10a1

Seq. No.	282888
Contig ID	131893_1.R1011
5'-most EST	uC-zmflmo17156g04b1

Seq. No.	282889
Contig ID	131935_1.R1011
5'-most EST	uC-zmflb73275f05a1

Seq. No.	282890
Contig ID	131937_1.R1011
5'-most EST	ceu700423671.h1

Seq. No.	282891
Contig ID	131950_1.R1011
5'-most EST	fdz701159677.h1

Seq. No.	282892
Contig ID	131950_2.R1011
5'-most EST	uC-zmflmo17158d07b1

Seq. No.	282893
Contig ID	131991_1.R1011
5'-most EST	uC-zmflmo17158h04b1

Seq. No.	282894
Contig ID	131994_1.R1011
5'-most EST	ymt700222786.h1
Method	BLASTX
NCBI GI	g4415912
BLAST score	566
E value	3.0e-58
Match length	198
% identity	55
NCBI Description	(AC006282) putative protease [Arabidopsis thaliana]

Seq. No.	282895
Contig ID	131997_1.R1011

5'-most EST	uC-zmf1b73130c11b2
Method	BLASTX
NCBI GI	g3377509
BLAST score	671
E value	2.0e-70
Match length	158
% identity	84
NCBI Description	(AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No.	282896
Contig ID	132004_1.R1011
5'-most EST	uC-zmflmo17159a05b1
Method	BLASTX
NCBI GI	g3328804
BLAST score	359
E value	4.0e-34
Match length	148
% identity	53
NCBI Description	(AE001311) GTP Binding Protein [Chlamydia trachomatis]

Seq. No.	282897
Contig ID	132018_1.R1011
5'-most EST	uC-zmflmo17164b02b1

Seq. No.	282898
Contig ID	132021_1.R1011
5'-most EST	uC-zmflmo17159b11b1

Seq. No.	282899
Contig ID	132030_1.R1011
5'-most EST	pmx700087218.h1

Seq. No.	282900
Contig ID	132031_1.R1011
5'-most EST	uC-zmflmo17159c10b1
Method	BLASTN
NCBI GI	g22332
BLAST score	245
E value	1.0e-135
Match length	383
% identity	90
NCBI Description	Z.mays HRGP gene

Seq. No.	282901
Contig ID	132052_1.R1011
5'-most EST	uC-zmflmo17159e07b1
Method	BLASTX
NCBI GI	g4455345
BLAST score	312
E value	1.0e-28
Match length	67
% identity	90
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	282902
Contig ID	132066_1.R1011
5'-most EST	ntr700075005.h1

Method	BLASTX
NCBI GI	g4538961
BLAST score	1876
E value	0.0e+00
Match length	445
% identity	77
NCBI Description	(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis thaliana]

Seq. No.	282903
Contig ID	132070_1.R1011
5'-most EST	uC-zmflmo17159g02b1
Method	BLASTX
NCBI GI	g1854378
BLAST score	163
E value	5.0e-11
Match length	46
% identity	72
NCBI Description	(AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No.	282904
Contig ID	132072_1.R1011
5'-most EST	uC-zmflmo17159g04b1

Seq. No.	282905
Contig ID	132076_1.R1011
5'-most EST	wyr700237108.h1
Method	BLASTX
NCBI GI	g4406820
BLAST score	659
E value	2.0e-68
Match length	226
% identity	65
NCBI Description	(AC006201) putative ras superfamily member [Arabidopsis thaliana]

Seq. No.	282906
Contig ID	132087_1.R1011
5'-most EST	uC-zmflmo17159h08a1

Seq. No.	282907
Contig ID	132102_1.R1011
5'-most EST	uC-zmflmo17160a12b1

Seq. No.	282908
Contig ID	132103_1.R1011
5'-most EST	uC-zmroteosinte099d08b2
Method	BLASTX
NCBI GI	g3024874
BLAST score	190
E value	6.0e-14
Match length	123
% identity	37
NCBI Description	HYPOTHETICAL 50.0 KD PROTEIN SLR0076 >gi_1001707_dbj_BAA10544_ (D64004) hypothetical protein [Synechocystis sp.]

Seq. No.	282909
Contig ID	132103_2.R1011
5'-most EST	pmx700088330.h1

Seq. No.	282910
Contig ID	132108_1.R1011
5'-most EST	uC-zmflmo17160b07b1

Seq. No.	282911
Contig ID	132120_1.R1011
5'-most EST	ymt700219831.h1
Method	BLASTX
NCBI GI	g1209703
BLAST score	290
E value	5.0e-26
Match length	106
% identity	49
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	282912
Contig ID	132134_1.R1011
5'-most EST	pmx700087392.h1
Method	BLASTX
NCBI GI	g2829895
BLAST score	439
E value	2.0e-44
Match length	186
% identity	58
NCBI Description	(AC002311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282913
Contig ID	132134_2.R1011
5'-most EST	uC-zmflmo17160d11b1
Method	BLASTX
NCBI GI	g2829895
BLAST score	458
E value	3.0e-45
Match length	129
% identity	69
NCBI Description	(AC002311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282914
Contig ID	132148_1.R1011
5'-most EST	wen700333061.h1
Method	BLASTX
NCBI GI	g4572676
BLAST score	164
E value	7.0e-11
Match length	174
% identity	26
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	282915
Contig ID	132164_1.R1011
5'-most EST	uC-zmflmo17160g08b1
Method	BLASTN

NCBI GI	g4416300
BLAST score	104
E value	4.0e-51
Match length	327
% identity	83
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	282916
Contig ID	132165_1.R1011
5'-most EST	uC-zmflmo17160g09b1
Method	BLASTX
NCBI GI	g2444174
BLAST score	400
E value	3.0e-41
Match length	155
% identity	58
NCBI Description	(U94781) unconventional myosin [Helianthus annuus]

Seq. No.	282917
Contig ID	132196_1.R1011
5'-most EST	uC-zmflmo17263c12b1
Method	BLASTX
NCBI GI	g4038036
BLAST score	327
E value	2.0e-30
Match length	78
% identity	73
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	282918
Contig ID	132214_1.R1011
5'-most EST	uC-zmflmo17161d06b1

Seq. No.	282919
Contig ID	132248_1.R1011
5'-most EST	wty700167956.h1
Method	BLASTX
NCBI GI	g3451074
BLAST score	495
E value	5.0e-50
Match length	163
% identity	57
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	282920
Contig ID	132251_1.R1011
5'-most EST	uC-zmflmo17161g09b1

Seq. No.	282921
Contig ID	132256_1.R1011
5'-most EST	uC-zmflmo17161h03b1
Method	BLASTX
NCBI GI	g4587547
BLAST score	193
E value	2.0e-14
Match length	67

% identity	52
NCBI Description	(AC006577) Contains similarity to DNA-binding protein Gt-2 gb_X68261 from Oryza sativa. [Arabidopsis thaliana]

Seq. No.	282922
Contig ID	132265_1.R1011
5'-most EST	uC-zmflmo17161h12b1

Seq. No.	282923
Contig ID	132280_1.R1011
5'-most EST	uC-zmflmo17163b03b1

Seq. No.	282924
Contig ID	132303_1.R1011
5'-most EST	uC-zmflmo17163d05b1
Method	BLASTX
NCBI GI	g3249095
BLAST score	338
E value	1.0e-31
Match length	99
% identity	64
NCBI Description	(AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb_L13703 from Schizosaccharomyces pombe. ESTs gb_N37567 and gb_T43002 come from this gene. [Arabidopsis thaliana]

Seq. No.	282925
Contig ID	132305_1.R1011
5'-most EST	uC-zmflmo17163d07b1
Method	BLASTX
NCBI GI	g4263827
BLAST score	189
E value	7.0e-14
Match length	118
% identity	36
NCBI Description	(AC006067) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	282926
Contig ID	132340_1.R1011
5'-most EST	uC-zmflmo17163g08b1

Seq. No.	282927
Contig ID	132341_1.R1011
5'-most EST	uC-zmflmo17163g09b1

Seq. No.	282928
Contig ID	132349_1.R1011
5'-most EST	uC-zmflmo17163h05b1
Method	BLASTX
NCBI GI	g4432841
BLAST score	274
E value	5.0e-24
Match length	147
% identity	48
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282929
Contig ID	132384_1.R1011
5'-most EST	uC-zmflmo17164c06b1
Method	BLASTX
NCBI GI	g2245000
BLAST score	190
E value	4.0e-14
Match length	147
% identity	35
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	282930
Contig ID	132446_1.R1011
5'-most EST	uC-zmflmo17164h09b1
Method	BLASTX
NCBI GI	g3608495
BLAST score	292
E value	4.0e-26
Match length	113
% identity	57
NCBI Description	(AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]

Seq. No.	282931
Contig ID	132447_1.R1011
5'-most EST	uC-zmflmo17164h10b1

Seq. No.	282932
Contig ID	132451_1.R1011
5'-most EST	uC-zmflmo17165a05b1
Method	BLASTN
NCBI GI	g2921303
BLAST score	260
E value	1.0e-144
Match length	435
% identity	91
NCBI Description	Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds

Seq. No.	282933
Contig ID	132474_1.R1011
5'-most EST	uC-zmflb73205a11b2

Seq. No.	282934
Contig ID	132504_1.R1011
5'-most EST	pmx700089482.h1
Method	BLASTX
NCBI GI	g100487
BLAST score	240
E value	5.0e-20
Match length	182
% identity	35
NCBI Description	TNP1 protein - garden snapdragon >gi_16057_emb_CAA40554_ (X57297) TNP1 [Antirrhinum majus]

Seq. No.	282935

Contig ID	132506_1.R1011
5'-most EST	uC-zmflmo17282d05b1
Seq. No.	282936
Contig ID	132535_1.R1011
5'-most EST	uC-zmflmo17166a03b1
Method	BLASTX
NCBI GI	g2257530
BLAST score	272
E value	7.0e-24
Match length	141
% identity	40
NCBI Description	(AB004537) hypothetical protein YPL063w [Schizosaccharomyces pombe]
Seq. No.	282937
Contig ID	132541_1.R1011
5'-most EST	rvt700551262.h1
Seq. No.	282938
Contig ID	132541_2.R1011
5'-most EST	cyk700048537.f1
Seq. No.	282939
Contig ID	132557_1.R1011
5'-most EST	uC-zmflmo17166c04b1
Seq. No.	282940
Contig ID	132566_1.R1011
5'-most EST	uC-zmflb73238e10b2
Seq. No.	282941
Contig ID	132572_1.R1011
5'-most EST	uC-zmflmo17166d07b1
Seq. No.	282942
Contig ID	132586_1.R1011
5'-most EST	ceu700425055.h1
Seq. No.	282943
Contig ID	132605_1.R1011
5'-most EST	uC-zmflmo17166g09b1
Seq. No.	282944
Contig ID	132611_1.R1011
5'-most EST	pmx700090056.h1
Seq. No.	282945
Contig ID	132612_1.R1011
5'-most EST	uC-zmflmo17166h06b1
Seq. No.	282946
Contig ID	132616_1.R1011
5'-most EST	ntr700073357.h1
Seq. No.	282947
Contig ID	132630_1.R1011

5'-most EST	xjt700095188.h1
Method	BLASTX
NCBI GI	g4204284
BLAST score	514
E value	3.0e-52
Match length	171
% identity	55
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	282948
Contig ID	132651_1.R1011
5'-most EST	uC-zmflmo17168d06b1
Method	BLASTX
NCBI GI	g3157910
BLAST score	839
E value	3.0e-90
Match length	177
% identity	93
NCBI Description	(AF003551) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Zea mays]

Seq. No.	282949
Contig ID	132653_1.R1011
5'-most EST	uC-zmflmo17168d08b1
Method	BLASTX
NCBI GI	g4582489
BLAST score	349
E value	7.0e-33
Match length	155
% identity	50
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	282950
Contig ID	132654_1.R1011
5'-most EST	uC-zmflmo17168d09b1

Seq. No.	282951
Contig ID	132663_1.R1011
5'-most EST	wyr700243456.h1

Seq. No.	282952
Contig ID	132695_1.R1011
5'-most EST	uC-zmflmo17168h10b1
Method	BLASTX
NCBI GI	g4091810
BLAST score	397
E value	2.0e-38
Match length	162
% identity	46
NCBI Description	(AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1 [Arabidopsis thaliana]

Seq. No.	282953
Contig ID	132701_1.R1011
5'-most EST	uC-zmflmo17169a10b1

Seq. No.	282954
Contig ID	132702_1.R1011
5'-most EST	uC-zmflmo17169a05b1
Method	BLASTX
NCBI GI	g3386597
BLAST score	162
E value	7.0e-11
Match length	48
% identity	67
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana] >gi_3702347 (AC005397) putative permease [Arabidopsis thaliana]

Seq. No.	282955
Contig ID	132710_1.R1011
5'-most EST	uC-zmflmo17169b01a1

Seq. No.	282956
Contig ID	132712_1.R1011
5'-most EST	uC-zmflmo17169b03b1
Method	BLASTX
NCBI GI	g3183088
BLAST score	308
E value	8.0e-28
Match length	96
% identity	55
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	282957
Contig ID	132723_1.R1011
5'-most EST	uC-zmflmo17169c02a1

Seq. No.	282958
Contig ID	132726_1.R1011
5'-most EST	uC-zmflmo17169c05b1
Method	BLASTX
NCBI GI	g4589062
BLAST score	791
E value	2.0e-84
Match length	163
% identity	95
NCBI Description	(AF120146) myo-inositol 1-phosphate synthase [Triticum aestivum] >gi_4589064_gb_AAD26331.1_AF120147_1 (AF120147) myo-inositol 1-phosphate synthase [Triticum aestivum] >gi_4589066_gb_AAD26332.1_AF120148_1 (AF120148) myo-inositol 1-phosphate synthase [Triticum aestivum]

Seq. No.	282959
Contig ID	132735_1.R1011
5'-most EST	uC-zmflmo17169d07b1
Method	BLASTX
NCBI GI	g3869255
BLAST score	295
E value	1.0e-47

Match length	112
% identity	89
NCBI Description	(U79562) defender against death homolog Peadad [Pisum sativum]

Seq. No.	282960
Contig ID	132750_1.R1011
5'-most EST	uC-zmflmo17169f01b1
Method	BLASTX
NCBI GI	g464846
BLAST score	365
E value	1.0e-34
Match length	70
% identity	100
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	282961
Contig ID	132759_1.R1011
5'-most EST	uC-zmflmo17169f10b1
Method	BLASTX
NCBI GI	g543565
BLAST score	235
E value	3.0e-19
Match length	74
% identity	58
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans] >gi_641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	282962
Contig ID	132762_1.R1011
5'-most EST	uC-zmflmo17169g01b1
Method	BLASTX
NCBI GI	g4033365
BLAST score	553
E value	1.0e-56
Match length	113
% identity	88
NCBI Description	(AJ223499) ATP sulfurylase [Brassica juncea]

Seq. No.	282963
Contig ID	132765_1.R1011
5'-most EST	uC-zmflmo17169g05b1

Seq. No.	282964
Contig ID	132766_1.R1011
5'-most EST	uC-zmflmo17169g06b1

Seq. No.	282965
Contig ID	132773_1.R1011
5'-most EST	uC-zmflmo17169h02b1
Method	BLASTX
NCBI GI	g1657855
BLAST score	319

E value	3.0e-29
Match length	104
% identity	58
NCBI Description	(U73216) cold acclimation protein WCOR413 [Triticum aestivum]

Seq. No.	282966
Contig ID	132776_1.R1011
5'-most EST	uC-zmflmo17169h05b1
Method	BLASTX
NCBI GI	g4508068
BLAST score	240
E value	1.0e-21
Match length	91
% identity	67
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	282967
Contig ID	132778_1.R1011
5'-most EST	uC-zmflmo17169h07b1
Method	BLASTX
NCBI GI	g3080435
BLAST score	311
E value	2.0e-28
Match length	97
% identity	67
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	282968
Contig ID	132790_1.R1011
5'-most EST	uC-zmflmo17171a07b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	38
E value	8.0e-12
Match length	38
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	282969
Contig ID	132806_1.R1011
5'-most EST	pwr700450427.h1
Method	BLASTX
NCBI GI	g3036810
BLAST score	210
E value	3.0e-16
Match length	159
% identity	33
NCBI Description	(AL022373) putative Myc-type transcription factor [Arabidopsis thaliana]

Seq. No.	282970
Contig ID	132819_1.R1011
5'-most EST	uC-zmflb73301g02b2
Method	BLASTX
NCBI GI	g1931639
BLAST score	216

E value	2.0e-17
Match length	126
% identity	33
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	282971
Contig ID	132823_1.R1011
5'-most EST	uC-zmflmo17171d09b1
Method	BLASTX
NCBI GI	g2618699
BLAST score	216
E value	3.0e-17
Match length	153
% identity	32
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	282972
Contig ID	132830_1.R1011
5'-most EST	nbm700468974.h1
Method	BLASTX
NCBI GI	g1181615
BLAST score	261
E value	1.0e-22
Match length	81
% identity	74
NCBI Description	(D83078) nitrilase [Nicotiana tabacum]

Seq. No.	282973
Contig ID	132833_1.R1011
5'-most EST	uC-zmroteosinte001f08b1
Method	BLASTX
NCBI GI	g2280530
BLAST score	610
E value	2.0e-63
Match length	117
% identity	91
NCBI Description	(AB005889) ATMYB4 [Arabidopsis thaliana]

Seq. No.	282974
Contig ID	132833_2.R1011
5'-most EST	uC-zmflmo17171e08b1
Method	BLASTX
NCBI GI	g3482929
BLAST score	233
E value	2.0e-19
Match length	45
% identity	87
NCBI Description	(AC003970) Putative transcription factor [Arabidopsis thaliana]

Seq. No.	282975
Contig ID	132840_1.R1011
5'-most EST	uC-zmflmo17171f04b1

Seq. No.	282976
Contig ID	132855_1.R1011
5'-most EST	uC-zmflb73191g10a1

Method	BLASTX
NCBI GI	g3775987
BLAST score	726
E value	9.0e-77
Match length	255
% identity	56
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.	282977
Contig ID	132869_1.R1011
5'-most EST	clt700044509.f1

Seq. No.	282978
Contig ID	132881_1.R1011
5'-most EST	cyk700050545.f1
Method	BLASTN
NCBI GI	g2924729
BLAST score	45
E value	8.0e-16
Match length	188
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	282979
Contig ID	132891_1.R1011
5'-most EST	uer700578426.h1

Seq. No.	282980
Contig ID	132908_1.R1011
5'-most EST	uC-zmflmo17173e08b1

Seq. No.	282981
Contig ID	132917_1.R1011
5'-most EST	uC-zmflb73129d04a1
Method	BLASTX
NCBI GI	g3204103
BLAST score	311
E value	2.0e-28
Match length	115
% identity	57
NCBI Description	(AJ006761) hypothetical protein [Cicer arietinum]

Seq. No.	282982
Contig ID	132918_1.R1011
5'-most EST	fC-zmfl700610803a1
Method	BLASTX
NCBI GI	g4544445
BLAST score	732
E value	9.0e-78
Match length	171
% identity	81
NCBI Description	(AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]

Seq. No.	282983
Contig ID	132919_1.R1011

5'-most EST	nbm700471070.h1
Seq. No.	282984
Contig ID	132930_1.R1011
5'-most EST	uC-zmflmo17173h10b1
Method	BLASTX
NCBI GI	g2224911
BLAST score	252
E value	2.0e-21
Match length	204
% identity	36
NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]
Seq. No.	282985
Contig ID	132941_1.R1011
5'-most EST	uC-zmflmo17174a10b1
Method	BLASTX
NCBI GI	g4376158
BLAST score	169
E value	8.0e-12
Match length	50
% identity	70
NCBI Description	(X98873) aspartate kinase [Arabidopsis thaliana]
Seq. No.	282986
Contig ID	132942_1.R1011
5'-most EST	pmx700085021.h1
Seq. No.	282987
Contig ID	132947_1.R1011
5'-most EST	uC-zmflmo17174b05b1
Method	BLASTX
NCBI GI	g421989
BLAST score	228
E value	2.0e-18
Match length	130
% identity	43
NCBI Description	serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx [Hordeum vulgare]
Seq. No.	282988
Contig ID	132952_1.R1011
5'-most EST	xjt700095727.h1
Method	BLASTX
NCBI GI	g3549656
BLAST score	358
E value	8.0e-34
Match length	165
% identity	48
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]
Seq. No.	282989
Contig ID	132961_1.R1011
5'-most EST	pwf700321780.h1
Method	BLASTX

NCBI GI	g1091678
BLAST score	251
E value	2.0e-21
Match length	105
% identity	50
NCBI Description	activator-like transposable element [Pennisetum glaucum]

Seq. No.	282990
Contig ID	132966_1.R1011
5'-most EST	uC-zmflmo17174d03b1

Seq. No.	282991
Contig ID	132967_1.R1011
5'-most EST	uC-zmroteosinte115h12b1

Seq. No.	282992
Contig ID	132974_1.R1011
5'-most EST	uwc700156105.h2

Seq. No.	282993
Contig ID	132982_1.R1011
5'-most EST	uC-zmflmo17174e11b1
Method	BLASTX
NCBI GI	g1840425
BLAST score	383
E value	7.0e-37
Match length	129
% identity	54
NCBI Description	(U36586) alcohol dehydrogenase [Vitis vinifera]

Seq. No.	282994
Contig ID	132993_1.R1011
5'-most EST	nwy700443820.h1
Method	BLASTX
NCBI GI	g4262174
BLAST score	1138
E value	1.0e-129
Match length	294
% identity	74
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	282995
Contig ID	132998_1.R1011
5'-most EST	clt700044191.f1

Seq. No.	282996
Contig ID	133022_1.R1011
5'-most EST	wyr700237196.h1
Method	BLASTX
NCBI GI	g3193297
BLAST score	479
E value	3.0e-48
Match length	140
% identity	62
NCBI Description	(AF069298) similar to epoxide hydrolases [Arabidopsis thaliana]

Seq. No.	282997
Contig ID	133031_1.R1011
5'-most EST	uC-zmflmo17175b07b1
Method	BLASTX
NCBI GI	g4455231
BLAST score	333
E value	7.0e-31
Match length	82
% identity	63
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	282998
Contig ID	133033_1.R1011
5'-most EST	uC-zmflmo17330c02b1

Seq. No.	282999
Contig ID	133034_1.R1011
5'-most EST	uC-zmflmo17198d08b1
Method	BLASTX
NCBI GI	g1263160
BLAST score	1004
E value	1.0e-109
Match length	262
% identity	26
NCBI Description	(X89226) leucine-rich repeat/receptor protein kinase [Oryza sativa]

Seq. No.	283000
Contig ID	133038_1.R1011
5'-most EST	ymt700222965.h1
Method	BLASTX
NCBI GI	g3915947
BLAST score	166
E value	2.0e-11
Match length	86
% identity	40
NCBI Description	HYPOTHETICAL 34.2 KD PROTEIN IN DING-GLNQ INTERGENIC REGION

Seq. No.	283001
Contig ID	133039_1.R1011
5'-most EST	uC-zmflmo17175c03b1

Seq. No.	283002
Contig ID	133051_1.R1011
5'-most EST	uC-zmflmo17266c04b1
Method	BLASTX
NCBI GI	g3746069
BLAST score	264
E value	1.0e-22
Match length	223
% identity	28
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	283003
Contig ID	133053_1.R1011
5'-most EST	uC-zmflmo17342a01a1

Method	BLASTX
NCBI GI	g3355717
BLAST score	427
E value	9.0e-79
Match length	180
% identity	88
NCBI Description	(Y13053) seryl-tRNA synthetase [Zea mays]

Seq. No.	283004
Contig ID	133072_1.R1011
5'-most EST	ntr700072534.h1
Method	BLASTX
NCBI GI	g3063445
BLAST score	325
E value	5.0e-30
Match length	141
% identity	8
NCBI Description	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq. No.	283005
Contig ID	133086_1.R1011
5'-most EST	xmt700266102.h1
Method	BLASTX
NCBI GI	g3037013
BLAST score	148
E value	3.0e-09
Match length	100
% identity	31
NCBI Description	(AF037448) Gry-rbp [Homo sapiens]

Seq. No.	283006
Contig ID	133100_1.R1011
5'-most EST	fdz701159518.h1
Method	BLASTX
NCBI GI	g2829885
BLAST score	319
E value	4.0e-29
Match length	87
% identity	64
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	283007
Contig ID	133127_1.R1011
5'-most EST	uC-zmflmo17176c02b1

Seq. No.	283008
Contig ID	133137_1.R1011
5'-most EST	uC-zmflmo17176c12b1

Seq. No.	283009
Contig ID	133163_1.R1011
5'-most EST	uC-zmflmo17176f02b1
Method	BLASTX
NCBI GI	g1762144
BLAST score	410
E value	9.0e-40
Match length	221

% identity	38
NCBI Description	(U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No.	283010
Contig ID	133169_1.R1011
5'-most EST	xmt700260621.h1
Method	BLASTX
NCBI GI	g2292978
BLAST score	422
E value	3.0e-41
Match length	148
% identity	59
NCBI Description	(Y10253) pantoate--beta-alanine ligase [Oryza sativa]

Seq. No.	283011
Contig ID	133184_1.R1011
5'-most EST	uC-zmflmo17176h02b1

Seq. No.	283012
Contig ID	133194_1.R1011
5'-most EST	uC-zmflmo17179a01b1
Method	BLASTX
NCBI GI	g4582783
BLAST score	757
E value	1.0e-80
Match length	183
% identity	75
NCBI Description	(AJ006752) starch synthase, isoform V [Vigna unguiculata]

Seq. No.	283013
Contig ID	133202_1.R1011
5'-most EST	uC-zmflmo17179a09b1

Seq. No.	283014
Contig ID	133242_1.R1011
5'-most EST	uC-zmflmo17179e07b1
Method	BLASTX
NCBI GI	g3023751
BLAST score	145
E value	8.0e-09
Match length	109
% identity	36
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	283015
Contig ID	133244_1.R1011
5'-most EST	uC-zmflmo17259a09b1
Method	BLASTX
NCBI GI	g4336747
BLAST score	1089
E value	1.0e-119
Match length	238
% identity	92

NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No.	283016
Contig ID	133248_1.R1011
5'-most EST	uC-zmflmo17245b07b1

Seq. No.	283017
Contig ID	133257_1.R1011
5'-most EST	xmt700263079.h1
Method	BLASTX
NCBI GI	g3046731
BLAST score	410
E value	6.0e-40
Match length	91
% identity	85
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	283018
Contig ID	133314_1.R1011
5'-most EST	uC-zmflmo17180d02b1

Seq. No.	283019
Contig ID	133322_1.R1011
5'-most EST	uC-zmflmo17180d11b1
Method	BLASTX
NCBI GI	g4204268
BLAST score	413
E value	2.0e-40
Match length	102
% identity	75
NCBI Description	(AC005223) 62134 [Arabidopsis thaliana]

Seq. No.	283020
Contig ID	133332_1.R1011
5'-most EST	uC-zmflmo17180e09b1

Seq. No.	283021
Contig ID	133333_1.R1011
5'-most EST	xsy700207933.h1
Method	BLASTX
NCBI GI	g2352799
BLAST score	867
E value	1.0e-93
Match length	188
% identity	90
NCBI Description	(AF007795) retinoblastoma-related protein 2b [Zea mays]

Seq. No.	283022
Contig ID	133335_1.R1011
5'-most EST	uC-zmflmo17295h04b1

Seq. No.	283023
Contig ID	133364_1.R1011
5'-most EST	uC-zmflmo17180h07b1

Seq. No.	283024
Contig ID	133377_1.R1011

5'-most EST	uC-zmflb73349g01a2
Method	BLASTX
NCBI GI	g4204282
BLAST score	490
E value	3.0e-49
Match length	163
% identity	53
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	283025
Contig ID	133411_1.R1011
5'-most EST	uC-zmflmo17184f04b1
Method	BLASTX
NCBI GI	g3885336
BLAST score	276
E value	3.0e-24
Match length	181
% identity	39
NCBI Description	(AC005623) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	283026
Contig ID	133447_1.R1011
5'-most EST	uC-zmflmo17185a04b1

Seq. No.	283027
Contig ID	133459_1.R1011
5'-most EST	uC-zmflb73217a08b2

Seq. No.	283028
Contig ID	133464_1.R1011
5'-most EST	uC-zmflmo17185b11b1
Method	BLASTX
NCBI GI	g2160694
BLAST score	207
E value	3.0e-16
Match length	85
% identity	51
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	283029
Contig ID	133467_1.R1011
5'-most EST	uC-zmflmo17185c02b1

Seq. No.	283030
Contig ID	133470_1.R1011
5'-most EST	uC-zmflmo17185c05b1

Seq. No.	283031
Contig ID	133485_1.R1011
5'-most EST	uC-zmflmo17185d09b1
Method	BLASTX
NCBI GI	g3059131
BLAST score	327
E value	3.0e-30
Match length	154

% identity	45
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	283032
Contig ID	133487_1.R1011
5'-most EST	uC-zmflmo17185d11b1
Method	BLASTX
NCBI GI	g135053
BLAST score	371
E value	2.0e-35
Match length	165
% identity	47
NCBI Description	SULFITE OXIDASE >gi_86440_pir__A34180 sulfite oxidase (EC 1.8.3.1), hepatic - chicken

Seq. No.	283033
Contig ID	133499_1.R1011
5'-most EST	uC-zmflmo17185e12b1
Method	BLASTX
NCBI GI	g1504012
BLAST score	168
E value	2.0e-11
Match length	64
% identity	50
NCBI Description	(D86969) similar to Human zinc-finger protein, BR140(P1:JC2069) [Homo sapiens]

Seq. No.	283034
Contig ID	133503_1.R1011
5'-most EST	uC-zmflmo17185g05b1

Seq. No.	283035
Contig ID	133506_1.R1011
5'-most EST	uC-zmflmo17185f08b1

Seq. No.	283036
Contig ID	133559_1.R1011
5'-most EST	uC-zmflmo17186c05b1

Seq. No.	283037
Contig ID	133593_1.R1011
5'-most EST	uC-zmflmo17186f05b1
Method	BLASTX
NCBI GI	g4468991
BLAST score	143
E value	9.0e-09
Match length	117
% identity	34
NCBI Description	(AL035605) ribosomal-like protein [Arabidopsis thaliana]

Seq. No.	283038
Contig ID	133601_1.R1011
5'-most EST	uC-zmflmo17186g08b1

Seq. No.	283039
Contig ID	133602_1.R1011
5'-most EST	uC-zmflmo17186g04b1

Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	283040
Contig ID	133617_1.R1011
5'-most EST	fC-zmle700444043f7
Method	BLASTX
NCBI GI	g2351097
BLAST score	1102
E value	1.0e-121
Match length	275
% identity	72
NCBI Description	(AB006810) ATMRK1 [Arabidopsis thaliana]

Seq. No.	283041
Contig ID	133618_1.R1011
5'-most EST	tzu700201565.h1

Seq. No.	283042
Contig ID	133664_1.R1011
5'-most EST	uC-zmflmo17187e03b1
Method	BLASTX
NCBI GI	g3892055
BLAST score	769
E value	5.0e-82
Match length	188
% identity	73
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	283043
Contig ID	133672_1.R1011
5'-most EST	uC-zmflmo17344g10b1

Seq. No.	283044
Contig ID	133675_1.R1011
5'-most EST	nbm700473713.h1

Seq. No.	283045
Contig ID	133692_1.R1011
5'-most EST	uC-zmflmo17266a05a1

Seq. No.	283046
Contig ID	133719_1.R1011
5'-most EST	uC-zmroteosinte120f06b2

Seq. No.	283047
Contig ID	133731_1.R1011
5'-most EST	uC-zmflmo17190c11b1

Seq. No.	283048
Contig ID	133747_1.R1011

5'-most EST	yyf700351468.h1
Seq. No.	283049
Contig ID	133771_1.R1011
5'-most EST	uC-zmflmo17058f09a1
Seq. No.	283050
Contig ID	133790_1.R1011
5'-most EST	clt700045969.f1
Method	BLASTX
NCBI GI	g575605
BLAST score	164
E value	3.0e-11
Match length	66
% identity	56
NCBI Description	(D42065) cationic peroxidase isozyme 40K precursor [Nicotiana tabacum]
Seq. No.	283051
Contig ID	133841_1.R1011
5'-most EST	uC-zmflb73132d09a1
Seq. No.	283052
Contig ID	133844_1.R1011
5'-most EST	uC-zmflmo17192g12b1
Seq. No.	283053
Contig ID	133852_1.R1011
5'-most EST	gwl700614444.h1
Seq. No.	283054
Contig ID	133852_2.R1011
5'-most EST	fC-zmle700579741f1
Method	BLASTX
NCBI GI	g4191775
BLAST score	198
E value	3.0e-15
Match length	110
% identity	54
NCBI Description	(AC005917) putative acyl-CoA cholesterol acyltransferase [Arabidopsis thaliana]
Seq. No.	283055
Contig ID	133865_1.R1011
5'-most EST	uC-zmflmo17193b03b1
Seq. No.	283056
Contig ID	133901_1.R1011
5'-most EST	nbm700469369.h1
Seq. No.	283057
Contig ID	133948_1.R1011
5'-most EST	uC-zmflmo17195g01b1
Method	BLASTX
NCBI GI	g1402888
BLAST score	422
E value	1.0e-41

Match length	142
% identity	58
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	283058
Contig ID	133956_1.R1011
5'-most EST	uC-zmflmo17195g09b1
Method	BLASTX
NCBI GI	g2623297
BLAST score	201
E value	2.0e-15
Match length	124
% identity	38
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3790583 (AF079180) RING-H2 finger protein RHC1a [Arabidopsis thaliana]

Seq. No.	283059
Contig ID	133961_1.R1011
5'-most EST	uC-zmflmo17195h03b1

Seq. No.	283060
Contig ID	133973_1.R1011
5'-most EST	uC-zmflmo17197a11b1

Seq. No.	283061
Contig ID	133986_1.R1011
5'-most EST	uC-zmflmo17204d08b1
Method	BLASTX
NCBI GI	g3281846
BLAST score	351
E value	4.0e-33
Match length	80
% identity	82
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	283062
Contig ID	133994_1.R1011
5'-most EST	uwc700153956.h1
Method	BLASTX
NCBI GI	g2243118
BLAST score	604
E value	1.0e-62
Match length	183
% identity	62
NCBI Description	(Y10984) glutathione synthetase [Brassica juncea]

Seq. No.	283063
Contig ID	134000_1.R1011
5'-most EST	uC-zmflmo17197d05a1

Seq. No.	283064
Contig ID	134060_1.R1011
5'-most EST	xtj700378286.h1

Seq. No.	283065
Contig ID	134070_1.R1011

5'-most EST	uC-zmflmo17289a07b1
Method	BLASTX
NCBI GI	g3790571
BLAST score	159
E value	2.0e-10
Match length	52
% identity	50
NCBI Description	(AF078823) RING-H2 finger protein RHA2b [Arabidopsis thaliana]

Seq. No.	283066
Contig ID	134076_1.R1011
5'-most EST	xdb700341757.h1
Method	BLASTX
NCBI GI	g2262113
BLAST score	200
E value	2.0e-15
Match length	56
% identity	62
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	283067
Contig ID	134104_1.R1011
5'-most EST	uC-zmflmo17198f06b1
Method	BLASTX
NCBI GI	g2443881
BLAST score	306
E value	8.0e-28
Match length	84
% identity	62
NCBI Description	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]

Seq. No.	283068
Contig ID	134120_1.R1011
5'-most EST	uC-zmflmo17198g12b1

Seq. No.	283069
Contig ID	134123_1.R1011
5'-most EST	uC-zmflb73166c04a1

Seq. No.	283070
Contig ID	134216_1.R1011
5'-most EST	uC-zmflmo17199h06b1

Seq. No.	283071
Contig ID	134220_1.R1011
5'-most EST	uC-zmflmo17199h10b1

Seq. No.	283072
Contig ID	134231_1.R1011
5'-most EST	uC-zmflmo17201a10b1
Method	BLASTX
NCBI GI	g113334
BLAST score	194
E value	9.0e-31
Match length	155

% identity	41
NCBI Description	ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) >gi_90291_pir__A30111 alpha-adaptin A - mouse >gi_49878_emb_CAA33096_ (X14971) alpha-adaptin (A) (AA 1-977) [Mus musculus]

Seq. No.	283073
Contig ID	134232_1.R1011
5'-most EST	uC-zmflmo17201a11b1
Method	BLASTX
NCBI GI	g4262174
BLAST score	594
E value	8.0e-76
Match length	219
% identity	63
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	283074
Contig ID	134266_1.R1011
5'-most EST	uC-zmflmo17201d11b1
Method	BLASTX
NCBI GI	g1175252
BLAST score	152
E value	2.0e-09
Match length	90
% identity	37
NCBI Description	HYPOTHETICAL PROTEIN HI0488 >gi_1074418_pir__D64008 hypothetical protein HI0488 - Haemophilus influenzae (strain Rd KW20) >gi_1573468 (U32731) conserved hypothetical protein [Haemophilus influenzae Rd]

Seq. No.	283075
Contig ID	134285_1.R1011
5'-most EST	uC-zmflmo17201f12b1

Seq. No.	283076
Contig ID	134294_1.R1011
5'-most EST	uC-zmflmo17201g03b1

Seq. No.	283077
Contig ID	134300_1.R1011
5'-most EST	fdz701166388.h1

Seq. No.	283078
Contig ID	134304_1.R1011
5'-most EST	uC-zmflmo17201h02b1

Seq. No.	283079
Contig ID	134319_1.R1011
5'-most EST	uC-zmflmo17202a07b1

Seq. No.	283080
Contig ID	134348_1.R1011
5'-most EST	uC-zmflmo17202d02b1
Method	BLASTX

NCBI GI	g2829910
BLAST score	168
E value	1.0e-11
Match length	162
% identity	30
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	283081
Contig ID	134354_1.R1011
5'-most EST	xyt700346911.h1
Method	BLASTX
NCBI GI	g2496950
BLAST score	257
E value	5.0e-22
Match length	140
% identity	41
NCBI Description	HYPOTHETICAL 41.7 KD PROTEIN F10B5.2 IN CHROMOSOME II >gi_3875710_emb_CAA88309_ (Z48334) F10B5.2 [Caenorhabditis elegans]

Seq. No.	283082
Contig ID	134362_1.R1011
5'-most EST	uC-zmflmo17309c11b1
Method	BLASTX
NCBI GI	g2130442
BLAST score	254
E value	1.0e-21
Match length	188
% identity	33
NCBI Description	hypothetical protein SPAC8A4.01c - fission yeast (Schizosaccharomyces pombe) (fragment) >gi_1052534_emb_CAA91511_ (Z66569) unknown [Schizosaccharomyces pombe]

Seq. No.	283083
Contig ID	134370_1.R1011
5'-most EST	uC-zmflmo17202f02b1
Method	BLASTX
NCBI GI	g4468812
BLAST score	389
E value	2.0e-37
Match length	118
% identity	62
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	283084
Contig ID	134374_1.R1011
5'-most EST	uC-zmflmo17202f06b1

Seq. No.	283085
Contig ID	134375_1.R1011
5'-most EST	rvt700552812.h1
Method	BLASTX
NCBI GI	g2330651
BLAST score	675
E value	8.0e-77

Match length	195
% identity	73
NCBI Description	(Y14559) topoisomerase II [Pisum sativum]

Seq. No.	283086
Contig ID	134381_1.R1011
5'-most EST	uC-zmflmo17202g01b1

Seq. No.	283087
Contig ID	134382_1.R1011
5'-most EST	cyk700050862.f1
Method	BLASTX
NCBI GI	g4587572
BLAST score	522
E value	5.0e-53
Match length	225
% identity	50
NCBI Description	(AC006550) Similar to gb_U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF_00400 WD40, G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from this gene. [Arabidopsis thaliana]

Seq. No.	283088
Contig ID	134391_1.R1011
5'-most EST	fwa700101849.h1

Seq. No.	283089
Contig ID	134396_1.R1011
5'-most EST	uC-zmflmo17202h05b1

Seq. No.	283090
Contig ID	134398_1.R1011
5'-most EST	uC-zmflmo17202h07b1
Method	BLASTN
NCBI GI	g507770
BLAST score	34
E value	3.0e-09
Match length	58
% identity	90
NCBI Description	Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete cds

Seq. No.	283091
Contig ID	134419_1.R1011
5'-most EST	uC-zmflmo17204b05b1
Method	BLASTX
NCBI GI	g4262176
BLAST score	193
E value	1.0e-14
Match length	44
% identity	73
NCBI Description	(AC005508) 18857 [Arabidopsis thaliana]

Seq. No.	283092
Contig ID	134435_1.R1011
5'-most EST	uC-zmflmo17204c11b1

Seq. No.	283093
Contig ID	134437_1.R1011
5'-most EST	uC-zmflmo17342g06b1

Seq. No.	283094
Contig ID	134447_1.R1011
5'-most EST	uC-zmflmo17204e01b1
Method	BLASTX
NCBI GI	g3269292
BLAST score	242
E value	2.0e-20
Match length	70
% identity	56
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	283095
Contig ID	134456_1.R1011
5'-most EST	uC-zmflmo17204e11b1

Seq. No.	283096
Contig ID	134469_1.R1011
5'-most EST	ntr700077415.h1
Method	BLASTX
NCBI GI	g3201615
BLAST score	429
E value	4.0e-42
Match length	192
% identity	47
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	283097
Contig ID	134477_1.R1011
5'-most EST	uC-zmflmo17204g09b1
Method	BLASTX
NCBI GI	g3860255
BLAST score	179
E value	6.0e-13
Match length	79
% identity	47
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283098
Contig ID	134477_2.R1011
5'-most EST	cat700022067.r1
Method	BLASTX
NCBI GI	g3860255
BLAST score	209
E value	2.0e-16
Match length	94
% identity	46
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283099
Contig ID	134480_1.R1011
5'-most EST	rvt700548921.h1

Seq. No.	283100

Contig ID	134488_1.R1011
5'-most EST	uC-zmflmo17204h10b1
Method	BLASTX
NCBI GI	g3269290
BLAST score	318
E value	5.0e-43
Match length	133
% identity	60
NCBI Description	(AL030978) putative receptor like kinase [Arabidopsis thaliana]

Seq. No.	283101
Contig ID	134498_1.R1011
5'-most EST	ymt700222407.h1

Seq. No.	283102
Contig ID	134500_1.R1011
5'-most EST	xyt700343076.h1
Method	BLASTX
NCBI GI	g1177022
BLAST score	422
E value	3.0e-41
Match length	241
% identity	37
NCBI Description	HYPOTHETICAL PROTEIN KIAA0052

Seq. No.	283103
Contig ID	134506_1.R1011
5'-most EST	xsy700211779.h1

Seq. No.	283104
Contig ID	134509_1.R1011
5'-most EST	uC-zmflmo17215b07b1
Method	BLASTX
NCBI GI	g4006856
BLAST score	648
E value	1.0e-67
Match length	210
% identity	61
NCBI Description	(Z99707) receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	283105
Contig ID	134513_1.R1011
5'-most EST	uC-zmflb73260c01b2

Seq. No.	283106
Contig ID	134549_1.R1011
5'-most EST	wen700333194.h1
Method	BLASTX
NCBI GI	g2194119
BLAST score	159
E value	4.0e-11
Match length	52
% identity	53
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	283107
Contig ID	134556_1.R1011
5'-most EST	uC-zmroteosinte057e09b1

Seq. No.	283108
Contig ID	134566_1.R1011
5'-most EST	nwy700444175.h1
Method	BLASTX
NCBI GI	g4581207
BLAST score	866
E value	7.0e-96
Match length	255
% identity	68
NCBI Description	(Y17914) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	283109
Contig ID	134566_2.R1011
5'-most EST	nbm700473264.h1

Seq. No.	283110
Contig ID	134573_1.R1011
5'-most EST	uC-zmflmo17215h05b1

Seq. No.	283111
Contig ID	134643_1.R1011
5'-most EST	uC-zmflmo17217f08b1

Seq. No.	283112
Contig ID	134645_1.R1011
5'-most EST	uC-zmflmo17217f10b1

Seq. No.	283113
Contig ID	134671_2.R1011
5'-most EST	uC-zmroteosinte028a06b1
Method	BLASTX
NCBI GI	g4454464
BLAST score	447
E value	2.0e-44
Match length	124
% identity	60
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	283114
Contig ID	134682_1.R1011
5'-most EST	uC-zmflmo17219b01b1
Method	BLASTN
NCBI GI	g3925238
BLAST score	41
E value	1.0e-13
Match length	116
% identity	85
NCBI Description	Zea mays 6-phosphogluconate dehydrogenase isoenzyme A gene, partial cds

Seq. No.	283115
Contig ID	134684_1.R1011

5'-most EST	uC-zmroteosinte006b11b1
Method	BLASTX
NCBI GI	g2772934
BLAST score	646
E value	2.0e-67
Match length	197
% identity	59
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	283116
Contig ID	134685_1.R1011
5'-most EST	uC-zmflmo17307f09b1

Seq. No.	283117
Contig ID	134696_1.R1011
5'-most EST	nwy700447833.h1

Seq. No.	283118
Contig ID	134708_1.R1011
5'-most EST	tzu700205964.h1
Method	BLASTX
NCBI GI	g4220527
BLAST score	185
E value	2.0e-13
Match length	130
% identity	38
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	283119
Contig ID	134713_1.R1011
5'-most EST	uC-zmflmo17219e02b1

Seq. No.	283120
Contig ID	134742_1.R1011
5'-most EST	uC-zmflmo17219g10b1

Seq. No.	283121
Contig ID	134747_1.R1011
5'-most EST	uC-zmflmo17219h03b1
Method	BLASTN
NCBI GI	g507770
BLAST score	58
E value	1.0e-23
Match length	130
% identity	86
NCBI Description	Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete cds

Seq. No.	283122
Contig ID	134755_1.R1011
5'-most EST	uC-zmflmo17219h12b1

Seq. No.	283123
Contig ID	134780_1.R1011
5'-most EST	uC-zmflmo17330g05b1
Method	BLASTX

NCBI GI	g3810592
BLAST score	424
E value	2.0e-41
Match length	153
% identity	56
NCBI Description	(AC005398) unknown protein [Arabidopsis thaliana]

Seq. No.	283124
Contig ID	134812_1.R1011
5'-most EST	uC-zmflmo17220f04b1
Method	BLASTX
NCBI GI	g4185794
BLAST score	281
E value	7.0e-27
Match length	92
% identity	66
NCBI Description	(AF097025) cysteine desulfurase [Homo sapiens]

Seq. No.	283125
Contig ID	134841_1.R1011
5'-most EST	uC-zmflmo17221a03b1
Method	BLASTX
NCBI GI	g4490756
BLAST score	327
E value	2.0e-30
Match length	103
% identity	55
NCBI Description	(AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283126
Contig ID	134848_1.R1011
5'-most EST	rv1700455223.h1
Method	BLASTX
NCBI GI	g1769895
BLAST score	159
E value	8.0e-11
Match length	38
% identity	74
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]

Seq. No.	283127
Contig ID	134851_1.R1011
5'-most EST	uC-zmflmo17221b01b1

Seq. No.	283128
Contig ID	134853_1.R1011
5'-most EST	uC-zmflb73063b11a1
Method	BLASTX
NCBI GI	g122772
BLAST score	263
E value	8.0e-23
Match length	106
% identity	57
NCBI Description	TRANSCRIPTION FACTOR HBP-1B >gi_100809_pir__S15347 transcription factor HBP-1b - wheat >gi_21635_emb_CAA40102_ (X56782) HBP-1b [Triticum aestivum]

Seq. No.	283129
Contig ID	134858_1.R1011
5'-most EST	mwy700441870.h1
Seq. No.	283130
Contig ID	134861_1.R1011
5'-most EST	uC-zmflmo17056g03a1
Seq. No.	283131
Contig ID	134865_1.R1011
5'-most EST	pmx700085254.h1
Method	BLASTX
NCBI GI	g3024577
BLAST score	273
E value	5.0e-24
Match length	135
% identity	48
NCBI Description	HOMEOBOX PROTEIN ROUGH SHEATH 1 >gi_1008879 (L44133) RS1 gene product [Zea mays]
Seq. No.	283132
Contig ID	134873_1.R1011
5'-most EST	uC-zmflmo17221c12b1
Seq. No.	283133
Contig ID	134888_1.R1011
5'-most EST	uC-zmflmo17287g04b1
Seq. No.	283134
Contig ID	134890_1.R1011
5'-most EST	fC-zmfl700350123f2
Method	BLASTX
NCBI GI	g4559351
BLAST score	151
E value	9.0e-10
Match length	111
% identity	36
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]
Seq. No.	283135
Contig ID	134916_1.R1011
5'-most EST	cjh700196212.h1
Method	BLASTX
NCBI GI	g4165154
BLAST score	804
E value	8.0e-86
Match length	335
% identity	53
NCBI Description	(AF115482) topoisomerase I [Nicotiana tabacum]
Seq. No.	283136
Contig ID	134924_1.R1011
5'-most EST	uC-zmflmo17222b08b1
Seq. No.	283137
Contig ID	134948_1.R1011
5'-most EST	cyk700050842.f1

Seq. No. 283138
Contig ID 134949_1.R1011
5'-most EST uC-zmflmo17344d11b1

Seq. No. 283139
Contig ID 134956_1.R1011
5'-most EST uC-zmflmo17222e09b1

Seq. No. 283140
Contig ID 134960_1.R1011
5'-most EST uC-zmflmo17222f01b1

Seq. No. 283141
Contig ID 134962_1.R1011
5'-most EST uwc700156233.h1

Seq. No. 283142
Contig ID 134994_1.R1011
5'-most EST yyf700350705.h1

Seq. No. 283143
Contig ID 134998_1.R1011
5'-most EST ntr700073339.h1

Seq. No. 283144
Contig ID 135043_1.R1011
5'-most EST uC-zmflmo17223e07b1

Seq. No. 283145
Contig ID 135059_1.R1011
5'-most EST uC-zmflmo17223f12b1

Seq. No. 283146
Contig ID 135076_1.R1011
5'-most EST uC-zmflmo17223h08b1

Seq. No. 283147
Contig ID 135076_2.R1011
5'-most EST xsy700208820.h1

Seq. No. 283148
Contig ID 135076_3.R1011
5'-most EST ceu700430309.h1

Seq. No. 283149
Contig ID 135081_1.R1011
5'-most EST uC-zmflmo17227a02b1
Method BLASTX
NCBI GI g1001382
BLAST score 537
E value 8.0e-55
Match length 105
% identity 98
NCBI Description (D64006) hypothetical protein [Synechocystis sp.]

Seq. No. 283150

Contig ID	135082_1.R1011
5'-most EST	uC-zmflmo17227a03b1
Method	BLASTX
NCBI GI	g1652097
BLAST score	830
E value	5.0e-89
Match length	156
% identity	99
NCBI Description	(D90902) cobyrinic acid a,c-diamide synthase [Synechocystis sp.]

Seq. No.	283151
Contig ID	135084_1.R1011
5'-most EST	uC-zmflmo17227a11b1
Method	BLASTX
NCBI GI	g1652558
BLAST score	1113
E value	1.0e-122
Match length	215
% identity	98
NCBI Description	(D90906) hypothetical protein [Synechocystis sp.]

Seq. No.	283152
Contig ID	135085_1.R1011
5'-most EST	uC-zmflmo17227a07b1
Method	BLASTX
NCBI GI	g1653081
BLAST score	153
E value	8.0e-10
Match length	151
% identity	26
NCBI Description	(D90910) sensory transduction histidine kinase [Synechocystis sp.]

Seq. No.	283153
Contig ID	135087_1.R1011
5'-most EST	uC-zmflmo17227a09b1
Method	BLASTX
NCBI GI	g1652840
BLAST score	659
E value	3.0e-69
Match length	129
% identity	98
NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]

Seq. No.	283154
Contig ID	135088_1.R1011
5'-most EST	uC-zmflmo17227a10b1
Method	BLASTX
NCBI GI	g1001724
BLAST score	474
E value	2.0e-48
Match length	102
% identity	95
NCBI Description	(D64004) phytoene dehydrogenase [Synechocystis sp.]

Seq. No.	283155

Contig ID	135091_1.R1011
5'-most EST	uC-zmflmo17227b01b1
Method	BLASTX
NCBI GI	g1001131
BLAST score	1014
E value	1.0e-110
Match length	211
% identity	93
NCBI Description	(D64001) hypothetical protein [Synechocystis sp.]

Seq. No.	283156
Contig ID	135092_1.R1011
5'-most EST	uC-zmflmo17227b02b1
Method	BLASTX
NCBI GI	g1653017
BLAST score	906
E value	4.0e-98
Match length	174
% identity	98
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	283157
Contig ID	135093_1.R1011
5'-most EST	uC-zmflmo17227b03b1
Method	BLASTN
NCBI GI	g1001701
BLAST score	467
E value	0.0e+00
Match length	498
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965

Seq. No.	283158
Contig ID	135095_1.R1011
5'-most EST	uC-zmflmo17227b06b1
Method	BLASTX
NCBI GI	g1652975
BLAST score	783
E value	8.0e-84
Match length	162
% identity	89
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	283159
Contig ID	135097_1.R1011
5'-most EST	uC-zmflmo17227b08b1
Method	BLASTN
NCBI GI	g1652225
BLAST score	589
E value	0.0e+00
Match length	629
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448

Seq. No.	283160

Contig ID	135100_1.R1011
5'-most EST	uC-zmflmo17227c01b1
Method	BLASTX
NCBI GI	g2492853
BLAST score	1237
E value	1.0e-137
Match length	240
% identity	99
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE (ACOAT) >gi_1652236_dbj_BAA17159_ (D90904) N-acetylornithine aminotransferase [Synechocystis sp.]

Seq. No.	283161
Contig ID	135103_1.R1011
5'-most EST	uC-zmflmo17227c04b1
Method	BLASTX
NCBI GI	g3122978
BLAST score	642
E value	4.0e-67
Match length	141
% identity	88
NCBI Description	PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE >gi_1652889_dbj_BAA17807_ (D90909) hypothetical protein [Synechocystis sp.]

Seq. No.	283162
Contig ID	135107_1.R1011
5'-most EST	uC-zmflmo17227c09b1
Method	BLASTN
NCBI GI	g1001200
BLAST score	634
E value	0.0e+00
Match length	638
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766

Seq. No.	283163
Contig ID	135109_1.R1011
5'-most EST	uC-zmflmo17227c11b1
Method	BLASTN
NCBI GI	g1653477
BLAST score	252
E value	1.0e-140
Match length	276
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 16/27, 1991550-2137258

Seq. No.	283164
Contig ID	135110_1.R1011
5'-most EST	uC-zmflmo17225c12a1
Method	BLASTX
NCBI GI	g1652015
BLAST score	460
E value	7.0e-66

Match length	176
% identity	71
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	283165
Contig ID	135112_1.R1011
5'-most EST	uC-zmflmo17227d02b1
Method	BLASTX
NCBI GI	g1001282
BLAST score	610
E value	4.0e-63
Match length	183
% identity	79
NCBI Description	(D64003) polyA polymerase [Synechocystis sp.]

Seq. No.	283166
Contig ID	135113_1.R1011
5'-most EST	uC-zmflmo17227d03b1
Method	BLASTX
NCBI GI	g1651718
BLAST score	781
E value	1.0e-83
Match length	151
% identity	99
NCBI Description	(D90899) phosphoribosylformyl glycinamidine synthetase II [Synechocystis sp.]

Seq. No.	283167
Contig ID	135114_1.R1011
5'-most EST	uC-zmflmo17227d04b1
Method	BLASTX
NCBI GI	g2493959
BLAST score	1131
E value	1.0e-124
Match length	218
% identity	99
NCBI Description	CYTOCHROME B6 >gi_683492_emb_CAA83452_ (Z31580) cytochrome b6 subunit of the cytochrome b6f complex [Synechocystis PCC6803] >gi_1001522_dbj_BAA10149_ (D64000) cytochrome b6 [Synechocystis sp.] >gi_1094919_prf__2107182A cytochrome b6 [Synechocystis sp.]

Seq. No.	283168
Contig ID	135115_1.R1011
5'-most EST	uC-zmflmo17227d05b1
Method	BLASTX
NCBI GI	g3287752
BLAST score	440
E value	1.0e-43
Match length	92
% identity	96
NCBI Description	PRECORRIN-6X REDUCTASE >gi_1651791_dbj_BAA16718_ (D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	283169
Contig ID	135116_1.R1011
5'-most EST	uC-zmflmo17227d06b1

Method	BLASTN
NCBI GI	g1651650
BLAST score	177
E value	4.0e-95
Match length	197
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859

Seq. No.	283170
Contig ID	135117_1.R1011
5'-most EST	uC-zmflmo17227d07b1
Method	BLASTX
NCBI GI	g2493483
BLAST score	388
E value	2.0e-37
Match length	77
% identity	96
NCBI Description	GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) >gi_1653440_dbj_BAA18354_ (D90913) glycerol kinase [Synechocystis sp.]

Seq. No.	283171
Contig ID	135118_1.R1011
5'-most EST	uC-zmflmo17227d08b1
Method	BLASTX
NCBI GI	g2496800
BLAST score	666
E value	1.0e-69
Match length	129
% identity	98
NCBI Description	HYPOTHETICAL 35.3 KD PROTEIN SLL1285 >gi_1652294_dbj_BAA17217_ (D90904) hypothetical protein [Synechocystis sp.]

Seq. No.	283172
Contig ID	135119_1.R1011
5'-most EST	uC-zmflmo17227d09b1
Method	BLASTX
NCBI GI	g1652249
BLAST score	782
E value	3.0e-83
Match length	152
% identity	98
NCBI Description	(D90904) hypothetical protein [Synechocystis sp.]

Seq. No.	283173
Contig ID	135120_1.R1011
5'-most EST	uC-zmflmo17227d10b1
Method	BLASTX
NCBI GI	g1001273
BLAST score	943
E value	1.0e-102
Match length	174
% identity	99
NCBI Description	(D64003) dTDP-glucose 4,6-dehydratase [Synechocystis sp.]

Seq. No.	283174

Contig ID	135121_1.R1011
5'-most EST	uC-zmflmo17227d11b1
Method	BLASTN
NCBI GI	g1652844
BLAST score	509
E value	0.0e+00
Match length	546
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418

Seq. No.	283175
Contig ID	135122_1.R1011
5'-most EST	uC-zmflmo17227d12b1
Method	BLASTX
NCBI GI	g1652478
BLAST score	1017
E value	1.0e-111
Match length	194
% identity	97
NCBI Description	(D90905) hypothetical protein [Synechocystis sp.]

Seq. No.	283176
Contig ID	135123_1.R1011
5'-most EST	uC-zmflmo17227e01b1
Method	BLASTX
NCBI GI	g1001594
BLAST score	880
E value	4.0e-95
Match length	176
% identity	98
NCBI Description	(D64000) sensory transduction histidine kinase [Synechocystis sp.]

Seq. No.	283177
Contig ID	135126_1.R1011
5'-most EST	uC-zmflmo17227e04b1
Method	BLASTX
NCBI GI	g1653935
BLAST score	247
E value	6.0e-21
Match length	70
% identity	73
NCBI Description	(D90917) hypothetical protein [Synechocystis sp.]

Seq. No.	283178
Contig ID	135128_1.R1011
5'-most EST	uC-zmflmo17227e06b1

Seq. No.	283179
Contig ID	135129_1.R1011
5'-most EST	uC-zmflmo17227e07b1
Method	BLASTX
NCBI GI	g1653109
BLAST score	803
E value	2.0e-89
Match length	200

% identity	84
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	283180
Contig ID	135132_1.R1011
5'-most EST	uC-zmflmo17227e10b1
Method	BLASTX
NCBI GI	g1651820
BLAST score	510
E value	1.0e-51
Match length	113
% identity	91
NCBI Description	(D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	283181
Contig ID	135136_1.R1011
5'-most EST	uC-zmflmo17229a03a1
Method	BLASTX
NCBI GI	g1653548
BLAST score	574
E value	5.0e-59
Match length	115
% identity	99
NCBI Description	(D90914) hypothetical protein [Synechocystis sp.]

Seq. No.	283182
Contig ID	135138_1.R1011
5'-most EST	uC-zmflmo17227f06b1
Method	BLASTX
NCBI GI	g2500385
BLAST score	1231
E value	1.0e-136
Match length	264
% identity	94
NCBI Description	30S RIBOSOMAL PROTEIN S1 HOMOLOG A >gi_1652650_dbj_BAA17570_ (D90907) 30S ribosomal protein S1 [Synechocystis sp.]

Seq. No.	283183
Contig ID	135142_1.R1011
5'-most EST	uC-zmflmo17227f10b1
Method	BLASTX
NCBI GI	g1651887
BLAST score	1419
E value	1.0e-158
Match length	274
% identity	100
NCBI Description	(D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	283184
Contig ID	135143_1.R1011
5'-most EST	uC-zmflmo17227f11b1
Method	BLASTX
NCBI GI	g1653640
BLAST score	885
E value	1.0e-95
Match length	166

% identity	99
NCBI Description	(D90915) serine/threonine protein kinase [Synechocystis sp.]

Seq. No.	283185
Contig ID	135144_1.R1011
5'-most EST	uC-zmflmo17227g01b1
Method	BLASTX
NCBI GI	g1001400
BLAST score	706
E value	9.0e-75
Match length	158
% identity	90
NCBI Description	(D63999) chemotaxis protein CheA [Synechocystis sp.]

Seq. No.	283186
Contig ID	135146_1.R1011
5'-most EST	uC-zmflmo17227g04b1
Method	BLASTX
NCBI GI	g1001731
BLAST score	548
E value	4.0e-56
Match length	119
% identity	94
NCBI Description	(D64004) low affinity sulfate transporter [Synechocystis sp.]

Seq. No.	283187
Contig ID	135149_1.R1011
5'-most EST	uC-zmflmo17227g07b1
Method	BLASTX
NCBI GI	g1652815
BLAST score	626
E value	2.0e-65
Match length	127
% identity	94
NCBI Description	(D90908) cell-cell signaling protein, C-factor [Synechocystis sp.]

Seq. No.	283188
Contig ID	135152_1.R1011
5'-most EST	uC-zmflmo17227g10b1
Method	BLASTX
NCBI GI	g3915583
BLAST score	1320
E value	1.0e-146
Match length	274
% identity	94
NCBI Description	HYPOTHETICAL SUGAR KINASE SLR0537 >gi_1001340_dbj_BAA10827_ (D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	283189
Contig ID	135153_1.R1011
5'-most EST	uC-zmflmo17227g11b1
Method	BLASTX
NCBI GI	g3023895
BLAST score	491

E value	2.0e-49
Match length	104
% identity	88
NCBI Description	PROBABLE GLUTAREDOXIN SLR1562 >gi_1653790_dbj_BAA18701_ (D90916) glutaredoxin [Synechocystis sp.]

Seq. No.	283190
Contig ID	135154_1.R1011
5'-most EST	uC-zmflmo17227g12b1
Method	BLASTX
NCBI GI	g97638
BLAST score	971
E value	1.0e-105
Match length	192
% identity	98
NCBI Description	translation elongation factor G - Synechocystis sp >gi_46483_emb_CAA46277_ (X65159) elongation factor G [Synechocystis PCC6803]

Seq. No.	283191
Contig ID	135158_1.R1011
5'-most EST	uC-zmflmo17227h04b1
Method	BLASTX
NCBI GI	g1652601
BLAST score	462
E value	2.0e-46
Match length	106
% identity	88
NCBI Description	(D90906) hypothetical protein [Synechocystis sp.]

Seq. No.	283192
Contig ID	135159_1.R1011
5'-most EST	uC-zmflmo17227h05b1
Method	BLASTX
NCBI GI	g3257120
BLAST score	162
E value	7.0e-11
Match length	152
% identity	26
NCBI Description	(AP000003) 230aa long hypothetical protein [Pyrococcus horikoshii]

Seq. No.	283193
Contig ID	135160_1.R1011
5'-most EST	uC-zmflmo17227h06b1
Method	BLASTX
NCBI GI	g1006592
BLAST score	814
E value	9.0e-89
Match length	179
% identity	96
NCBI Description	(D64005) magnesium and cobalt transport protein [Synechocystis sp.]

Seq. No.	283194
Contig ID	135166_1.R1011
5'-most EST	uC-zmflmo17227h12b1

Method	BLASTX
NCBI GI	g1651718
BLAST score	1343
E value	1.0e-149
Match length	257
% identity	99
NCBI Description	(D90899) phosphoribosylformyl glycinamidine synthetase II [Synechocystis sp.]

Seq. No.	283195
Contig ID	135168_1.R1011
5'-most EST	uC-zmflmo17229a02b1
Method	BLASTX
NCBI GI	g1346061
BLAST score	822
E value	2.0e-88
Match length	168
% identity	97
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 1 (GAPDH 1) (GAP-1) >gi_1084175_pir__S54150 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Synechocystis sp. (PCC 6803) >gi_785044_emb_CAA60134_ (X86375) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Synechocystis sp.]

Seq. No.	283196
Contig ID	135172_1.R1011
5'-most EST	uC-zmflmo17229a08b1
Method	BLASTX
NCBI GI	g732097
BLAST score	206
E value	4.0e-16
Match length	95
% identity	42
NCBI Description	HYPOTHETICAL 53.0 KD PROTEIN IN IADA-MCRD INTERGENIC REGION (F470) >gi_1361109_pir__S56565 hypothetical protein f470 - Escherichia coli >gi_537181 (U14003) ORF_f470 [Escherichia coli] >gi_1790797 (AE000504) putative regulator [Escherichia coli]

Seq. No.	283197
Contig ID	135174_1.R1011
5'-most EST	uC-zmflmo17255h10b1

Seq. No.	283198
Contig ID	135179_1.R1011
5'-most EST	uC-zmflmo17229b04b1
Method	BLASTN
NCBI GI	g1652956
BLAST score	640
E value	0.0e+00
Match length	699
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592

Seq. No.	283199

Contig ID	135181_1.R1011
5'-most EST	uC-zmflmo17229b06b1
Method	BLASTX
NCBI GI	g1001819
BLAST score	342
E value	4.0e-42
Match length	171
% identity	58
NCBI Description	(D64005) cation efflux system protein [Synechocystis sp.]

Seq. No.	283200
Contig ID	135182_1.R1011
5'-most EST	uC-zmflmo17229b08b1
Method	BLASTX
NCBI GI	g1653747
BLAST score	566
E value	4.0e-58
Match length	127
% identity	88
NCBI Description	(D90916) phycobilisome core component [Synechocystis sp.]

Seq. No.	283201
Contig ID	135184_1.R1011
5'-most EST	uC-zmflmo17229b10b1
Method	BLASTN
NCBI GI	g1652618
BLAST score	645
E value	0.0e+00
Match length	645
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885

Seq. No.	283202
Contig ID	135186_1.R1011
5'-most EST	uC-zmflmo17229b12b1
Method	BLASTX
NCBI GI	g1001743
BLAST score	1539
E value	1.0e-172
Match length	311
% identity	95
NCBI Description	(D64004) protochlorophyllide oxido-reductase [Synechocystis sp.]

Seq. No.	283203
Contig ID	135187_1.R1011
5'-most EST	uC-zmflmo17229c01b1
Method	BLASTX
NCBI GI	g118451
BLAST score	1011
E value	1.0e-110
Match length	198
% identity	91
NCBI Description	FATTY ACID DESATURASE (DELTA 12 DESATURASE) >gi_97671_pir__S11519 stearoyl-CoA desaturase (EC 1.14.99.5) - Synechocystis sp >gi_40652_emb_CAA37584_

(X53508) fatty acid desaturase [Synechocystis sp.] >gi_1653254_dbj_BAA18169_ (D90912) fatty acid desaturase [Synechocystis sp.] >gi_227121_prf__1614346A desA gene [Synechocystis sp.]

Seq. No.	283204
Contig ID	135188_1.R1011
5'-most EST	uC-zmflmo17229c02b1
Method	BLASTX
NCBI GI	g1001756
BLAST score	775
E value	8.0e-83
Match length	170
% identity	94
NCBI Description	(D64004) sensory transduction histidine kinase [Synechocystis sp.]

Seq. No.	283205
Contig ID	135190_1.R1011
5'-most EST	uC-zmflmo17229c05b1
Method	BLASTX
NCBI GI	g3024871
BLAST score	780
E value	4.0e-83
Match length	192
% identity	77
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	283206
Contig ID	135192_1.R1011
5'-most EST	uC-zmflmo17229c08b1

Seq. No.	283207
Contig ID	135193_1.R1011
5'-most EST	uC-zmflmo17230b06a1
Method	BLASTX
NCBI GI	g1652730
BLAST score	560
E value	2.0e-57
Match length	110
% identity	98
NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]

Seq. No.	283208
Contig ID	135194_1.R1011
5'-most EST	uC-zmflmo17229c10b1
Method	BLASTX
NCBI GI	g1723171
BLAST score	835
E value	2.0e-89
Match length	171
% identity	92
NCBI Description	PUTATIVE AMMONIUM TRANSPORTER SLL0537 >gi_1001374_dbj_BAA10864_ (D64006) ammonium transport protein Amt1 [Synechocystis sp.]

Seq. No.	283209
Contig ID	135196_1.R1011
5'-most EST	uC-zmflmo17229d02b1
Method	BLASTX
NCBI GI	g1652157
BLAST score	894
E value	1.0e-96
Match length	195
% identity	91
NCBI Description	(D90903) mercuric reductase [Synechocystis sp.]

Seq. No.	283210
Contig ID	135197_1.R1011
5'-most EST	uC-zmflmo17229d04b1
Method	BLASTX
NCBI GI	g1653940
BLAST score	596
E value	1.0e-104
Match length	243
% identity	93
NCBI Description	(D90917) ATP-binding protein [Synechocystis sp.]

Seq. No.	283211
Contig ID	135198_1.R1011
5'-most EST	uC-zmflmo17228c04a1
Method	BLASTX
NCBI GI	g1001827
BLAST score	649
E value	8.0e-68
Match length	140
% identity	91
NCBI Description	(D64005) sensory transduction histidine kinase [Synechocystis sp.]

Seq. No.	283212
Contig ID	135202_1.R1011
5'-most EST	uC-zmflmo17229d11b1
Method	BLASTN
NCBI GI	g1653836
BLAST score	616
E value	0.0e+00
Match length	636
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470

Seq. No.	283213
Contig ID	135203_1.R1011
5'-most EST	uC-zmflmo17255f01a1
Method	BLASTX
NCBI GI	g1652978
BLAST score	423
E value	3.0e-43
Match length	93
% identity	99
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	283214
Contig ID	135206_1.R1011
5'-most EST	uC-zmflmo17229e03b1
Method	BLASTX
NCBI GI	g1001241
BLAST score	803
E value	4.0e-86
Match length	165
% identity	90
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	283215
Contig ID	135207_1.R1011
5'-most EST	uC-zmflmo17229e04b1
Method	BLASTN
NCBI GI	g1653715
BLAST score	686
E value	0.0e+00
Match length	735
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851

Seq. No.	283216
Contig ID	135211_1.R1011
5'-most EST	uC-zmflmo17229e08b1
Method	BLASTX
NCBI GI	g1653629
BLAST score	1487
E value	1.0e-166
Match length	314
% identity	93
NCBI Description	(D90915) hypothetical protein [Synechocystis sp.]

Seq. No.	283217
Contig ID	135212_1.R1011
5'-most EST	uC-zmflmo17229e09b1
Method	BLASTX
NCBI GI	g1652841
BLAST score	493
E value	1.0e-49
Match length	100
% identity	97
NCBI Description	(D90908) sensory transduction histidine kinase [Synechocystis sp.]

Seq. No.	283218
Contig ID	135213_1.R1011
5'-most EST	uC-zmflmo17229e10b1
Method	BLASTX
NCBI GI	g1652187
BLAST score	623
E value	1.0e-64
Match length	143
% identity	86
NCBI Description	(D90903) ABC transporter [Synechocystis sp.]

Seq. No.	283219
Contig ID	135214_1.R1011
5'-most EST	uC-zmflmo17229e11b1
Method	BLASTX
NCBI GI	g1653858
BLAST score	703
E value	8.0e-82
Match length	166
% identity	98
NCBI Description	(D90917) haemolysin secretion ATP-binding protein [Synechocystis sp.]

Seq. No.	283220
Contig ID	135215_1.R1011
5'-most EST	uC-zmflmo17229e12b1
Method	BLASTX
NCBI GI	g1652965
BLAST score	709
E value	5.0e-75
Match length	178
% identity	82
NCBI Description	(D90910) acetyl coenzyme A acetyltransferase (thiolase) [Synechocystis sp.]

Seq. No.	283221
Contig ID	135216_1.R1011
5'-most EST	uC-zmflmo17229f01b1
Method	BLASTX
NCBI GI	g1653116
BLAST score	758
E value	8.0e-81
Match length	144
% identity	100
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	283222
Contig ID	135217_1.R1011
5'-most EST	uC-zmflmo17229f02b1
Method	BLASTN
NCBI GI	g1651768
BLAST score	624
E value	0.0e+00
Match length	742
% identity	96
NCBI Description	Synechocystis sp. PCC6803 complete genome, 2/27, 133860-271599

Seq. No.	283223
Contig ID	135218_1.R1011
5'-most EST	uC-zmflmo17229f03a1
Method	BLASTX
NCBI GI	g1653480
BLAST score	499
E value	9.0e-51
Match length	101
% identity	99

NCBI Description	(D90914) phosphoenolpyruvate carboxylase [Synechocystis sp.]

Seq. No.	283224
Contig ID	135219_1.R1011
5'-most EST	uC-zmflmo17229f04b1
Method	BLASTX
NCBI GI	g1001255
BLAST score	453
E value	1.0e-44
Match length	107
% identity	76
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	283225
Contig ID	135221_1.R1011
5'-most EST	uC-zmflmo17229f06b1

Seq. No.	283226
Contig ID	135223_1.R1011
5'-most EST	uC-zmflmo17229f09b1
Method	BLASTX
NCBI GI	g1651873
BLAST score	946
E value	1.0e-103
Match length	171
% identity	99
NCBI Description	(D90900) 4-alpha-glucanotransferase [Synechocystis sp.]

Seq. No.	283227
Contig ID	135225_1.R1011
5'-most EST	uC-zmflmo17229f11b1
Method	BLASTX
NCBI GI	g1001820
BLAST score	846
E value	6.0e-91
Match length	156
% identity	100
NCBI Description	(D64005) hypothetical protein [Synechocystis sp.]

Seq. No.	283228
Contig ID	135227_1.R1011
5'-most EST	uC-zmflmo17229g02b1
Method	BLASTX
NCBI GI	g538869
BLAST score	654
E value	8.0e-69
Match length	122
% identity	100
NCBI Description	replication protein A - Synechocystis sp. plasmid pCA2.4 >gi_290013 (L13739) replication initiation protein [Cyanobacterium synechocystis]

Seq. No.	283229
Contig ID	135231_1.R1011
5'-most EST	uC-zmflmo17229g06b1
Method	BLASTX

NCBI GI	g3915410
BLAST score	920
E value	2.0e-99
Match length	224
% identity	84
NCBI Description	HYPOTHETICAL 74.4 KD PROTEIN SLL1021 >gi_1652020_dbj_BAA16946_ (D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	283230
Contig ID	135232_1.R1011
5'-most EST	uC-zmflmo17229g07b1
Method	BLASTX
NCBI GI	g2829610
BLAST score	531
E value	5.0e-54
Match length	102
% identity	99
NCBI Description	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG >gi_1653027_dbj_BAA17944_ (D90910) pantothenate metabolism flavoprotein [Synechocystis sp.]

Seq. No.	283231
Contig ID	135234_1.R1011
5'-most EST	uC-zmflmo17229g10b1
Method	BLASTX
NCBI GI	g461732
BLAST score	449
E value	1.0e-44
Match length	90
% identity	99
NCBI Description	10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) >gi_348350_pir__A44425 heat shock protein groES - Synechocystis sp. (PCC 6803) >gi_287462_dbj_BAA02179_ (D12677) GroES [Synechocystis sp.]

Seq. No.	283232
Contig ID	135235_1.R1011
5'-most EST	uC-zmflmo17229g11b1
Method	BLASTN
NCBI GI	g1001200
BLAST score	968
E value	0.0e+00
Match length	972
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766

Seq. No.	283233
Contig ID	135244_1.R1011
5'-most EST	uC-zmflmo17229h08b1
Method	BLASTX
NCBI GI	g1651666
BLAST score	784
E value	8.0e-84
Match length	171
% identity	95

NCBI Description	(D90899) ferric aerobactin receptor [Synechocystis sp.]

Seq. No.	283234
Contig ID	135246_1.R1011
5'-most EST	uC-zmflmo17229h10b1

Seq. No.	283235
Contig ID	135248_1.R1011
5'-most EST	uC-zmflmo17229h12b1
Method	BLASTN
NCBI GI	g1001701
BLAST score	474
E value	0.0e+00
Match length	485
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965

Seq. No.	283236
Contig ID	135251_1.R1011
5'-most EST	uC-zmflmo17230a11b1
Method	BLASTX
NCBI GI	g1001495
BLAST score	485
E value	1.0e-48
Match length	115
% identity	84
NCBI Description	(D64000) UDP-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase [Synechocystis sp.]

Seq. No.	283237
Contig ID	135251_2.R1011
5'-most EST	uC-zmflmo17230a06b1
Method	BLASTX
NCBI GI	g1350688
BLAST score	198
E value	2.0e-15
Match length	47
% identity	87
NCBI Description	50S RIBOSOMAL PROTEIN L20 >gi_1001496_dbj_BAA10121_ (D64000) 50S ribosomal protein L20 [Synechocystis sp.]

Seq. No.	283238
Contig ID	135258_1.R1011
5'-most EST	uC-zmflmo17230b03b1
Method	BLASTX
NCBI GI	g1001236
BLAST score	1066
E value	1.0e-117
Match length	231
% identity	94
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	283239
Contig ID	135259_1.R1011
5'-most EST	uC-zmflmo17230b04b1
Method	BLASTX

NCBI GI	g1653767
BLAST score	782
E value	1.0e-83
Match length	155
% identity	98
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	283240
Contig ID	135264_1.R1011
5'-most EST	uC-zmflmo17230b11b1

Seq. No.	283241
Contig ID	135265_1.R1011
5'-most EST	uC-zmflmo17230b12a1
Method	BLASTX
NCBI GI	g2500952
BLAST score	735
E value	3.0e-78
Match length	144
% identity	97
NCBI Description	SUN PROTEIN (FMU PROTEIN) >gi_1652035_dbj_BAA16960_ (D90902) fmu and fmv protein [Synechocystis sp.]

Seq. No.	283242
Contig ID	135266_1.R1011
5'-most EST	uC-zmflmo17230c01a1
Method	BLASTN
NCBI GI	g1653715
BLAST score	179
E value	2.0e-96
Match length	187
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851

Seq. No.	283243
Contig ID	135267_2.R1011
5'-most EST	uC-zmflmo17230c02b1

Seq. No.	283244
Contig ID	135270_1.R1011
5'-most EST	uC-zmflmo17230c05b1
Method	BLASTX
NCBI GI	g1652563
BLAST score	575
E value	2.0e-59
Match length	130
% identity	89
NCBI Description	(D90906) RfbJ protein [Synechocystis sp.]

Seq. No.	283245
Contig ID	135273_1.R1011
5'-most EST	uC-zmflmo17230c08b1
Method	BLASTX
NCBI GI	g1653153
BLAST score	940
E value	1.0e-102

Match length	206
% identity	94
NCBI Description	(D90911) acriflavin resistance protein [Synechocystis sp.]

Seq. No.	283246
Contig ID	135275_1.R1011
5'-most EST	uC-zmflmo17230c10b1
Method	BLASTX
NCBI GI	g1001714
BLAST score	244
E value	8.0e-21
Match length	51
% identity	92
NCBI Description	(D64004) general secretion pathway protein E [Synechocystis sp.]

Seq. No.	283247
Contig ID	135276_1.R1011
5'-most EST	uC-zmflmo17230c11b1

Seq. No.	283248
Contig ID	135277_1.R1011
5'-most EST	uC-zmflmo17230c12b1
Method	BLASTX
NCBI GI	g1653765
BLAST score	786
E value	1.0e-87
Match length	209
% identity	59
NCBI Description	(D90916) aspartate kinase [Synechocystis sp.]

Seq. No.	283249
Contig ID	135278_1.R1011
5'-most EST	uC-zmflmo17230d01a1
Method	BLASTX
NCBI GI	g1652811
BLAST score	402
E value	4.0e-39
Match length	81
% identity	100
NCBI Description	(D90908) glucose dehydrogenase [Synechocystis sp.]

Seq. No.	283250
Contig ID	135279_1.R1011
5'-most EST	uC-zmflmo17230d02b1
Method	BLASTX
NCBI GI	g1651968
BLAST score	551
E value	2.0e-56
Match length	116
% identity	89
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	283251
Contig ID	135281_1.R1011
5'-most EST	uC-zmflmo17230d04b1
Method	BLASTN

NCBI GI	g1653836
BLAST score	431
E value	0.0e+00
Match length	709
% identity	100
NCBI Description	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470

Seq. No.	283252
Contig ID	135282_1.R1011
5'-most EST	uC-zmflmo17230d05b1
Method	BLASTX
NCBI GI	g4376185
BLAST score	491
E value	2.0e-49
Match length	183
% identity	53
NCBI Description	(AF001355) hybrid histidine protein kinase-phosphate acceptor regulatory protein CvgSY [Pseudomonas syringae pv. syringae]

Seq. No.	283253
Contig ID	135283_1.R1011
5'-most EST	uC-zmflmo17230d06b1
Method	BLASTX
NCBI GI	g2496196
BLAST score	179
E value	7.0e-13
Match length	143
% identity	36
NCBI Description	HYPOTHETICAL PROTEIN MJECS02 >gi_2129058_pir__B64516 hypothetical protein MJECS02 - Methanococcus jannaschii plasmid pURB801 >gi_1522636 (L77119) M. jannaschii predicted coding region MJECS02 [Methanococcus jannaschii]

Seq. No.	283254
Contig ID	135284_1.R1011
5'-most EST	uC-zmflmo17230d07b1
Method	BLASTX
NCBI GI	g3023705
BLAST score	790
E value	1.0e-84
Match length	163
% identity	94
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_1653839_dbj_BAA18749_ (D90917) enolase [Synechocystis sp.]

Seq. No.	283255
Contig ID	135286_1.R1011
5'-most EST	uC-zmflmo17230d09b1
Method	BLASTX
NCBI GI	g2500005
BLAST score	816
E value	1.0e-91
Match length	181

% identity	100
NCBI Description	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE 2 (GART 2) (GAR TRANSFORMYLASE 2) (5'-PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE 2) (FORMATE-DEPENDENT GAR TRANSFORMYLASE) >gi_558138 (L36958) glycinamide ribonucleotide transformylase [Synechocystis sp.] >gi_1652885_dbj_BAA17803_ (D90909) glycinamide ribonucleotide transformylase [Synechocystis sp.]

Seq. No.	283256
Contig ID	135287_1.R1011
5'-most EST	uC-zmflmo17230d10b1
Method	BLASTX
NCBI GI	g2126522
BLAST score	947
E value	1.0e-102
Match length	171
% identity	99
NCBI Description	desaturase delta 15 - Synechocystis sp. (strain PCC6803) >gi_600598_dbj_BAA02924_ (D13780) delta 15 desaturase [Synechocystis sp.] >gi_1653388_dbj_BAA18302_ (D90913) delta 15 desaturase [Synechocystis sp.]

Seq. No.	283257
Contig ID	135288_1.R1011
5'-most EST	uC-zmflmo17230d11b1
Method	BLASTX
NCBI GI	g1652652
BLAST score	841
E value	2.0e-90
Match length	184
% identity	90
NCBI Description	(D90907) RecF protein [Synechocystis sp.]

Seq. No.	283258
Contig ID	135290_1.R1011
5'-most EST	uC-zmflmo17230e03b1
Method	BLASTN
NCBI GI	g1001200
BLAST score	596
E value	0.0e+00
Match length	688
% identity	96
NCBI Description	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766

Seq. No.	283259
Contig ID	135291_1.R1011
5'-most EST	uC-zmflmo17230e04b1
Method	BLASTX
NCBI GI	g1652042
BLAST score	453
E value	5.0e-45
Match length	172
% identity	53
NCBI Description	(D90902) lipophilic protein [Synechocystis sp.]

Seq. No.	283260
Contig ID	135292_1.R1011
5'-most EST	uC-zmflmo17230e05b1
Method	BLASTX
NCBI GI	g1652437
BLAST score	445
E value	1.0e-111
Match length	228
% identity	98
NCBI Description	(D90905) ABC transporter [Synechocystis sp.]

Seq. No.	283261
Contig ID	135296_1.R1011
5'-most EST	uC-zmflmo17230e09b1
Method	BLASTX
NCBI GI	g1001461
BLAST score	408
E value	3.0e-40
Match length	81
% identity	18
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	283262
Contig ID	135300_1.R1011
5'-most EST	uC-zmflmo17230f01b1
Method	BLASTX
NCBI GI	g1006612
BLAST score	532
E value	2.0e-54
Match length	148
% identity	75
NCBI Description	(D64005) phospho-N-acetylmuramoyl-pentapeptide-transferas e [Synechocystis sp.]

Seq. No.	283263
Contig ID	135301_1.R1011
5'-most EST	uC-zmflmo17256a04a1
Method	BLASTX
NCBI GI	g1001771
BLAST score	630
E value	1.0e-65
Match length	143
% identity	86
NCBI Description	(D64004) hypothetical protein [Synechocystis sp.]

Seq. No.	283264
Contig ID	135302_1.R1011
5'-most EST	uC-zmflmo17230f04b1
Method	BLASTX
NCBI GI	g1651899
BLAST score	204
E value	9.0e-16
Match length	47
% identity	87
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	283265

Contig ID	135303_1.R1011
5'-most EST	uC-zmflmo17230f05b1
Method	BLASTX
NCBI GI	g1653770
BLAST score	410
E value	6.0e-40
Match length	81
% identity	99
NCBI Description	(D90916) hypothetical protein [Synechocystis sp.]

Seq. No.	283266
Contig ID	135304_1.R1011
5'-most EST	uC-zmflmo17251d09a1
Method	BLASTN
NCBI GI	g1651650
BLAST score	740
E value	0.0e+00
Match length	756
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859

Seq. No.	283267
Contig ID	135312_1.R1011
5'-most EST	uC-zmflmo17230g02a1
Method	BLASTN
NCBI GI	g1652956
BLAST score	141
E value	9.0e-74
Match length	165
% identity	96
NCBI Description	Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592

Seq. No.	283268
Contig ID	135323_1.R1011
5'-most EST	uC-zmflmo17230h02b1
Method	BLASTX
NCBI GI	g1001384
BLAST score	396
E value	7.0e-39
Match length	90
% identity	93
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	283269
Contig ID	135326_1.R1011
5'-most EST	uC-zmflmo17230h06a1
Method	BLASTX
NCBI GI	g1652483
BLAST score	397
E value	1.0e-38
Match length	74
% identity	99
NCBI Description	(D90905) hypothetical protein [Synechocystis sp.]

Seq. No.	283270
Contig ID	135328_1.R1011

5'-most EST	uC-zmflmo17230h09b1
Method	BLASTX
NCBI GI	g1653465
BLAST score	342
E value	5.0e-32
Match length	68
% identity	97
NCBI Description	(D90913) mannose-1-phosphate guanyltransferase [Synechocystis sp.]

Seq. No.	283271
Contig ID	135330_1.R1011
5'-most EST	uC-zmflmo17230h11b1
Method	BLASTN
NCBI GI	g1652618
BLAST score	488
E value	0.0e+00
Match length	512
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885

Seq. No.	283272
Contig ID	135331_1.R1011
5'-most EST	uC-zmflmo17230h12b1
Method	BLASTX
NCBI GI	g1652639
BLAST score	1165
E value	1.0e-131
Match length	292
% identity	88
NCBI Description	(D90907) sensory transduction histidine kinase [Synechocystis sp.]

Seq. No.	283273
Contig ID	135333_1.R1011
5'-most EST	uC-zmflmo17235a02b1

Seq. No.	283274
Contig ID	135335_1.R1011
5'-most EST	uC-zmflmo17289f04b1

Seq. No.	283275
Contig ID	135339_1.R1011
5'-most EST	uC-zmflmo17235a09b1
Method	BLASTX
NCBI GI	g550542
BLAST score	769
E value	4.0e-82
Match length	178
% identity	87
NCBI Description	(X81831) cytochrome P450 [Zea mays] >gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea mays]

Seq. No.	283276
Contig ID	135341_1.R1011

5'-most EST	uC-zmflmo17235a11b1
Method	BLASTX
NCBI GI	g132166
BLAST score	186
E value	6.0e-14
Match length	77
% identity	56
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	283277
Contig ID	135361_1.R1011
5'-most EST	uC-zmflmo17235c10b1

Seq. No.	283278
Contig ID	135367_1.R1011
5'-most EST	uC-zmflmo17235d04b1
Method	BLASTX
NCBI GI	g1402906
BLAST score	430
E value	4.0e-43
Match length	127
% identity	72
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]

Seq. No.	283279
Contig ID	135388_1.R1011
5'-most EST	uC-zmflmo17235f02b1

Seq. No.	283280
Contig ID	135392_1.R1011
5'-most EST	uC-zmflmo17235f06b1
Method	BLASTX
NCBI GI	g4454480
BLAST score	457
E value	2.0e-50
Match length	216
% identity	47
NCBI Description	(AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]

Seq. No.	283281
Contig ID	135402_1.R1011
5'-most EST	xsy700214854.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	283282
Contig ID	135408_1.R1011
5'-most EST	uC-zmflb73257h05b3
Method	BLASTX
NCBI GI	g2833390
BLAST score	845
E value	6.0e-91
Match length	200
% identity	77
NCBI Description	GLYCOGEN (STARCH) SYNTHASE PRECURSOR (GBSSII) (GRANULE-BOUND STARCH SYNTHASE II) >gi_887649_emb_CAA61241_ (X87988) glycogen (starch) synthase [Solanum tuberosum]

Seq. No.	283283
Contig ID	135410_1.R1011
5'-most EST	uC-zmflmo17235g12b1

Seq. No.	283284
Contig ID	135410_2.R1011
5'-most EST	uC-zmflb73253a02a1

Seq. No.	283285
Contig ID	135416_1.R1011
5'-most EST	uC-zmflmo17235h07b1

Seq. No.	283286
Contig ID	135423_1.R1011
5'-most EST	uC-zmflmo17300g05a1

Seq. No.	283287
Contig ID	135446_1.R1011
5'-most EST	ntr700073712.h1
Method	BLASTX
NCBI GI	g3831463
BLAST score	265
E value	5.0e-23
Match length	137
% identity	39
NCBI Description	(AC005700) unknown protein [Arabidopsis thaliana]

Seq. No.	283288
Contig ID	135484_1.R1011
5'-most EST	uC-zmflb73235a10b2

Seq. No.	283289
Contig ID	135485_1.R1011
5'-most EST	uC-zmflmo17236h10b1

Seq. No.	283290
Contig ID	135489_1.R1011
5'-most EST	pmx700091906.h1
Method	BLASTX
NCBI GI	g1170089
BLAST score	178
E value	7.0e-13
Match length	125
% identity	44

NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	283291
Contig ID	135504_1.R1011
5'-most EST	uC-zmflmo17238b07b1
Method	BLASTX
NCBI GI	g3641661
BLAST score	462
E value	7.0e-46
Match length	183
% identity	49
NCBI Description	(AB008519) high affinity nitrate transporter [Oryza sativa]

Seq. No.	283292
Contig ID	135509_1.R1011
5'-most EST	uC-zmflmo17238b12b1

Seq. No.	283293
Contig ID	135544_1.R1011
5'-most EST	uC-zmflmo17238e11b1

Seq. No.	283294
Contig ID	135554_1.R1011
5'-most EST	uC-zmflmo17234f11a1

Seq. No.	283295
Contig ID	135561_1.R1011
5'-most EST	uC-zmflmo17238g08b1

Seq. No.	283296
Contig ID	135603_1.R1011
5'-most EST	uC-zmflmo17240c03b1
Method	BLASTX
NCBI GI	g2191134
BLAST score	163
E value	9.0e-11
Match length	182
% identity	34
NCBI Description	(AF007269) contains weak similarity to Galectin-3 binding protein [Arabidopsis thaliana]

Seq. No.	283297
Contig ID	135629_1.R1011
5'-most EST	uC-zmflmo17240e07b1
Method	BLASTX
NCBI GI	g4544383
BLAST score	443
E value	7.0e-44
Match length	171
% identity	54
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283298
Contig ID	135644_1.R1011
5'-most EST	tzu700202977.h1
Method	BLASTX
NCBI GI	g4582448
BLAST score	204
E value	1.0e-15
Match length	49
% identity	82
NCBI Description	(AC007071) putative preprotein translocase SecY subunit [Arabidopsis thaliana]

Seq. No.	283299
Contig ID	135653_1.R1011
5'-most EST	uC-zmflmo17240g10b1

Seq. No.	283300
Contig ID	135670_1.R1011
5'-most EST	uC-zmflmo17242a03b1

Seq. No.	283301
Contig ID	135680_1.R1011
5'-most EST	hbs701184454.h1
Method	BLASTX
NCBI GI	g2618698
BLAST score	635
E value	2.0e-66
Match length	150
% identity	85
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	283302
Contig ID	135695_1.R1011
5'-most EST	uC-zmflmo17242c05b1

Seq. No.	283303
Contig ID	135698_1.R1011
5'-most EST	uC-zmflmo17242c08b1

Seq. No.	283304
Contig ID	135709_1.R1011
5'-most EST	uC-zmflmo17242d09b1
Method	BLASTX
NCBI GI	g4585972
BLAST score	361
E value	4.0e-34
Match length	107
% identity	63
NCBI Description	(AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No.	283305
Contig ID	135716_1.R1011
5'-most EST	uC-zmflmo17242e06b1

Seq. No.	283306
Contig ID	135725_2.R1011
5'-most EST	yyf700352010.h1

Seq. No.	283307
Contig ID	135733_1.R1011
5'-most EST	uC-zmflmo17242g01b1

Seq. No.	283308
Contig ID	135750_1.R1011
5'-most EST	uwc700151767.h1
Method	BLASTX
NCBI GI	g4559380
BLAST score	186
E value	2.0e-14
Match length	55
% identity	60
NCBI Description	(AC006526) putative auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	283309
Contig ID	135751_1.R1011
5'-most EST	uC-zmroteosinte019a08b1
Method	BLASTX
NCBI GI	g1931638
BLAST score	353
E value	3.0e-33
Match length	200
% identity	47
NCBI Description	(U95973) transcription factor RUSH-1alpha isolog [Arabidopsis thaliana]

Seq. No.	283310
Contig ID	135755_1.R1011
5'-most EST	uC-zmflmo17242h12b1
Method	BLASTX
NCBI GI	g4191785
BLAST score	353
E value	4.0e-33
Match length	131
% identity	55
NCBI Description	(AC005917) putative hydrolase [Arabidopsis thaliana]

Seq. No.	283311
Contig ID	135758_1.R1011
5'-most EST	uC-zmflmo17245a03b1

Seq. No.	283312
Contig ID	135789_1.R1011
5'-most EST	cjh700195890.h1
Method	BLASTX
NCBI GI	g2651300
BLAST score	143
E value	3.0e-09
Match length	71
% identity	45
NCBI Description	(AC002336) putative initiator tRNA phosphoribosyl-transferase [Arabidopsis thaliana]

Seq. No.	283313

Contig ID 135797_1.R1011
5'-most EST uC-zmflmo17359c09a1

Seq. No. 283314
Contig ID 135798_1.R1011
5'-most EST gct701167273.h1
Method BLASTX
NCBI GI g3075397
BLAST score 156
E value 3.0e-10
Match length 68
% identity 47
NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No. 283315
Contig ID 135799_1.R1011
5'-most EST yyf700350812.h1

Seq. No. 283316
Contig ID 135811_1.R1011
5'-most EST uC-zmflmo17245g04b1

Seq. No. 283317
Contig ID 135832_1.R1011
5'-most EST uC-zmflmo17246a01b1

Seq. No. 283318
Contig ID 135846_1.R1011
5'-most EST uC-zmflmo17246b04b1
Method BLASTX
NCBI GI g3063697
BLAST score 259
E value 6.0e-22
Match length 93
% identity 62
NCBI Description (AL022537) putative myb-protein (partial) [Arabidopsis thaliana]

Seq. No. 283319
Contig ID 135851_1.R1011
5'-most EST uC-zmflmo17421g05a1

Seq. No. 283320
Contig ID 135887_1.R1011
5'-most EST uC-zmflmo17246f09b1
Method BLASTX
NCBI GI g2244855
BLAST score 218
E value 9.0e-18
Match length 72
% identity 61
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 283321
Contig ID 135897_1.R1011
5'-most EST gwl700612732.h1
Method BLASTX

NCBI GI	g2245378
BLAST score	589
E value	2.0e-61
Match length	171
% identity	68
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	283322
Contig ID	135898_1.R1011
5'-most EST	uC-zmflmo17246g11b1
Method	BLASTX
NCBI GI	g3924611
BLAST score	301
E value	3.0e-27
Match length	172
% identity	42
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283323
Contig ID	135933_1.R1011
5'-most EST	uC-zmflmo17248c04b1

Seq. No.	283324
Contig ID	135955_1.R1011
5'-most EST	uC-zmflmo17292d06b1

Seq. No.	283325
Contig ID	135956_1.R1011
5'-most EST	uC-zmflmo17248e05b1

Seq. No.	283326
Contig ID	135989_1.R1011
5'-most EST	uC-zmflmo17248h03b1

Seq. No.	283327
Contig ID	136006_1.R1011
5'-most EST	uC-zmflmo17255a08b1
Method	BLASTN
NCBI GI	g1653604
BLAST score	205
E value	1.0e-111
Match length	310
% identity	96
NCBI Description	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259

Seq. No.	283328
Contig ID	136011_1.R1011
5'-most EST	uC-zmflmo17255b02b1
Method	BLASTX
NCBI GI	g2495539
BLAST score	159
E value	2.0e-10
Match length	116
% identity	34
NCBI Description	HYPOTHETICAL 58.9 KD PROTEIN IN TESB-HHA INTERGENIC REGION >gi_1773140 (U82664) similar to the 60.8kd protein in

SSB-SOXS intergenic region [Escherichia coli] >gi_1786662 (AE000152) orf, hypothetical protein [Escherichia coli]

Seq. No.	283329
Contig ID	136013_1.R1011
5'-most EST	uC-zmflmo17255b11b1
Method	BLASTX
NCBI GI	g2689699
BLAST score	216
E value	4.0e-17
Match length	114
% identity	42
NCBI Description	(AF034786) modification subunit [Lactococcus lactis bv. diacetylactis]

Seq. No.	283330
Contig ID	136016_1.R1011
5'-most EST	uC-zmflmo17255c12b1
Method	BLASTX
NCBI GI	g1652331
BLAST score	787
E value	1.0e-87
Match length	199
% identity	88
NCBI Description	(D90904) NADH dehydrogenase subunit 5 [Synechocystis sp.]

Seq. No.	283331
Contig ID	136023_1.R1011
5'-most EST	uC-zmflmo17255f04b1
Method	BLASTX
NCBI GI	g1208477
BLAST score	682
E value	9.0e-72
Match length	139
% identity	96
NCBI Description	(D64004) hypothetical protein [Synechocystis sp.]

Seq. No.	283332
Contig ID	136026_1.R1011
5'-most EST	uC-zmflmo17255g02b1
Method	BLASTN
NCBI GI	g1652956
BLAST score	437
E value	0.0e+00
Match length	449
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592

Seq. No.	283333
Contig ID	136040_1.R1011
5'-most EST	uC-zmflmo17256a02b1
Method	BLASTX
NCBI GI	g1652841
BLAST score	844
E value	7.0e-91
Match length	170

% identity	98
NCBI Description	(D90908) sensory transduction histidine kinase [Synechocystis sp.]

Seq. No.	283334
Contig ID	136043_1.R1011
5'-most EST	uC-zmflmo17256a05b1
Method	BLASTX
NCBI GI	g1653694
BLAST score	660
E value	5.0e-69
Match length	145
% identity	88
NCBI Description	(D90915) hypothetical protein [Synechocystis sp.]

Seq. No.	283335
Contig ID	136044_1.R1011
5'-most EST	uC-zmflmo17256c12b1
Method	BLASTX
NCBI GI	g2492989
BLAST score	577
E value	2.0e-59
Match length	113
% identity	97
NCBI Description	ARGININOSUCCINATE SYNTHASE (CITRULLINE--ASPARTATE LIGASE) >gi_1653931_dbj_BAA18841_ (D90917) argininosuccinate synthetase [Synechocystis sp.]

Seq. No.	283336
Contig ID	136045_1.R1011
5'-most EST	uC-zmflmo17256a07b1
Method	BLASTX
NCBI GI	g1001304
BLAST score	761
E value	3.0e-81
Match length	143
% identity	98
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	283337
Contig ID	136050_1.R1011
5'-most EST	uC-zmflmo17256a12b1
Method	BLASTN
NCBI GI	g1653715
BLAST score	387
E value	0.0e+00
Match length	435
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851

Seq. No.	283338
Contig ID	136052_1.R1011
5'-most EST	uC-zmflmo17256b02b1
Method	BLASTN
NCBI GI	g1653715
BLAST score	528

E value	0.0e+00
Match length	569
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851

Seq. No.	283339
Contig ID	136053_1.R1011
5'-most EST	uC-zmflmo17256b03b1
Method	BLASTX
NCBI GI	g1653249
BLAST score	675
E value	7.0e-71
Match length	128
% identity	99
NCBI Description	(D90912) hypothetical protein [Synechocystis sp.]

Seq. No.	283340
Contig ID	136054_1.R1011
5'-most EST	uC-zmflmo17256b04b1
Method	BLASTX
NCBI GI	g1001219
BLAST score	633
E value	6.0e-66
Match length	128
% identity	96
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	283341
Contig ID	136055_1.R1011
5'-most EST	uC-zmflmo17256b05b1
Method	BLASTN
NCBI GI	g1653715
BLAST score	597
E value	0.0e+00
Match length	641
% identity	98
NCBI Description	Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851

Seq. No.	283342
Contig ID	136056_1.R1011
5'-most EST	uC-zmflmo17256b07b1
Method	BLASTX
NCBI GI	g2500139
BLAST score	1375
E value	1.0e-153
Match length	273
% identity	100
NCBI Description	PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1) >gi_1653916_dbj_BAA18826_ (D90917) peptide chain release factor [Synechocystis sp.]

Seq. No.	283343
Contig ID	136057_1.R1011
5'-most EST	uC-zmflmo17256b08b1
Method	BLASTX

NCBI GI	g1653498
BLAST score	811
E value	5.0e-87
Match length	191
% identity	65
NCBI Description	(D90914) ABC transporter [Synechocystis sp.]

Seq. No.	283344
Contig ID	136061_1.R1011
5'-most EST	uC-zmflmo17256b12b1
Method	BLASTN
NCBI GI	g1001102
BLAST score	544
E value	0.0e+00
Match length	572
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794

Seq. No.	283345
Contig ID	136066_1.R1011
5'-most EST	uC-zmflmo17251f06a1
Method	BLASTX
NCBI GI	g1652896
BLAST score	766
E value	9.0e-82
Match length	167
% identity	92
NCBI Description	(D90909) hypothetical protein [Synechocystis sp.]

Seq. No.	283346
Contig ID	136067_1.R1011
5'-most EST	uC-zmflmo17256c07b1
Method	BLASTN
NCBI GI	g1001779
BLAST score	633
E value	0.0e+00
Match length	674
% identity	78
NCBI Description	Synechocystis sp. PCC6803 complete genome, 24/27, 3002966-3138603

Seq. No.	283347
Contig ID	136070_1.R1011
5'-most EST	uC-zmflmo17256c10b1
Method	BLASTX
NCBI GI	g2120953
BLAST score	238
E value	8.0e-20
Match length	117
% identity	44
NCBI Description	ORF2 - Alcaligenes eutrophus >gi_695280 (L36817) ORF2 [Alcaligenes eutrophus] >gi_1093467_prf__2104199H ORF 2 [Ralstonia eutropha]

Seq. No.	283348
Contig ID	136074_1.R1011

5'-most EST	uC-zmflmo17256d03b1
Method	BLASTX
NCBI GI	g1001117
BLAST score	424
E value	1.0e-41
Match length	93
% identity	86
NCBI Description	(D64001) glycolate oxidase subunit GlcD [Synechocystis sp.]

Seq. No.	283349
Contig ID	136075_1.R1011
5'-most EST	uC-zmflmo17256d04b1
Method	BLASTX
NCBI GI	g1001462
BLAST score	761
E value	4.0e-81
Match length	149
% identity	34
NCBI Description	(D63999) hypothetical protein [Synechocystis sp.]

Seq. No.	283350
Contig ID	136076_1.R1011
5'-most EST	uC-zmflmo17256d05b1
Method	BLASTX
NCBI GI	g1652783
BLAST score	291
E value	7.0e-26
Match length	60
% identity	93
NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]

Seq. No.	283351
Contig ID	136077_1.R1011
5'-most EST	uC-zmflmo17256d06b1
Method	BLASTX
NCBI GI	g1653057
BLAST score	1113
E value	1.0e-122
Match length	246
% identity	92
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	283352
Contig ID	136083_1.R1011
5'-most EST	uC-zmflmo17256d12b1
Method	BLASTX
NCBI GI	g1651934
BLAST score	712
E value	2.0e-75
Match length	136
% identity	99
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	283353
Contig ID	136084_1.R1011
5'-most EST	uC-zmflmo17256e01b1
Method	BLASTN

NCBI GI g1652844
BLAST score 539
E value 0.0e+00
Match length 631
% identity 96
NCBI Description Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418

Seq. No. 283354
Contig ID 136085_1.R1011
5'-most EST uC-zmflmo17256e02b1
Method BLASTX
NCBI GI g1652837
BLAST score 742
E value 1.0e-79
Match length 178
% identity 25
NCBI Description (D90908) hypothetical protein [Synechocystis sp.]

Seq. No. 283355
Contig ID 136087_1.R1011
5'-most EST uC-zmflmo17256e04b1
Method BLASTN
NCBI GI g1653083
BLAST score 471
E value 0.0e+00
Match length 515
% identity 98
NCBI Description Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643

Seq. No. 283356
Contig ID 136098_1.R1011
5'-most EST uC-zmflmo17256f03b1
Method BLASTN
NCBI GI g1651768
BLAST score 207
E value 1.0e-113
Match length 235
% identity 98
NCBI Description Synechocystis sp. PCC6803 complete genome, 2/27, 133860-271599

Seq. No. 283357
Contig ID 136101_1.R1011
5'-most EST uC-zmflmo17256f06b1

Seq. No. 283358
Contig ID 136105_1.R1011
5'-most EST uC-zmflmo17256f11b1
Method BLASTN
NCBI GI g1653836
BLAST score 739
E value 0.0e+00
Match length 759
% identity 99
NCBI Description Synechocystis sp. PCC6803 complete genome, 27/27,

3418852-3573470

Seq. No.	283359
Contig ID	136107_1.R1011
5'-most EST	uC-zmflmo17256g01b1
Method	BLASTX
NCBI GI	g2313556
BLAST score	383
E value	1.0e-36
Match length	206
% identity	40
NCBI Description	(AE000560) conserved hypothetical protein [Helicobacter pylori 26695]

Seq. No.	283360
Contig ID	136108_1.R1011
5'-most EST	uC-zmflmo17256g02b1
Method	BLASTX
NCBI GI	g1477448
BLAST score	165
E value	2.0e-11
Match length	34
% identity	97
NCBI Description	(X96599) magnesium chelatase [Synechocystis sp.]

Seq. No.	283361
Contig ID	136109_1.R1011
5'-most EST	uC-zmflmo17256g03b1
Method	BLASTN
NCBI GI	g1001612
BLAST score	569
E value	0.0e+00
Match length	588
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 21/27, 2644795-2755702

Seq. No.	283362
Contig ID	136110_1.R1011
5'-most EST	uC-zmflmo17256g04b1
Method	BLASTN
NCBI GI	g1653604
BLAST score	475
E value	0.0e+00
Match length	499
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259

Seq. No.	283363
Contig ID	136111_1.R1011
5'-most EST	uC-zmflmo17256g05b1
Method	BLASTN
NCBI GI	g1652225
BLAST score	456
E value	0.0e+00
Match length	468

% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448

Seq. No.	283364
Contig ID	136124_1.R1011
5'-most EST	uC-zmflmo17256h07b1
Method	BLASTN
NCBI GI	g1653477
BLAST score	494
E value	0.0e+00
Match length	513
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 16/27, 1991550-2137258

Seq. No.	283365
Contig ID	136126_1.R1011
5'-most EST	uC-zmflmo17256h10b1
Method	BLASTN
NCBI GI	g1653715
BLAST score	499
E value	0.0e+00
Match length	599
% identity	95
NCBI Description	Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851

Seq. No.	283366
Contig ID	136134_1.R1011
5'-most EST	uC-zmflmo17257a12b1

Seq. No.	283367
Contig ID	136182_1.R1011
5'-most EST	uC-zmflmo17257e10b1

Seq. No.	283368
Contig ID	136190_1.R1011
5'-most EST	wyr700238707.h1
Method	BLASTX
NCBI GI	g3176664
BLAST score	161
E value	8.0e-11
Match length	65
% identity	51
NCBI Description	(AC004393) Contains similarity to beta scruin gb_Z47541 from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955 come from this gene. [Arabidopsis thaliana]

Seq. No.	283369
Contig ID	136220_1.R1011
5'-most EST	uC-zmflmo17258a04b1
Method	BLASTX
NCBI GI	g4531442
BLAST score	465
E value	1.0e-46
Match length	131

% identity	67
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]
Seq. No.	283370
Contig ID	136228_1.R1011
5'-most EST	uC-zmflmo17258a12b1
Seq. No.	283371
Contig ID	136239_1.R1011
5'-most EST	uC-zmflmo17309h11b1
Seq. No.	283372
Contig ID	136282_1.R1011
5'-most EST	uC-zmflmo17258f11b1
Seq. No.	283373
Contig ID	136286_1.R1011
5'-most EST	uC-zmflmo17258g03b1
Method	BLASTX
NCBI GI	g3894187
BLAST score	193
E value	1.0e-14
Match length	40
% identity	90
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.	283374
Contig ID	136305_1.R1011
5'-most EST	uC-zmflmo17258h12b1
Method	BLASTX
NCBI GI	g3790658
BLAST score	163
E value	4.0e-11
Match length	135
% identity	34
NCBI Description	(AF098999) contains similarity to ABC transporters (Pfam: ABC_tran.hmm, score: 39.76) [Caenorhabditis elegans]
Seq. No.	283375
Contig ID	136362_1.R1011
5'-most EST	ceu700427172.h1
Method	BLASTX
NCBI GI	g3142300
BLAST score	175
E value	6.0e-13
Match length	69
% identity	52
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]
Seq. No.	283376
Contig ID	136440_1.R1011
5'-most EST	uC-zmflmo17261e08b1
Seq. No.	283377

Contig ID	136459_1.R1011
5'-most EST	nbm700467085.h1
Seq. No.	283378
Contig ID	136464_1.R1011
5'-most EST	uC-zmflmo17261g12b1
Seq. No.	283379
Contig ID	136471_1.R1011
5'-most EST	uC-zmflmo17261h08b1
Seq. No.	283380
Contig ID	136483_1.R1011
5'-most EST	uC-zmflmo17270d02b1
Seq. No.	283381
Contig ID	136512_1.R1011
5'-most EST	uC-zmflmo17181f07b1
Method	BLASTX
NCBI GI	g2062176
BLAST score	251
E value	2.0e-21
Match length	60
% identity	75
NCBI Description	(AC001645) Myb-related transcription activator (MybSt1) isolog [Arabidopsis thaliana]
Seq. No.	283382
Contig ID	136513_1.R1011
5'-most EST	uC-zmflmo17262d04b1
Seq. No.	283383
Contig ID	136516_1.R1011
5'-most EST	tfd700570238.h1
Seq. No.	283384
Contig ID	136537_1.R1011
5'-most EST	uC-zmflmo17262f09b1
Seq. No.	283385
Contig ID	136550_1.R1011
5'-most EST	rvt700552739.h1
Seq. No.	283386
Contig ID	136551_1.R1011
5'-most EST	wyr700241322.h1
Seq. No.	283387
Contig ID	136552_1.R1011
5'-most EST	nbm700471545.h1
Seq. No.	283388
Contig ID	136565_1.R1011
5'-most EST	uC-zmflb73155g09b2
Method	BLASTX
NCBI GI	g3832528
BLAST score	170

E value	1.0e-11
Match length	55
% identity	64
NCBI Description	(AF100167) unknown [Glycine max]

Seq. No.	283389
Contig ID	136576_1.R1011
5'-most EST	wyr700238628.h1
Method	BLASTX
NCBI GI	g4204268
BLAST score	339
E value	4.0e-32
Match length	92
% identity	72
NCBI Description	(AC005223) 62134 [Arabidopsis thaliana]

Seq. No.	283390
Contig ID	136607_1.R1011
5'-most EST	uC-zmflmo17263e01b1
Method	BLASTX
NCBI GI	g461753
BLAST score	150
E value	4.0e-09
Match length	41
% identity	73
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi_169128 (L09547) nuclear encoded precursor to chloroplast protein [Pisum sativum]

Seq. No.	283391
Contig ID	136619_1.R1011
5'-most EST	uC-zmflmo17263f02b1

Seq. No.	283392
Contig ID	136637_1.R1011
5'-most EST	uC-zmflmo17265d05b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	283393
Contig ID	136650_1.R1011
5'-most EST	uC-zmflmo17263h11b1
Method	BLASTX
NCBI GI	g3776084
BLAST score	152
E value	7.0e-10
Match length	51
% identity	51
NCBI Description	(Y18251) NtN2 [Medicago truncatula]

Seq. No.	283394
Contig ID	136667_1.R1011
5'-most EST	pmx700089155.h1
Method	BLASTX
NCBI GI	g4539324
BLAST score	814
E value	2.0e-87
Match length	172
% identity	92
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	283395
Contig ID	136671_1.R1011
5'-most EST	nwy700447218.h1
Method	BLASTX
NCBI GI	g1946355
BLAST score	640
E value	6.0e-67
Match length	183
% identity	66
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	283396
Contig ID	136686_1.R1011
5'-most EST	nbm700474872.h1
Method	BLASTN
NCBI GI	g168654
BLAST score	65
E value	9.0e-28
Match length	256
% identity	82
NCBI Description	Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene, complete cds

Seq. No.	283397
Contig ID	136687_1.R1011
5'-most EST	uC-zmflmo17265d03b1

Seq. No.	283398
Contig ID	136695_1.R1011
5'-most EST	uC-zmflmo17265d12b1

Seq. No.	283399
Contig ID	136710_1.R1011
5'-most EST	uC-zmflmo17265f05b1

Seq. No.	283400
Contig ID	136715_1.R1011
5'-most EST	uC-zmflmo17265f10b1

Seq. No.	283401
Contig ID	136751_1.R1011
5'-most EST	uC-zmflmo17266b01b1
Method	BLASTX
NCBI GI	g3452263

BLAST score	934
E value	1.0e-101
Match length	237
% identity	77
NCBI Description	(AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No.	283402
Contig ID	136754_1.R1011
5'-most EST	ymt700219285.h1

Seq. No.	283403
Contig ID	136759_1.R1011
5'-most EST	uC-zmflmo17266b10b1
Method	BLASTX
NCBI GI	g1255448
BLAST score	541
E value	2.0e-55
Match length	150
% identity	71
NCBI Description	(D50468) mitogen-activated protein kinase [Arabidopsis thaliana]

Seq. No.	283404
Contig ID	136774_1.R1011
5'-most EST	uwc700151083.h1
Method	BLASTX
NCBI GI	g3241943
BLAST score	753
E value	3.0e-80
Match length	162
% identity	82
NCBI Description	(AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283405
Contig ID	136783_1.R1011
5'-most EST	fwa700098530.h1

Seq. No.	283406
Contig ID	136796_1.R1011
5'-most EST	pmx700087760.h1

Seq. No.	283407
Contig ID	136814_1.R1011
5'-most EST	wyr700235453.h1

Seq. No.	283408
Contig ID	136841_1.R1011
5'-most EST	uC-zmflmo17267b06b1
Method	BLASTX
NCBI GI	g4115379
BLAST score	232
E value	4.0e-33
Match length	176
% identity	47
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	283409
Contig ID	136846_1.R1011
5'-most EST	pmx700090817.h1
Method	BLASTX
NCBI GI	g3805765
BLAST score	201
E value	2.0e-15
Match length	90
% identity	52
NCBI Description	(AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No.	283410
Contig ID	136856_1.R1011
5'-most EST	ypc700803470.h1

Seq. No.	283411
Contig ID	136863_1.R1011
5'-most EST	uC-zmflmo17267d05b1

Seq. No.	283412
Contig ID	136866_1.R1011
5'-most EST	ntr700072768.h1
Method	BLASTX
NCBI GI	g2494119
BLAST score	155
E value	1.0e-21
Match length	94
% identity	65
NCBI Description	(AC002376) EST gb_T04104 comes from this gene. [Arabidopsis thaliana]

Seq. No.	283413
Contig ID	136868_1.R1011
5'-most EST	uC-zmflmo17267d11b1
Method	BLASTX
NCBI GI	g4263825
BLAST score	298
E value	1.0e-26
Match length	272
% identity	33
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283414
Contig ID	136869_1.R1011
5'-most EST	uC-zmflmo17267d12b1

Seq. No.	283415
Contig ID	136873_1.R1011
5'-most EST	qmh700026164.f1
Method	BLASTX
NCBI GI	g3319876
BLAST score	637
E value	3.0e-70
Match length	210
% identity	62
NCBI Description	(AJ007791) Msh3 protein [Arabidopsis thaliana]

Seq. No. 283416
Contig ID 136901_1.R1011
5'-most EST uC-zmflmo17267g12b1

Seq. No. 283417
Contig ID 136902_1.R1011
5'-most EST uC-zmflmo17267h01b1
Method BLASTX
NCBI GI g2262157
BLAST score 525
E value 2.0e-53
Match length 179
% identity 60
NCBI Description (AC002329) putative ligand-gated ion channel protein [Arabidopsis thaliana]

Seq. No. 283418
Contig ID 136912_1.R1011
5'-most EST uC-zmflmo17267h12b1

Seq. No. 283419
Contig ID 136937_1.R1011
5'-most EST uC-zmflb73259h01a1

Seq. No. 283420
Contig ID 136986_1.R1011
5'-most EST uC-zmflmo17268g07b1

Seq. No. 283421
Contig ID 137009_1.R1011
5'-most EST uC-zmflmo17269a07b1

Seq. No. 283422
Contig ID 137025_1.R1011
5'-most EST xsy700208434.h1

Seq. No. 283423
Contig ID 137051_1.R1011
5'-most EST uC-zmflmo17269e02b1

Seq. No. 283424
Contig ID 137088_1.R1011
5'-most EST uC-zmflmo17269h06b1

Seq. No. 283425
Contig ID 137092_1.R1011
5'-most EST xmt700263250.h1
Method BLASTX
NCBI GI g2252632
BLAST score 397
E value 3.0e-38
Match length 193
% identity 45
NCBI Description (U95973) Barley Mlo protein isolog [Arabidopsis thaliana]

Seq. No. 283426

Contig ID	137111_1.R1011
5'-most EST	uC-zmflmo17398h10a1
Seq. No.	283427
Contig ID	137177_1.R1011
5'-most EST	uC-zmflmo17271a02b1
Seq. No.	283428
Contig ID	137190_1.R1011
5'-most EST	uwc700151370.h1
Method	BLASTX
NCBI GI	g421941
BLAST score	770
E value	8.0e-82
Match length	188
% identity	81
NCBI Description	GTP-binding protein, ras-related - common tobacco >gi_296878_emb_CAA50609_ (X71609) ras-related GTP-binding protein [Nicotiana tabacum]
Seq. No.	283429
Contig ID	137190_2.R1011
5'-most EST	ceu700425007.h1
Seq. No.	283430
Contig ID	137241_1.R1011
5'-most EST	cyk700048764.f1
Method	BLASTX
NCBI GI	g4039153
BLAST score	178
E value	8.0e-13
Match length	43
% identity	70
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302_ (AF122005) hydrophobic protein [Arabidopsis thaliana]
Seq. No.	283431
Contig ID	137247_1.R1011
5'-most EST	xyt700346239.h1
Seq. No.	283432
Contig ID	137264_1.R1011
5'-most EST	uC-zmflmo17273b03b1
Seq. No.	283433
Contig ID	137266_1.R1011
5'-most EST	pmx700087493.h1
Seq. No.	283434
Contig ID	137279_1.R1011
5'-most EST	uC-zmflmo17273c07b1
Method	BLASTN
NCBI GI	g3411265
BLAST score	55
E value	5.0e-22
Match length	71

% identity	94
NCBI Description	Zea mays pullulanase-type starch debranching enzyme (zpu1) mRNA, complete cds

Seq. No.	283435
Contig ID	137284_2.R1011
5'-most EST	uer700580219.h1

Seq. No.	283436
Contig ID	137291_1.R1011
5'-most EST	uC-zmflmo17273d09b1

Seq. No.	283437
Contig ID	137294_1.R1011
5'-most EST	gwl700612676.h1
Method	BLASTX
NCBI GI	g1532171
BLAST score	469
E value	5.0e-47
Match length	156
% identity	62
NCBI Description	(U63815) AT.I.24-9 gene product [Arabidopsis thaliana]

Seq. No.	283438
Contig ID	137342_1.R1011
5'-most EST	uC-zmflmo17277a06b1

Seq. No.	283439
Contig ID	137343_1.R1011
5'-most EST	uC-zmflmo17277a07b1
Method	BLASTX
NCBI GI	g1709758
BLAST score	171
E value	5.0e-12
Match length	49
% identity	71
NCBI Description	PROTEASOME COMPONENT C2 (MACROPAIN SUBUNIT C2) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2) >gi_1066151_dbj_BAA07128_ (D37886) proteasome C2 subunit [Oryza sativa]

Seq. No.	283440
Contig ID	137374_1.R1011
5'-most EST	uC-zmflmo17277d05b1

Seq. No.	283441
Contig ID	137407_1.R1011
5'-most EST	cat700021488.r1
Method	BLASTX
NCBI GI	g3927827
BLAST score	155
E value	4.0e-10
Match length	101
% identity	37
NCBI Description	(AC005727) osmotin-like protein precursor [Arabidopsis thaliana]

Seq. No.	283442
Contig ID	137410_1.R1011
5'-most EST	uC-zmflmo17277g07b1
Method	BLASTX
NCBI GI	g2104908
BLAST score	301
E value	2.0e-39
Match length	121
% identity	73
NCBI Description	(Y07632) potassium channel [Zea mays]

Seq. No.	283443
Contig ID	137426_1.R1011
5'-most EST	pmx700085714.h1
Method	BLASTX
NCBI GI	g3287679
BLAST score	627
E value	1.0e-113
Match length	305
% identity	70
NCBI Description	(AC003979) T22J18.6 [Arabidopsis thaliana]

Seq. No.	283444
Contig ID	137434_1.R1011
5'-most EST	uer700580207.h1

Seq. No.	283445
Contig ID	137438_1.R1011
5'-most EST	uwc700150430.h1

Seq. No.	283446
Contig ID	137440_1.R1011
5'-most EST	uC-zmflmo17278b06b1

Seq. No.	283447
Contig ID	137449_1.R1011
5'-most EST	uC-zmflmo17278c06b1
Method	BLASTX
NCBI GI	g1931641
BLAST score	355
E value	2.0e-33
Match length	173
% identity	44
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]

Seq. No.	283448
Contig ID	137453_1.R1011
5'-most EST	uC-zmflmo17278c10b1
Method	BLASTX
NCBI GI	g2914697
BLAST score	289
E value	1.0e-25
Match length	114
% identity	54
NCBI Description	(AC003974) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283449

Contig ID	137509_1.R1011
5'-most EST	uC-zmflmo17278h11b1
Method	BLASTX
NCBI GI	g3377800
BLAST score	583
E value	3.0e-60
Match length	154
% identity	70
NCBI Description	(AF075597) similar to glycosyl hydrolases family 9 (PFam:glycosyl_hydro5.hmm, score: 100.70) [Arabidopsis thaliana]

Seq. No.	283450
Contig ID	137517_1.R1011
5'-most EST	uC-zmflmo17070e03a1

Seq. No.	283451
Contig ID	137526_1.R1011
5'-most EST	uC-zmflmo17280b06b1

Seq. No.	283452
Contig ID	137530_1.R1011
5'-most EST	pmx700083818.h1
Method	BLASTX
NCBI GI	g2335096
BLAST score	169
E value	2.0e-11
Match length	83
% identity	43
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283453
Contig ID	137576_1.R1011
5'-most EST	uC-zmflmo17280g04b1
Method	BLASTN
NCBI GI	g602605
BLAST score	38
E value	7.0e-12
Match length	82
% identity	87
NCBI Description	Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No.	283454
Contig ID	137586_1.R1011
5'-most EST	uC-zmflmo17280h05b1

Seq. No.	283455
Contig ID	137594_1.R1011
5'-most EST	uC-zmflmo17282a02b1
Method	BLASTX
NCBI GI	g3236240
BLAST score	259
E value	1.0e-22
Match length	108
% identity	54
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	283456
Contig ID	137618_1.R1011
5'-most EST	uC-zmflmo17282c03b1
Method	BLASTX
NCBI GI	g161752
BLAST score	283
E value	7.0e-25
Match length	181
% identity	15
NCBI Description	(L03710) cnjB [Tetrahymena thermophila] >gi_737494_prf__1922371A cnjB gene [Tetrahymena thermophila]

Seq. No.	283457
Contig ID	137629_1.R1011
5'-most EST	rvt700551543.h1
Method	BLASTX
NCBI GI	g2529677
BLAST score	219
E value	2.0e-17
Match length	113
% identity	45
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No.	283458
Contig ID	137664_1.R1011
5'-most EST	uC-zmflmo17282g12b1
Method	BLASTX
NCBI GI	g1001294
BLAST score	144
E value	7.0e-09
Match length	56
% identity	46
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	283459
Contig ID	137683_1.R1011
5'-most EST	uC-zmflmo17283a08b1
Method	BLASTX
NCBI GI	g4490323
BLAST score	153
E value	1.0e-16
Match length	94
% identity	59
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	283460
Contig ID	137685_1.R1011
5'-most EST	xdb700341527.h1
Method	BLASTX
NCBI GI	g2618725
BLAST score	199
E value	3.0e-15
Match length	54
% identity	67
NCBI Description	(U49074) IAA18 [Arabidopsis thaliana]

Seq. No.	283461
Contig ID	137704_1.R1011
5'-most EST	fdz701l61436.h1

Seq. No.	283462
Contig ID	137716_1.R1011
5'-most EST	pmx700083352.h1
Method	BLASTX
NCBI GI	g4467098
BLAST score	239
E value	4.0e-20
Match length	103
% identity	42
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	283463
Contig ID	137727_1.R1011
5'-most EST	pmx700083910.h1

Seq. No.	283464
Contig ID	137735_1.R1011
5'-most EST	ymt700221102.h1
Method	BLASTX
NCBI GI	g4335754
BLAST score	201
E value	1.0e-15
Match length	124
% identity	35
NCBI Description	(AC006284) putative acid phophatase (contains metallo-phosphoesterase motif, prosite: QDOC50185) [Arabidopsis thaliana]

Seq. No.	283465
Contig ID	137757_1.R1011
5'-most EST	nwy700445619.h1

Seq. No.	283466
Contig ID	137778_1.R1011
5'-most EST	uC-zmflmo17285b03b1

Seq. No.	283467
Contig ID	137779_1.R1011
5'-most EST	uC-zmflb73165f12b2

Seq. No.	283468
Contig ID	137788_1.R1011
5'-most EST	uC-zmflmo17285c01b1

Seq. No.	283469
Contig ID	137809_1.R1011
5'-most EST	uC-zmflmo17285e01b1
Method	BLASTX
NCBI GI	g1361985
BLAST score	214
E value	3.0e-17
Match length	129

% identity	39
NCBI Description	disease resistance protein RPM1 - Arabidopsis thaliana >gi_963017_emb_CAA61131_ (X87851) disease resistance gene [Arabidopsis thaliana]

Seq. No.	283470
Contig ID	137822_1.R1011
5'-most EST	uC-zmflmo17285f03b1

Seq. No.	283471
Contig ID	137833_1.R1011
5'-most EST	tzu700201754.h1
Method	BLASTX
NCBI GI	g4587513
BLAST score	452
E value	2.0e-44
Match length	160
% identity	56
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	283472
Contig ID	137840_1.R1011
5'-most EST	uC-zmflmo17309g07b1
Method	BLASTX
NCBI GI	g4512630
BLAST score	171
E value	5.0e-16
Match length	254
% identity	26
NCBI Description	(AC004793) Contains reverse transcriptase domain (rvt) PF_00078. [Arabidopsis thaliana]

Seq. No.	283473
Contig ID	137852_1.R1011
5'-most EST	uC-zmflmo17286a02b1
Method	BLASTX
NCBI GI	g1752734
BLAST score	315
E value	7.0e-29
Match length	165
% identity	41
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	283474
Contig ID	137870_1.R1011
5'-most EST	uC-zmflmo17400h04a1
Method	BLASTX
NCBI GI	g1667607
BLAST score	164
E value	3.0e-11
Match length	38
% identity	84
NCBI Description	(U76747) Tap [Triticum aestivum]

Seq. No.	283475
Contig ID	137875_1.R1011

5'-most EST	uC-zmflmo17286c05b1
Method	BLASTX
NCBI GI	g3169716
BLAST score	506
E value	2.0e-51
Match length	149
% identity	63
NCBI Description	(U60986) NADP-dependent glutamate dehydrogenase [Giardia intestinalis]

Seq. No.	283476
Contig ID	137910_1.R1011
5'-most EST	uC-zmflmo17286f06b1

Seq. No.	283477
Contig ID	137911_1.R1011
5'-most EST	uC-zmflb73300e06a1

Seq. No.	283478
Contig ID	137922_1.R1011
5'-most EST	uC-zmflmo17286g07b1
Method	BLASTX
NCBI GI	g2827635
BLAST score	544
E value	9.0e-56
Match length	132
% identity	80
NCBI Description	(AL021636) predicted protein [Arabidopsis thaliana]

Seq. No.	283479
Contig ID	137966_1.R1011
5'-most EST	uC-zmflmo17287c08b1

Seq. No.	283480
Contig ID	137974_1.R1011
5'-most EST	uC-zmflmo17287d04b1
Method	BLASTX
NCBI GI	g2130141
BLAST score	474
E value	2.0e-47
Match length	204
% identity	47
NCBI Description	mudrA protein - maize transposon MuDR >gi_540581 (M76978) mudrA [Zea mays] >gi_595816 (U14597) mudrA gene product [Zea mays]

Seq. No.	283481
Contig ID	137981_1.R1011
5'-most EST	bdu700382010.h1
Method	BLASTX
NCBI GI	g3668088
BLAST score	236
E value	1.0e-19
Match length	77
% identity	53
NCBI Description	(AC004667) G9a-like protein [Arabidopsis thaliana]

Seq. No.	283482
Contig ID	137985_1.R1011
5'-most EST	uC-zmflmo17287e03b1
Method	BLASTX
NCBI GI	g4588012
BLAST score	1068
E value	1.0e-116
Match length	394
% identity	56
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	283483
Contig ID	137996_1.R1011
5'-most EST	tfd700572114.h1

Seq. No.	283484
Contig ID	138051_1.R1011
5'-most EST	ntr700075983.h1
Method	BLASTX
NCBI GI	g4539423
BLAST score	215
E value	5.0e-17
Match length	51
% identity	75
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	283485
Contig ID	138069_1.R1011
5'-most EST	uC-zmflmo17288d12b1

Seq. No.	283486
Contig ID	138070_1.R1011
5'-most EST	uC-zmflmo17288e01b1

Seq. No.	283487
Contig ID	138074_1.R1011
5'-most EST	uC-zmflmo17288e05b1

Seq. No.	283488
Contig ID	138086_1.R1011
5'-most EST	ymt700220017.h1

Seq. No.	283489
Contig ID	138090_1.R1011
5'-most EST	uC-zmflmo17288f10b1
Method	BLASTX
NCBI GI	g4538965
BLAST score	304
E value	1.0e-27
Match length	117
% identity	47
NCBI Description	(AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283490
Contig ID	138091_1.R1011

5'-most EST	uC-zmflmo17288f12b1
Method	BLASTX
NCBI GI	g2827139
BLAST score	318
E value	4.0e-33
Match length	116
% identity	60
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	283491
Contig ID	138098_1.R1011
5'-most EST	xmt700259129.h2
Method	BLASTX
NCBI GI	g2648032
BLAST score	658
E value	4.0e-73
Match length	167
% identity	79
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	283492
Contig ID	138099_1.R1011
5'-most EST	uC-zmflmo17288g08b1
Method	BLASTX
NCBI GI	g2760843
BLAST score	234
E value	3.0e-19
Match length	119
% identity	43
NCBI Description	(AC003105) unknown protein [Arabidopsis thaliana]

Seq. No.	283493
Contig ID	138099_2.R1011
5'-most EST	xdb700341961.h1

Seq. No.	283494
Contig ID	138134_1.R1011
5'-most EST	pmx700083934.h1
Method	BLASTX
NCBI GI	g4103857
BLAST score	143
E value	8.0e-09
Match length	74
% identity	51
NCBI Description	(AF028722) fetal globin inducing factor [Mus musculus]

Seq. No.	283495
Contig ID	138143_1.R1011
5'-most EST	wuj700282188.h1
Method	BLASTX
NCBI GI	g469072
BLAST score	267
E value	2.0e-23
Match length	85

% identity	58
NCBI Description	(D16206) RNA-binding gricine-rich protein-1 (RGP-1c) [Nicotiana sylvestris]

Seq. No.	283496
Contig ID	138163_1.R1011
5'-most EST	uC-zmflmo17289e08b1
Method	BLASTX
NCBI GI	g1619300
BLAST score	269
E value	1.0e-23
Match length	63
% identity	76
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	283497
Contig ID	138175_1.R1011
5'-most EST	uC-zmflmo17289f08b1

Seq. No.	283498
Contig ID	138182_1.R1011
5'-most EST	pwr700451629.h1
Method	BLASTX
NCBI GI	g2827282
BLAST score	228
E value	9.0e-19
Match length	122
% identity	43
NCBI Description	(AF040701) TATA binding protein associated factor [Homo sapiens]

Seq. No.	283499
Contig ID	138212_1.R1011
5'-most EST	uC-zmflmo17290a11b1

Seq. No.	283500
Contig ID	138218_1.R1011
5'-most EST	wyr700238449.h1
Method	BLASTX
NCBI GI	g4432825
BLAST score	752
E value	9.0e-80
Match length	261
% identity	74
NCBI Description	(AC006593) putative SOP2p protein [Arabidopsis thaliana]

Seq. No.	283501
Contig ID	138220_1.R1011
5'-most EST	uC-zmflmo17290b07b1

Seq. No.	283502
Contig ID	138243_1.R1011
5'-most EST	uC-zmflmo17290d08b1
Method	BLASTX
NCBI GI	g2346976
BLAST score	184
E value	1.0e-13

Match length	84
% identity	44
NCBI Description	(AB006600) ZPT2-13 [Petunia x hybrida]

Seq. No.	283503
Contig ID	138264_1.R1011
5'-most EST	uC-zmflmo17290f07b1
Method	BLASTX
NCBI GI	g3132479
BLAST score	743
E value	6.0e-79
Match length	217
% identity	69
NCBI Description	(AC003096) multidrug resistance-associated protein, AtMRP2 [Arabidopsis thaliana]

Seq. No.	283504
Contig ID	138280_1.R1011
5'-most EST	uC-zmflmo17290g11b1
Method	BLASTX
NCBI GI	g551167
BLAST score	186
E value	8.0e-14
Match length	66
% identity	58
NCBI Description	(L35241) moesin actin-binding domain homologue [Arabidopsis thaliana]

Seq. No.	283505
Contig ID	138290_1.R1011
5'-most EST	wty700171110.h1
Method	BLASTX
NCBI GI	g4415913
BLAST score	168
E value	1.0e-11
Match length	54
% identity	67
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	283506
Contig ID	138328_1.R1011
5'-most EST	uC-zmflmo17292c12b1

Seq. No.	283507
Contig ID	138342_1.R1011
5'-most EST	uC-zmflmo17292e04b1

Seq. No.	283508
Contig ID	138352_1.R1011
5'-most EST	yyf700351961.h1

Seq. No.	283509
Contig ID	138353_1.R1011
5'-most EST	uC-zmflmo17292f03b1

Seq. No.	283510
Contig ID	138356_1.R1011

5'-most EST	uC-zmflmo17313c04b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	283511
Contig ID	138361_1.R1011
5'-most EST	xmt700259535.h1

Seq. No.	283512
Contig ID	138380_1.R1011
5'-most EST	qmh700029589.f1

Seq. No.	283513
Contig ID	138417_1.R1011
5'-most EST	uC-zmflmo17293d04b1

Seq. No.	283514
Contig ID	138434_1.R1011
5'-most EST	uC-zmflb73135d06b2
Method	BLASTX
NCBI GI	g2618689
BLAST score	236
E value	2.0e-19
Match length	56
% identity	82
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	283515
Contig ID	138447_1.R1011
5'-most EST	nbm700467706.h1
Method	BLASTX
NCBI GI	g4559353
BLAST score	688
E value	1.0e-72
Match length	156
% identity	83
NCBI Description	(AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]

Seq. No.	283516
Contig ID	138464_1.R1011
5'-most EST	pmx700087416.h1

Seq. No.	283517
Contig ID	138480_1.R1011
5'-most EST	uC-zmflmo17294b06b1
Method	BLASTX
NCBI GI	g3928871
BLAST score	1320
E value	1.0e-146
Match length	252
% identity	99

NCBI Description	(AF093627) poly(ADP)-ribose polymerase [Zea mays]
Seq. No.	283518
Contig ID	138502_1.R1011
5'-most EST	uwc700154209.h1
Method	BLASTX
NCBI GI	g3043712
BLAST score	313
E value	2.0e-28
Match length	92
% identity	63
NCBI Description	(AB011166) KIAA0594 protein [Homo sapiens]
Seq. No.	283519
Contig ID	138519_1.R1011
5'-most EST	uC-zmflmo17294f01b1
Method	BLASTX
NCBI GI	g3882183
BLAST score	165
E value	2.0e-11
Match length	85
% identity	44
NCBI Description	(AB018274) KIAA0731 protein [Homo sapiens]
Seq. No.	283520
Contig ID	138557_1.R1011
5'-most EST	vqh700053155.r1
Seq. No.	283521
Contig ID	138559_1.R1011
5'-most EST	xsy700208428.h1
Method	BLASTX
NCBI GI	g2673914
BLAST score	343
E value	6.0e-32
Match length	144
% identity	51
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.	283522
Contig ID	138581_1.R1011
5'-most EST	uC-zmflmo17295c05b1
Seq. No.	283523
Contig ID	138581_2.R1011
5'-most EST	cyk700049572.f1
Seq. No.	283524
Contig ID	138583_1.R1011
5'-most EST	uC-zmflmo17295c07b1
Seq. No.	283525
Contig ID	138598_1.R1011
5'-most EST	uC-zmflmo17295d11b1
Seq. No.	283526
Contig ID	138603_1.R1011

5'-most EST	pmx700084182.h1
Seq. No.	283527
Contig ID	138662_1.R1011
5'-most EST	tzu700204729.h1
Seq. No.	283528
Contig ID	138694_1.R1011
5'-most EST	xsy700211480.h1
Method	BLASTX
NCBI GI	g2213600
BLAST score	725
E value	1.0e-76
Match length	258
% identity	55
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]
Seq. No.	283529
Contig ID	138726_1.R1011
5'-most EST	xyt700343972.h1
Method	BLASTX
NCBI GI	g2660677
BLAST score	392
E value	6.0e-38
Match length	120
% identity	58
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]
Seq. No.	283530
Contig ID	138765_1.R1011
5'-most EST	uC-zmflmo17299c12b1
Seq. No.	283531
Contig ID	138784_1.R1011
5'-most EST	yyf700350391.h1
Seq. No.	283532
Contig ID	138820_1.R1011
5'-most EST	uC-zmflmo17300b01b1
Seq. No.	283533
Contig ID	138828_1.R1011
5'-most EST	uC-zmflmo17300b10b1
Seq. No.	283534
Contig ID	138834_1.R1011
5'-most EST	uC-zmflmo17300c05b1
Seq. No.	283535
Contig ID	138843_1.R1011
5'-most EST	uC-zmflmo17300d04a1
Seq. No.	283536
Contig ID	138844_1.R1011
5'-most EST	uC-zmflmo17300d05b1
Seq. No.	283537

Contig ID	138846_1.R1011
5'-most EST	uC-zmflmo17300d07b1
Method	BLASTX
NCBI GI	g4262239
BLAST score	234
E value	3.0e-19
Match length	136
% identity	36
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	283538
Contig ID	138852_1.R1011
5'-most EST	xmt700267688.h1
Method	BLASTX
NCBI GI	g2583121
BLAST score	527
E value	1.0e-53
Match length	131
% identity	78
NCBI Description	(AC002387) putative phosphotransferase [Arabidopsis thaliana]

Seq. No.	283539
Contig ID	138854_1.R1011
5'-most EST	uC-zmflmo17300e05b1
Method	BLASTX
NCBI GI	g4468804
BLAST score	357
E value	8.0e-34
Match length	169
% identity	24
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	283540
Contig ID	138900_1.R1011
5'-most EST	uC-zmflmo17342f03b1
Method	BLASTX
NCBI GI	g345790
BLAST score	383
E value	1.0e-36
Match length	136
% identity	54
NCBI Description	CDC4L protein - human (fragment)

Seq. No.	283541
Contig ID	138900_2.R1011
5'-most EST	uC-zmflmo17301a11b1

Seq. No.	283542
Contig ID	138904_1.R1011
5'-most EST	wty700172529.h1

Seq. No.	283543
Contig ID	138906_1.R1011
5'-most EST	uC-zmflmo17425d03a1

Seq. No.	283544
Contig ID	138939_1.R1011
5'-most EST	uC-zmflb73234f08b2
Method	BLASTX
NCBI GI	g4262147
BLAST score	228
E value	1.0e-18
Match length	113
% identity	43
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	283545
Contig ID	138966_1.R1011
5'-most EST	uC-zmroteosinte006d03b1

Seq. No.	283546
Contig ID	138968_1.R1011
5'-most EST	ceu700432880.h1
Method	BLASTX
NCBI GI	g3182915
BLAST score	155
E value	3.0e-16
Match length	86
% identity	50
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1842150_dbj_BAA19225_ (AB001051) ADP-ribosylation factor [Dugesia japonica]

Seq. No.	283547
Contig ID	138974_1.R1011
5'-most EST	uC-zmflmo17303a03b1
Method	BLASTX
NCBI GI	g3548803
BLAST score	447
E value	2.0e-44
Match length	141
% identity	65
NCBI Description	(AC005313) putative DNA-binding protein [Arabidopsis thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No.	283548
Contig ID	139037_1.R1011
5'-most EST	uC-zmflmo17303f11b1
Method	BLASTX
NCBI GI	g2827630
BLAST score	183
E value	3.0e-13
Match length	102
% identity	36
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	283549
Contig ID	139039_1.R1011
5'-most EST	xdb700338423.h1

Seq. No.	283550

Contig ID	139051_1.R1011
5'-most EST	uC-zmflmo17303h02b1
Method	BLASTX
NCBI GI	g4581111
BLAST score	194
E value	2.0e-14
Match length	177
% identity	29
NCBI Description	(AC005825) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	283551
Contig ID	139051_2.R1011
5'-most EST	uC-zmflmo17027g04a1

Seq. No.	283552
Contig ID	139059_1.R1011
5'-most EST	tfd700571984.h1
Method	BLASTX
NCBI GI	g3935181
BLAST score	514
E value	4.0e-56
Match length	133
% identity	81
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	283553
Contig ID	139081_1.R1011
5'-most EST	uC-zmflmo17306b12b1

Seq. No.	283554
Contig ID	139085_1.R1011
5'-most EST	uC-zmflmo17306c04b1

Seq. No.	283555
Contig ID	139087_1.R1011
5'-most EST	hbs701182558.h1

Seq. No.	283556
Contig ID	139106_1.R1011
5'-most EST	uC-zmflmo17028g10a1

Seq. No.	283557
Contig ID	139144_1.R1011
5'-most EST	uC-zmflmo17342e05a1
Method	BLASTX
NCBI GI	g100226
BLAST score	155
E value	4.0e-10
Match length	99
% identity	38
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	283558

Contig ID	139148_1.R1011
5'-most EST	ymt700222492.h1
Seq. No.	283559
Contig ID	139150_1.R1011
5'-most EST	uC-zmflmo17307a04b1
Seq. No.	283560
Contig ID	139170_1.R1011
5'-most EST	tzu700206774.h1
Method	BLASTX
NCBI GI	g4322421
BLAST score	539
E value	4.0e-55
Match length	146
% identity	64
NCBI Description	(AF085230) cadmium resistance factor 1 [Arabidopsis thaliana]
Seq. No.	283561
Contig ID	139220_1.R1011
5'-most EST	uC-zmflmo17307g09b1
Method	BLASTX
NCBI GI	g3132825
BLAST score	742
E value	5.0e-79
Match length	147
% identity	97
NCBI Description	(AF063403) putative cytosine-5 DNA methyltransferase [Zea mays]
Seq. No.	283562
Contig ID	139221_1.R1011
5'-most EST	uC-zmflmo17307g10b1
Method	BLASTX
NCBI GI	g3157949
BLAST score	218
E value	2.0e-17
Match length	75
% identity	49
NCBI Description	(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb_Z28697 from Nicotiana tabacum. ESTs gb_Z18185 and gb_AA605362 come from this gene. [Arabidopsis thaliana]
Seq. No.	283563
Contig ID	139270_1.R1011
5'-most EST	xtj700378210.h1
Seq. No.	283564
Contig ID	139277_1.R1011
5'-most EST	nbm700474787.h1
Method	BLASTX
NCBI GI	g2244940
BLAST score	154
E value	1.0e-20
Match length	137
% identity	53

NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 283565
Contig ID 139301_1.R1011
5'-most EST uC-zmflmo17308g09b1

Seq. No. 283566
Contig ID 139311_1.R1011
5'-most EST uC-zmflmo17308h07b1

Seq. No. 283567
Contig ID 139325_1.R1011
5'-most EST uC-zmflmo17309a12b1

Seq. No. 283568
Contig ID 139346_1.R1011
5'-most EST uer700583628.h1

Seq. No. 283569
Contig ID 139348_1.R1011
5'-most EST uC-zmflmo17309d04b1
Method BLASTX
NCBI GI g3608412
BLAST score 432
E value 1.0e-42
Match length 139
% identity 60
NCBI Description (AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No. 283570
Contig ID 139360_1.R1011
5'-most EST uC-zmflmo17309e07b1
Method BLASTX
NCBI GI g627969
BLAST score 187
E value 8.0e-14
Match length 189
% identity 10
NCBI Description apomucin precursor - rat >gi_476097 (U03407) apomucin [Rattus norvegicus]

Seq. No. 283571
Contig ID 139360_2.R1011
5'-most EST uwc700154973.h1
Method BLASTX
NCBI GI g627969
BLAST score 182
E value 2.0e-13
Match length 122
% identity 7
NCBI Description apomucin precursor - rat >gi_476097 (U03407) apomucin [Rattus norvegicus]

Seq. No. 283572
Contig ID 139389_1.R1011
5'-most EST uC-zmflb73072b07a1

Seq. No.	283573
Contig ID	139410_1.R1011
5'-most EST	wen700334655.h1

Seq. No.	283574
Contig ID	139412_1.R1011
5'-most EST	gct701175701.h1
Method	BLASTN
NCBI GI	g22549
BLAST score	49
E value	2.0e-18
Match length	77
% identity	91
NCBI Description	Maize gene for a 27kDa storage protein, zein

Seq. No.	283575
Contig ID	139416_1.R1011
5'-most EST	uC-zmflmo17310b09b1
Method	BLASTX
NCBI GI	g3560166
BLAST score	286
E value	2.0e-25
Match length	154
% identity	42
NCBI Description	(AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]

Seq. No.	283576
Contig ID	139439_1.R1011
5'-most EST	uwc700150696.h1
Method	BLASTX
NCBI GI	g3355477
BLAST score	545
E value	7.0e-56
Match length	159
% identity	39
NCBI Description	(AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No.	283577
Contig ID	139495_1.R1011
5'-most EST	uC-zmflmo17312a09b1
Method	BLASTX
NCBI GI	g4218535
BLAST score	179
E value	1.0e-12
Match length	58
% identity	64
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	283578
Contig ID	139506_1.R1011
5'-most EST	fC-zmle700432739a3
Method	BLASTX
NCBI GI	g2801536
BLAST score	323

Draft - 10/27/2000

E value	1.0e-29
Match length	122
% identity	56
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	283579
Contig ID	139513_1.R1011
5'-most EST	uC-zmflmo17312c04b1
Method	BLASTX
NCBI GI	g4586055
BLAST score	515
E value	2.0e-52
Match length	159
% identity	59
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283580
Contig ID	139515_1.R1011
5'-most EST	uC-zmflmo17312c12b1

Seq. No.	283581
Contig ID	139527_1.R1011
5'-most EST	uC-zmflmo17312d06b1

Seq. No.	283582
Contig ID	139529_1.R1011
5'-most EST	wty700173002.h1

Seq. No.	283583
Contig ID	139535_1.R1011
5'-most EST	uC-zmflmo17344b11b1
Method	BLASTX
NCBI GI	g3402679
BLAST score	340
E value	1.0e-31
Match length	212
% identity	43
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	283584
Contig ID	139549_1.R1011
5'-most EST	uC-zmflmo17312f06b1
Method	BLASTN
NCBI GI	g433039
BLAST score	45
E value	5.0e-16
Match length	61
% identity	93
NCBI Description	Zea mays W-22 clone PREM-1 retroelement PREM-1, partial sequence

Seq. No.	283585
Contig ID	139563_1.R1011
5'-most EST	uC-zmflmo17352c06a1

Seq. No.	283586
Contig ID	139582_1.R1011

5'-most EST	tfd700571326.h1
Method	BLASTX
NCBI GI	g2979544
BLAST score	381
E value	1.0e-36
Match length	118
% identity	59
NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	283587
Contig ID	139611_1.R1011
5'-most EST	uC-zmflmo17313d02b1

Seq. No.	283588
Contig ID	139613_1.R1011
5'-most EST	qmh700027052.f1
Method	BLASTX
NCBI GI	g3860275
BLAST score	595
E value	1.0e-61
Match length	171
% identity	66
NCBI Description	(AC005824) putative GTP-binding protein [Arabidopsis thaliana] >gi_4314395_gb_AAD15605_ (AC006232) putative terminal flower 1 (TFL1) [Arabidopsis thaliana] >gi_4521159_dbj_BAA75933.1_ (AB024712) ATC [Arabidopsis thaliana] >gi_4521161_dbj_BAA75931.1_ (AB024714) ATC [Arabidopsis thaliana] >gi_4521163_dbj_BAA75932.1_ (AB024715) ATC [Arabidopsis thaliana]

Seq. No.	283589
Contig ID	139624_1.R1011
5'-most EST	cyk700051679.f1

Seq. No.	283590
Contig ID	139637_1.R1011
5'-most EST	ymt700219345.h1

Seq. No.	283591
Contig ID	139690_1.R1011
5'-most EST	fwa700101332.h1
Method	BLASTX
NCBI GI	g4539452
BLAST score	340
E value	8.0e-33
Match length	162
% identity	48
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	283592
Contig ID	139705_1.R1011
5'-most EST	uC-zmflmo17320d05a1

Seq. No.	283593
Contig ID	139706_1.R1011
5'-most EST	uC-zmflmo17320d06b1

Method	BLASTN
NCBI GI	g3287498
BLAST score	36
E value	1.0e-10
Match length	64
% identity	89
NCBI Description	Oryza sativa gene for importin alpha, complete cds

Seq. No.	283594
Contig ID	139708_1.R1011
5'-most EST	cyk700049482.f1
Method	BLASTX
NCBI GI	g4325341
BLAST score	684
E value	6.0e-72
Match length	162
% identity	77
NCBI Description	(AF128393) similar to the Drosophila DES-1 protein (GB:X94180) [Arabidopsis thaliana]

Seq. No.	283595
Contig ID	139722_1.R1011
5'-most EST	uC-zmflmo17320e11b1
Method	BLASTX
NCBI GI	g1183961
BLAST score	435
E value	6.0e-49
Match length	161
% identity	63
NCBI Description	(Z69382) RNA elicase [Saccharomyces cerevisiae]

Seq. No.	283596
Contig ID	139744_1.R1011
5'-most EST	wyr700244349.h1
Method	BLASTX
NCBI GI	g2781351
BLAST score	510
E value	1.0e-66
Match length	197
% identity	69
NCBI Description	(AC003113) F24O1.7 [Arabidopsis thaliana]

Seq. No.	283597
Contig ID	139807_1.R1011
5'-most EST	uC-zmflmo17321e08b1

Seq. No.	283598
Contig ID	139819_1.R1011
5'-most EST	wty700171911.h1
Method	BLASTX
NCBI GI	g3608155
BLAST score	777
E value	6.0e-83
Match length	208
% identity	73
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	283599
Contig ID	139825_1.R1011
5'-most EST	uC-zmflmo17321g03b1
Method	BLASTX
NCBI GI	g2494034
BLAST score	526
E value	1.0e-53
Match length	137
% identity	66
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	283600
Contig ID	139832_2.R1011
5'-most EST	uC-zmflb73251f07b3

Seq. No.	283601
Contig ID	139856_1.R1011
5'-most EST	uC-zmflmo17322b02b1
Method	BLASTX
NCBI GI	g4510377
BLAST score	628
E value	1.0e-65
Match length	181
% identity	70
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	283602
Contig ID	139859_1.R1011
5'-most EST	uC-zmflmo17322b05b1

Seq. No.	283603
Contig ID	139869_1.R1011
5'-most EST	nbm700468241.h1

Seq. No.	283604
Contig ID	139877_1.R1011
5'-most EST	uC-zmflmo17322c12b1
Method	BLASTX
NCBI GI	g4185311
BLAST score	880
E value	4.0e-95
Match length	180
% identity	93
NCBI Description	(AF090446) polyprotein [Zea mays]

Seq. No.	283605
Contig ID	139907_1.R1011
5'-most EST	uC-zmflmo17322f09b1

Seq. No.	283606
Contig ID	139932_1.R1011
5'-most EST	uC-zmflmo17322h12b1
Method	BLASTX
NCBI GI	g3080423

BLAST score	263
E value	2.0e-37
Match length	154
% identity	53
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	283607
Contig ID	139946_1.R1011
5'-most EST	uC-zmflmo17330b02b1

Seq. No.	283608
Contig ID	139967_1.R1011
5'-most EST	pmx700087534.h1
Method	BLASTX
NCBI GI	g3242729
BLAST score	1346
E value	1.0e-149
Match length	297
% identity	82
NCBI Description	(AC003040) curly leaf protein (polycomb-group) [Arabidopsis thaliana]

Seq. No.	283609
Contig ID	139997_1.R1011
5'-most EST	hbs701185413.h1

Seq. No.	283610
Contig ID	140011_1.R1011
5'-most EST	uC-zmflmo17330h01b1

Seq. No.	283611
Contig ID	140018_1.R1011
5'-most EST	rvt700551803.h1

Seq. No.	283612
Contig ID	140019_1.R1011
5'-most EST	uC-zmflmo17330h09b1
Method	BLASTX
NCBI GI	g464900
BLAST score	254
E value	9.0e-22
Match length	144
% identity	35
NCBI Description	PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR >gi_539008_pir__S39476 kinase-like transmembrane protein TMKL1 precursor - Arabidopsis thaliana >gi_313190_emb_CAA51385_ (X72863) TMKL1 [Arabidopsis thaliana]

Seq. No.	283613
Contig ID	140021_1.R1011
5'-most EST	uC-zmflmo17330h11b1

Seq. No.	283614
Contig ID	140035_1.R1011
5'-most EST	uC-zmflmo17333b01b1
Method	BLASTX

NCBI GI	g2765817
BLAST score	502
E value	1.0e-50
Match length	129
% identity	71
NCBI Description	(Z95352) AtMlo-h1 [Arabidopsis thaliana] >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No.	283615
Contig ID	140055_1.R1011
5'-most EST	yyf700349229.h1
Method	BLASTX
NCBI GI	g2462829
BLAST score	149
E value	2.0e-09
Match length	104
% identity	34
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	283616
Contig ID	140061_1.R1011
5'-most EST	uC-zmflmo17333d07b1
Method	BLASTX
NCBI GI	g99741
BLAST score	657
E value	8.0e-69
Match length	230
% identity	30
NCBI Description	P-glycoprotein pgp1 - Arabidopsis thaliana

Seq. No.	283617
Contig ID	140083_1.R1011
5'-most EST	uC-zmflmo17333f05b1

Seq. No.	283618
Contig ID	140090_1.R1011
5'-most EST	uC-zmflmo17333f12b1
Method	BLASTX
NCBI GI	g3341899
BLAST score	167
E value	1.0e-11
Match length	74
% identity	47
NCBI Description	(AB009285) BCNT [Homo sapiens]

Seq. No.	283619
Contig ID	140095_1.R1011
5'-most EST	ntr700072390.h1
Method	BLASTX
NCBI GI	g2894445
BLAST score	228
E value	1.0e-18
Match length	124
% identity	48
NCBI Description	(Y14333) transketolase [Arabidopsis thaliana]

Seq. No.	283620
Contig ID	140098_1.R1011
5'-most EST	uC-zmflmo17333g09b1

Seq. No.	283621
Contig ID	140107_1.R1011
5'-most EST	uC-zmflmo17333h06a1

Seq. No.	283622
Contig ID	140129_1.R1011
5'-most EST	ceu700433649.h1

Seq. No.	283623
Contig ID	140141_1.R1011
5'-most EST	uC-zmflmo17334c11b1

Seq. No.	283624
Contig ID	140154_1.R1011
5'-most EST	ymt700221618.h1
Method	BLASTX
NCBI GI	g4309758
BLAST score	243
E value	3.0e-20
Match length	64
% identity	72
NCBI Description	(AC006217) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283625
Contig ID	140174_1.R1011
5'-most EST	tfd700572111.h1

Seq. No.	283626
Contig ID	140197_1.R1011
5'-most EST	uC-zmflmo17335b05b1

Seq. No.	283627
Contig ID	140218_1.R1011
5'-most EST	uC-zmflmo17335d04b1
Method	BLASTN
NCBI GI	g517492
BLAST score	70
E value	8.0e-31
Match length	122
% identity	89
NCBI Description	Z.Mays Zm38 gene, intron

Seq. No.	283628
Contig ID	140266_1.R1011
5'-most EST	uC-zmflmo17335h09b1
Method	BLASTX
NCBI GI	g4262222
BLAST score	385
E value	3.0e-37
Match length	119
% identity	61
NCBI Description	(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]

Seq. No.	283629
Contig ID	140269_1.R1011
5'-most EST	uC-zmflmo17336a02b1
Seq. No.	283630
Contig ID	140285_1.R1011
5'-most EST	uC-zmflmo17336b10b1
Seq. No.	283631
Contig ID	140299_1.R1011
5'-most EST	uC-zmflmo17336d01b1
Method	BLASTX
NCBI GI	g1352245
BLAST score	243
E value	8.0e-29
Match length	118
% identity	58
NCBI Description	FATTY ALDEHYDE DEHYDROGENASE (ALDEHYDE DEHYDROGENASE, MICROSOMAL) (CLASS 3) >gi_687254 (U14390) aldehyde deydrogenase [Mus musculus]
Seq. No.	283632
Contig ID	140302_1.R1011
5'-most EST	fwa700099305.h1
Seq. No.	283633
Contig ID	140314_1.R1011
5'-most EST	uC-zmflmo17336e09b1
Method	BLASTX
NCBI GI	g3540207
BLAST score	163
E value	5.0e-11
Match length	96
% identity	47
NCBI Description	(AC004260) Putative protein kinase [Arabidopsis thaliana]
Seq. No.	283634
Contig ID	140351_1.R1011
5'-most EST	wty700165213.h1
Seq. No.	283635
Contig ID	140351_2.R1011
5'-most EST	fdz701167012.h1
Seq. No.	283636
Contig ID	140378_1.R1011
5'-most EST	mwy700443296.h2
Seq. No.	283637
Contig ID	140382_1.R1011
5'-most EST	uC-zmflmo17339c11b1
Method	BLASTX
NCBI GI	g4469020
BLAST score	395
E value	4.0e-38
Match length	93

% identity	81
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	283638
Contig ID	140389_1.R1011
5'-most EST	yyf700351734.h1
Method	BLASTX
NCBI GI	g4646217
BLAST score	203
E value	3.0e-24
Match length	110
% identity	63
NCBI Description	(AC007290) putative phosphoprotein phosphatase [Arabidopsis thaliana]

Seq. No.	283639
Contig ID	140396_1.R1011
5'-most EST	uC-zmflmo17339e01b1
Method	BLASTX
NCBI GI	g2827549
BLAST score	769
E value	4.0e-82
Match length	172
% identity	87
NCBI Description	(AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]

Seq. No.	283640
Contig ID	140419_1.R1011
5'-most EST	xyt700343644.h1
Method	BLASTX
NCBI GI	g3924596
BLAST score	901
E value	3.0e-97
Match length	340
% identity	56
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	283641
Contig ID	140430_1.R1011
5'-most EST	gct701172533.h1

Seq. No.	283642
Contig ID	140455_1.R1011
5'-most EST	cyk700049064.f1

Seq. No.	283643
Contig ID	140469_1.R1011
5'-most EST	uC-zmflmo17340d01b1

Seq. No.	283644
Contig ID	140474_1.R1011
5'-most EST	uC-zmflmo17340d08b1
Method	BLASTX
NCBI GI	g4538947

BLAST score	472
E value	5.0e-47
Match length	159
% identity	30
NCBI Description	(AL049483) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	283645
Contig ID	140475_1.R1011
5'-most EST	uC-zmflmo17340d09b1

Seq. No.	283646
Contig ID	140481_1.R1011
5'-most EST	uC-zmflmo17340e03b1
Method	BLASTX
NCBI GI	g3123231
BLAST score	151
E value	1.0e-09
Match length	61
% identity	48
NCBI Description	GENERAL STRESS PROTEIN 13 (GSP13) >gi_1934792_emb_CAB07921_ (Z93934) unknown [Bacillus subtilis] >gi_2635635_emb_CAB15128_ (Z99120) similar to polyribonucleotide nucleotidyltransferase [Bacillus subtilis]

Seq. No.	283647
Contig ID	140488_1.R1011
5'-most EST	uC-zmflmo17340e11b1

Seq. No.	283648
Contig ID	140547_1.R1011
5'-most EST	lhp700053490.r1

Seq. No.	283649
Contig ID	140554_1.R1011
5'-most EST	uwc700152172.h1

Seq. No.	283650
Contig ID	140567_1.R1011
5'-most EST	xmt700265938.h1
Method	BLASTX
NCBI GI	g3047104
BLAST score	168
E value	1.0e-11
Match length	74
% identity	50
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	283651
Contig ID	140596_1.R1011
5'-most EST	uC-zmflmo17341g08b1
Method	BLASTX
NCBI GI	g4508083
BLAST score	280
E value	1.0e-24
Match length	191

% identity	21
NCBI Description	(AC005882) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	283652
Contig ID	140602_1.R1011
5'-most EST	dyk700102139.h1
Method	BLASTX
NCBI GI	g4558568
BLAST score	269
E value	2.0e-26
Match length	136
% identity	49
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283653
Contig ID	140673_1.R1011
5'-most EST	nbm700469710.h1
Method	BLASTX
NCBI GI	g1800215
BLAST score	913
E value	1.0e-131
Match length	250
% identity	96
NCBI Description	(U56729) phytochrome A [Sorghum bicolor]

Seq. No.	283654
Contig ID	140683_1.R1011
5'-most EST	uC-zmflmo17342g05b1
Method	BLASTX
NCBI GI	g2292907
BLAST score	591
E value	3.0e-61
Match length	122
% identity	93
NCBI Description	(Y10099) P-glycoprotein homologue [Hordeum vulgare]

Seq. No.	283655
Contig ID	140685_1.R1011
5'-most EST	uC-zmflmo17342g07b1
Method	BLASTX
NCBI GI	g4432857
BLAST score	162
E value	1.0e-10
Match length	108
% identity	40
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283656
Contig ID	140692_1.R1011
5'-most EST	uC-zmflmo17342h06b1

Seq. No.	283657
Contig ID	140734_1.R1011
5'-most EST	uC-zmflmo17344d06b1
Method	BLASTX
NCBI GI	g3075392
BLAST score	257

E value	3.0e-22
Match length	100
% identity	52
NCBI Description	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]

Seq. No.	283658
Contig ID	140746_1.R1011
5'-most EST	clt700045142.f1
Method	BLASTX
NCBI GI	g3953458
BLAST score	294
E value	2.0e-26
Match length	90
% identity	64
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	283659
Contig ID	140756_1.R1011
5'-most EST	uC-zmflmo17344f09b1

Seq. No.	283660
Contig ID	140810_1.R1011
5'-most EST	uC-zmflmo17d02b1

Seq. No.	283661
Contig ID	140826_1.R1011
5'-most EST	uC-zmflmo17e07b1
Method	BLASTX
NCBI GI	g3779024
BLAST score	673
E value	5.0e-71
Match length	141
% identity	94
NCBI Description	(AC005171) unknown protein [Arabidopsis thaliana]

Seq. No.	283662
Contig ID	140885_1.R1011
5'-most EST	dyk700105544.h1

Seq. No.	283663
Contig ID	140886_1.R1011
5'-most EST	bdu700382092.h1

Seq. No.	283664
Contig ID	140910_1.R1011
5'-most EST	dyk700106320.h1
Method	BLASTN
NCBI GI	g3821780
BLAST score	34
E value	3.0e-09
Match length	34
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	283665
Contig ID	140910_2.R1011

5'-most EST	uC-zmroteosinte001e01b1
Seq. No.	283666
Contig ID	140913_1.R1011
5'-most EST	uC-zmroteosinte001e04b1
Method	BLASTX
NCBI GI	g1854378
BLAST score	1387
E value	1.0e-154
Match length	278
% identity	96
NCBI Description	(AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]
Seq. No.	283667
Contig ID	140916_1.R1011
5'-most EST	uC-zmroteosinte001e07b1
Seq. No.	283668
Contig ID	140936_1.R1011
5'-most EST	uC-zmroteosinte001g04b1
Seq. No.	283669
Contig ID	140993_1.R1011
5'-most EST	uC-zmroteosinte002d03b1
Method	BLASTX
NCBI GI	g1717870
BLAST score	236
E value	2.0e-19
Match length	269
% identity	30
NCBI Description	PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C8A4.01C (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)
Seq. No.	283670
Contig ID	140994_1.R1011
5'-most EST	uC-zmroteosinte002d04b1
Method	BLASTX
NCBI GI	g3157910
BLAST score	522
E value	3.0e-53
Match length	149
% identity	78
NCBI Description	(AF003551) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Zea mays]
Seq. No.	283671
Contig ID	141008_1.R1011
5'-most EST	uC-zmroteosinte002e07b1
Seq. No.	283672
Contig ID	141036_1.R1011
5'-most EST	uC-zmflmo17371g07a1
Seq. No.	283673
Contig ID	141037_1.R1011

5'-most EST	uC-zmroteosinte025g05b1
Method	BLASTX
NCBI GI	g4240539
BLAST score	911
E value	1.0e-105
Match length	194
% identity	95
NCBI Description	(AF100455) knotted class 1 homeodomain protein liguleless3 [Zea mays]

Seq. No.	283674
Contig ID	141058_1.R1011
5'-most EST	tzu700204077.h1
Method	BLASTX
NCBI GI	g4249382
BLAST score	987
E value	1.0e-107
Match length	244
% identity	74
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	283675
Contig ID	141092_1.R1011
5'-most EST	wty700170780.h1

Seq. No.	283676
Contig ID	141095_1.R1011
5'-most EST	uC-zmroteosinte003e04b1

Seq. No.	283677
Contig ID	141107_1.R1011
5'-most EST	ntr700074248.h1
Method	BLASTX
NCBI GI	g1619602
BLAST score	233
E value	5.0e-35
Match length	214
% identity	37
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	283678
Contig ID	141114_1.R1011
5'-most EST	uC-zmroteosinte003g01b1
Method	BLASTX
NCBI GI	g98837
BLAST score	154
E value	4.0e-10
Match length	112
% identity	34
NCBI Description	enantiomer-selective amidase - Rhodococcus sp >gi_152052 (M74531) enantiomerase-selective amidase [Rhodococcus sp.]

Seq. No.	283679
Contig ID	141165_1.R1011
5'-most EST	uC-zmroteosinte004c06b1

Seq. No.	283680
Contig ID	141209_1.R1011
5'-most EST	uC-zmroteosinte004g02b1

Seq. No.	283681
Contig ID	141222_1.R1011
5'-most EST	tzu700201171.h1
Method	BLASTX
NCBI GI	g3309575
BLAST score	347
E value	2.0e-53
Match length	183
% identity	60
NCBI Description	(AF060553) calcium sensor homolog [Arabidopsis thaliana] >gi_4538989_emb_CAB39731.1_ (Y18870) CBL4 protein [Arabidopsis thaliana]

Seq. No.	283682
Contig ID	141249_1.R1011
5'-most EST	xsy700208328.h1
Method	BLASTX
NCBI GI	g3335359
BLAST score	505
E value	4.0e-51
Match length	139
% identity	65
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	283683
Contig ID	141267_1.R1011
5'-most EST	wyr700235934.h1

Seq. No.	283684
Contig ID	141288_1.R1011
5'-most EST	xmt700266118.h1
Method	BLASTX
NCBI GI	g4503617
BLAST score	196
E value	7.0e-15
Match length	125
% identity	42
NCBI Description	exostoses (multiple)-like 3 >gi_2723391_dbj_BAA24080_ (AB007042) EXTR1 [Homo sapiens] >gi_2897905_(AF001690) EXT like protein 3 [Homo sapiens] >gi_3043562_dbj_BAA25445_ (AB011091) KIAA0519 protein [Homo sapiens] >gi_4103884_ (AF029231) EXT homolog [Homo sapiens]

Seq. No.	283685
Contig ID	141297_1.R1011
5'-most EST	hvj700621633.h1
Method	BLASTX
NCBI GI	g3885327
BLAST score	694
E value	6.0e-73
Match length	174
% identity	70

NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283686
Contig ID	141313_1.R1011
5'-most EST	nbm700476240.h1
Method	BLASTX
NCBI GI	g2950395
BLAST score	1089
E value	1.0e-119
Match length	228
% identity	93
NCBI Description	(AJ224847) oxidoreductase [Zea mays]

Seq. No.	283687
Contig ID	141313_2.R1011
5'-most EST	hbs701184374.h1
Method	BLASTN
NCBI GI	g2950394
BLAST score	74
E value	3.0e-33
Match length	152
% identity	98
NCBI Description	Zea mays me gene, exons 1 to

Seq. No.	283688
Contig ID	141372_1.R1011
5'-most EST	uC-zmroteosinte006e07b1

Seq. No.	283689
Contig ID	141383_1.R1011
5'-most EST	uC-zmroteosinte061c10b2
Method	BLASTX
NCBI GI	g2213907
BLAST score	150
E value	1.0e-14
Match length	143
% identity	38
NCBI Description	(AF004837) putative vacuolar protein sorting homolog [Aspergillus fumigatus]

Seq. No.	283690
Contig ID	141398_1.R1011
5'-most EST	wen700334983.h1
Method	BLASTX
NCBI GI	g4115377
BLAST score	242
E value	9.0e-21
Match length	91
% identity	48
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	283691
Contig ID	141403_1.R1011
5'-most EST	nbm700466985.h1

Seq. No.	283692
Contig ID	141433_1.R1011

5'-most EST	uC-zmroteosinte007c08b1
Seq. No.	283693
Contig ID	141450_1.R1011
5'-most EST	wty700171417.h1
Method	BLASTX
NCBI GI	g548702
BLAST score	379
E value	2.0e-36
Match length	111
% identity	56
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9) (RPB14.5) >gi_543001_pir__S41621 DNA-directed RNA polymerase (EC 2.7.7.6) II 14.5K chain - human >gi_397150_emb_CAA80649_ (Z23102) RNA Polymerase II subunit 14.5 kD [Homo sapiens] >gi_1905901 (AD001527) HUMAN DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo sapiens]
Seq. No.	283694
Contig ID	141453_1.R1011
5'-most EST	uC-zmroteosinte026a03b1
Seq. No.	283695
Contig ID	141503_1.R1011
5'-most EST	nbm700475048.h1
Method	BLASTX
NCBI GI	g3176671
BLAST score	474
E value	2.0e-47
Match length	176
% identity	52
NCBI Description	(AC004393) Contains similarity to hypothetical gene B0495.7 gb_687822 from C. elegans cosmid gb_U21317. [Arabidopsis thaliana]
Seq. No.	283696
Contig ID	141508_2.R1011
5'-most EST	uC-zmroteosinte083d03b1
Seq. No.	283697
Contig ID	141510_1.R1011
5'-most EST	uC-zmroteosinte008b11b1
Seq. No.	283698
Contig ID	141513_1.R1011
5'-most EST	uC-zmroteosinte008c02b1
Method	BLASTX
NCBI GI	g4406801
BLAST score	254
E value	1.0e-21
Match length	91
% identity	55
NCBI Description	(AC006304) unknown protein [Arabidopsis thaliana]
Seq. No.	283699
Contig ID	141561_1.R1011

5'-most EST	uC-zmroteosinte008g02b1
Seq. No.	283700
Contig ID	141563_1.R1011
5'-most EST	gct701173771.h1
Seq. No.	283701
Contig ID	141583_1.R1011
5'-most EST	nbm700476462.h1
Seq. No.	283702
Contig ID	141591_1.R1011
5'-most EST	wyr700236753.h1
Method	BLASTX
NCBI GI	g627584
BLAST score	255
E value	9.0e-22
Match length	124
% identity	46
NCBI Description	protein p84 - human >gi_550058 (L36529) protein p84 [Homo sapiens]
Seq. No.	283703
Contig ID	141597_1.R1011
5'-most EST	nwy700447531.h1
Seq. No.	283704
Contig ID	141607_1.R1011
5'-most EST	ymt700223339.h1
Seq. No.	283705
Contig ID	141626_1.R1011
5'-most EST	uC-zmroteosinte009e01b1
Seq. No.	283706
Contig ID	141626_2.R1011
5'-most EST	jfc700968538.h1
Seq. No.	283707
Contig ID	141647_1.R1011
5'-most EST	uC-zmroteosinte106h04b2
Seq. No.	283708
Contig ID	141670_1.R1011
5'-most EST	uC-zmroteosinte009h11b1
Method	BLASTX
NCBI GI	g4558672
BLAST score	349
E value	8.0e-33
Match length	170
% identity	39
NCBI Description	(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis thaliana]
Seq. No.	283709
Contig ID	141672_1.R1011
5'-most EST	wyr700237767.h1

Method	BLASTX
NCBI GI	g2245015
BLAST score	412
E value	4.0e-40
Match length	170
% identity	46
NCBI Description	(Z97341) unnamed protein product [Arabidopsis thaliana]

Seq. No.	283710
Contig ID	141679_1.R1011
5'-most EST	wyr700236277.h1
Method	BLASTX
NCBI GI	g2982272
BLAST score	492
E value	2.0e-49
Match length	173
% identity	54
NCBI Description	(AF051220) hypothetical protein [Picea mariana]

Seq. No.	283711
Contig ID	141680_2.R1011
5'-most EST	uC-zmflmo17336e02a1

Seq. No.	283712
Contig ID	141711_1.R1011
5'-most EST	dyk700106765.h1
Method	BLASTX
NCBI GI	g418548
BLAST score	377
E value	6.0e-36
Match length	139
% identity	53
NCBI Description	HYPOTHETICAL 15.7 KD PROTEIN IN APHA-UVRA INTERGENIC REGION (O138) >gi_396391 (U00006) No definition line found [Escherichia coli] >gi_1790491 (AE000479) orf, hypothetical protein [Escherichia coli]

Seq. No.	283713
Contig ID	141729_1.R1011
5'-most EST	xyt700344384.h1
Method	BLASTX
NCBI GI	g4160280
BLAST score	1630
E value	0.0e+00
Match length	344
% identity	83
NCBI Description	(AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No.	283714
Contig ID	141746_1.R1011
5'-most EST	xsy700212289.h1
Method	BLASTX
NCBI GI	g1652591
BLAST score	225
E value	4.0e-18
Match length	158
% identity	34

NCBI Description	(D90906) chloroplast import-associated channel IAP75 [Synechocystis sp.]
Seq. No.	283715
Contig ID	141757_1.R1011
5'-most EST	xyt700345653.h1
Seq. No.	283716
Contig ID	141782_1.R1011
5'-most EST	uC-zmroteosinte011b05b1
Seq. No.	283717
Contig ID	141823_1.R1011
5'-most EST	uC-zmflmo17393h04a1
Seq. No.	283718
Contig ID	141853_1.R1011
5'-most EST	ymt700221125.h1
Seq. No.	283719
Contig ID	141941_1.R1011
5'-most EST	uC-zmroteosinte012h01b1
Seq. No.	283720
Contig ID	141966_1.R1011
5'-most EST	uC-zmroteosinte013b03b1
Seq. No.	283721
Contig ID	141972_1.R1011
5'-most EST	nbm700473239.h1
Seq. No.	283722
Contig ID	141979_1.R1011
5'-most EST	uC-zmroteosinte013c04b1
Seq. No.	283723
Contig ID	142006_1.R1011
5'-most EST	uC-zmroteosinte013e07b1
Seq. No.	283724
Contig ID	142017_1.R1011
5'-most EST	uC-zmroteosinte013f06b1
Method	BLASTX
NCBI GI	g4406759
BLAST score	321
E value	1.0e-29
Match length	149
% identity	51
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]
Seq. No.	283725
Contig ID	142039_1.R1011
5'-most EST	rvl700454466.h1
Method	BLASTX
NCBI GI	g3641252
BLAST score	360
E value	5.0e-34

Match length	210
% identity	40
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	283726
Contig ID	142041_1.R1011
5'-most EST	dyk700105880.h1
Method	BLASTX
NCBI GI	g2961356
BLAST score	480
E value	6.0e-48
Match length	198
% identity	52
NCBI Description	(AL022140) alcohol dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	283727
Contig ID	142049_1.R1011
5'-most EST	lhp700053347.r1
Method	BLASTX
NCBI GI	g559713
BLAST score	254
E value	9.0e-22
Match length	129
% identity	36
NCBI Description	(D38552) The ha1539 protein is related to cyclophilin. [Homo sapiens]

Seq. No.	283728
Contig ID	142056_1.R1011
5'-most EST	uC-zmroteosinte014a11b1
Method	BLASTX
NCBI GI	g4587563
BLAST score	717
E value	7.0e-76
Match length	184
% identity	73
NCBI Description	(AC006550) Similar to gb_U51990 pre-mRNA-splicing factor hPrp18 from Homo sapiens. ESTs gb_T46391 and gb_AA721815 come from this gene. [Arabidopsis thaliana]

Seq. No.	283729
Contig ID	142079_1.R1011
5'-most EST	wyr700238096.h1

Seq. No.	283730
Contig ID	142090_1.R1011
5'-most EST	wty700165220.h1

Seq. No.	283731
Contig ID	142091_1.R1011
5'-most EST	uC-zmroteosinte014d11b1

Seq. No.	283732
Contig ID	142107_1.R1011
5'-most EST	xmt700267732.h1

Method	BLASTX
NCBI GI	g3080414
BLAST score	914
E value	7.0e-99
Match length	244
% identity	76
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	283733
Contig ID	142110_1.R1011
5'-most EST	cjh700194035.h1
Method	BLASTX
NCBI GI	g2462838
BLAST score	731
E value	2.0e-77
Match length	227
% identity	67
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	283734
Contig ID	142112_1.R1011
5'-most EST	uC-zmroteosinte014f08b1

Seq. No.	283735
Contig ID	142114_1.R1011
5'-most EST	uC-zmroteosinte014f10b1
Method	BLASTX
NCBI GI	g4263820
BLAST score	604
E value	9.0e-63
Match length	160
% identity	66
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283736
Contig ID	142123_1.R1011
5'-most EST	rvt700553211.h1

Seq. No.	283737
Contig ID	142135_1.R1011
5'-most EST	ntr700072531.h1

Seq. No.	283738
Contig ID	142154_1.R1011
5'-most EST	wyr700238641.h1

Seq. No.	283739
Contig ID	142161_1.R1011
5'-most EST	mwy700442858.h1
Method	BLASTX
NCBI GI	g3928519
BLAST score	664
E value	1.0e-69
Match length	209
% identity	65
NCBI Description	(AB011670) wpk4 protein kinase [Triticum aestivum]

Seq. No.	283740
Contig ID	142181_1.R1011
5'-most EST	wuj700282144.h1

Seq. No.	283741
Contig ID	142181_2.R1011
5'-most EST	ymt700219371.h1

Seq. No.	283742
Contig ID	142191_1.R1011
5'-most EST	rvl700456612.h1

Seq. No.	283743
Contig ID	142202_1.R1011
5'-most EST	uC-zmroteosinte015f05b1
Method	BLASTX
NCBI GI	g2827663
BLAST score	341
E value	1.0e-31
Match length	245
% identity	6
NCBI Description	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]

Seq. No.	283744
Contig ID	142315_1.R1011
5'-most EST	uC-zmroteosinte016h03b1
Method	BLASTX
NCBI GI	g4206196
BLAST score	270
E value	1.0e-23
Match length	126
% identity	48
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283745
Contig ID	142320_1.R1011
5'-most EST	uC-zmroteosinte016h08b1
Method	BLASTX
NCBI GI	g2262105
BLAST score	496
E value	6.0e-50
Match length	139
% identity	67
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	283746
Contig ID	142334_2.R1011
5'-most EST	uC-zmroteosinte100f01b2
Method	BLASTX
NCBI GI	g1703143
BLAST score	278
E value	2.0e-40
Match length	112
% identity	70
NCBI Description	ACTIN-LIKE PROTEIN 3 >gi_881635 (U29610) Arp3 [Acanthamoeba castellanii]

Seq. No.	283747
Contig ID	142365_1.R1011
5'-most EST	zuv700353759.h1

Seq. No.	283748
Contig ID	142367_1.R1011
5'-most EST	uC-zmroteosinte017d11b1
Method	BLASTX
NCBI GI	g2920587
BLAST score	218
E value	2.0e-17
Match length	103
% identity	46
NCBI Description	(AF038362) TBP-associated factor 172 [Homo sapiens] >gi_2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo sapiens]

Seq. No.	283749
Contig ID	142384_1.R1011
5'-most EST	uC-zmroteosinte024e06b1

Seq. No.	283750
Contig ID	142387_1.R1011
5'-most EST	wen700333768.h1

Seq. No.	283751
Contig ID	142444_1.R1011
5'-most EST	xyt700344140.h1

Seq. No.	283752
Contig ID	142444_3.R1011
5'-most EST	nwy700445787.h1

Seq. No.	283753
Contig ID	142458_1.R1011
5'-most EST	uC-zmroteosinte119g04b2
Method	BLASTX
NCBI GI	g2444174
BLAST score	653
E value	6.0e-81
Match length	230
% identity	68
NCBI Description	(U94781) unconventional myosin [Helianthus annuus]

Seq. No.	283754
Contig ID	142481_1.R1011
5'-most EST	ymt700222046.h1
Method	BLASTX
NCBI GI	g4322107
BLAST score	383
E value	8.0e-37
Match length	161
% identity	49
NCBI Description	(AF072717) pEg7 [Xenopus laevis]

Seq. No.	283755

Contig ID	142490_1.R1011
5'-most EST	uC-zmroteosinte018g04b1

Seq. No.	283756
Contig ID	142492_1.R1011
5'-most EST	hbs701182008.h1
Method	BLASTX
NCBI GI	g2245135
BLAST score	530
E value	6.0e-54
Match length	174
% identity	57
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283757
Contig ID	142500_1.R1011
5'-most EST	uC-zmflb73255e09b1
Method	BLASTX
NCBI GI	g3128228
BLAST score	262
E value	7.0e-27
Match length	130
% identity	62
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	283758
Contig ID	142500_2.R1011
5'-most EST	wty700162795.h1
Method	BLASTX
NCBI GI	g3128228
BLAST score	286
E value	9.0e-32
Match length	169
% identity	35
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	283759
Contig ID	142500_3.R1011
5'-most EST	zuv700356896.h1

Seq. No.	283760
Contig ID	142594_1.R1011
5'-most EST	uC-zmroteosinte019h06b1
Method	BLASTX
NCBI GI	g2880049
BLAST score	162
E value	4.0e-11
Match length	47
% identity	66
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283761
Contig ID	142597_1.R1011

5'-most EST	cat700018281.r1
Seq. No.	283762
Contig ID	142613_1.R1011
5'-most EST	uC-zmroteosinte020b02b1
Method	BLASTX
NCBI GI	g2832686
BLAST score	510
E value	1.0e-51
Match length	163
% identity	63
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]
Seq. No.	283763
Contig ID	142620_1.R1011
5'-most EST	cyk700052228.f1
Seq. No.	283764
Contig ID	142621_1.R1011
5'-most EST	xsy700214692.h1
Method	BLASTX
NCBI GI	g1171747
BLAST score	232
E value	4.0e-19
Match length	121
% identity	42
NCBI Description	PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120) >gi_482505_pir__A48168 proliferating-cell nucleolar antigen P120 - human >gi_287723_emb_CAA39119_ (X55504) P120 antigen [Homo sapiens]
Seq. No.	283765
Contig ID	142629_1.R1011
5'-most EST	pmx700084639.h1
Seq. No.	283766
Contig ID	142652_1.R1011
5'-most EST	uC-zmroteosinte020e06b1
Seq. No.	283767
Contig ID	142688_1.R1011
5'-most EST	xmt700266360.h1
Method	BLASTX
NCBI GI	g4558550
BLAST score	402
E value	3.0e-39
Match length	115
% identity	67
NCBI Description	(AC007138) putative protein transport factor [Arabidopsis thaliana]
Seq. No.	283768
Contig ID	142692_1.R1011
5'-most EST	uC-zmroteosinte020h10b1
Method	BLASTX
NCBI GI	g3881461

BLAST score	156
E value	3.0e-10
Match length	49
% identity	57
NCBI Description	(Z68753) predicted using Genefinder; Similarity to Glucose-repressible alcoihol dehydrogenase transcriptional effector (SW:CCR4_YEAST); cDNA EST EMBL:T01851 comes from this gene; cDNA EST yk240e8.5 comes from this gene; cDNA ES

Seq. No.	283769
Contig ID	142723_1.R1011
5'-most EST	uC-zmroteosinte021c06b1
Method	BLASTX
NCBI GI	g481815
BLAST score	150
E value	2.0e-09
Match length	131
% identity	32
NCBI Description	vegetative storage protein - western balsam poplar x cottonwood >gi_309839 (L20233) vegetative storage protein [Populus trichocarpa x Populus deltoides]

Seq. No.	283770
Contig ID	142763_1.R1011
5'-most EST	uC-zmroteosinte021f10b1
Method	BLASTX
NCBI GI	g2190540
BLAST score	478
E value	6.0e-48
Match length	156
% identity	58
NCBI Description	(AC001229) Similar to Arabidopsis TFL1 (gb_U77674). [Arabidopsis thaliana]

Seq. No.	283771
Contig ID	142772_1.R1011
5'-most EST	wty700167073.h1
Method	BLASTX
NCBI GI	g3860842
BLAST score	211
E value	2.0e-16
Match length	89
% identity	47
NCBI Description	(AJ235271) PROTEASE II (ptrB) [Rickettsia prowazekii]

Seq. No.	283772
Contig ID	142780_1.R1011
5'-most EST	uC-zmroteosinte021h05b1
Method	BLASTX
NCBI GI	g2829892
BLAST score	266
E value	3.0e-23
Match length	114
% identity	47
NCBI Description	(AC002311) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 283773

Contig ID	142781_1.R1011
5'-most EST	yne700379032.h1
Method	BLASTX
NCBI GI	g1330343
BLAST score	148
E value	1.0e-09
Match length	51
% identity	53
NCBI Description	(U58755) C34D4.12 gene product [Caenorhabditis elegans]

Seq. No.	283774
Contig ID	142784_1.R1011
5'-most EST	uC-zmroteosinte021h09b1
Method	BLASTX
NCBI GI	g3702321
BLAST score	601
E value	9.0e-68
Match length	170
% identity	76
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No.	283775
Contig ID	142795_1.R1011
5'-most EST	uC-zmroteosinte022a08b1
Method	BLASTX
NCBI GI	g3068705
BLAST score	264
E value	7.0e-23
Match length	165
% identity	36
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	283776
Contig ID	142841_1.R1011
5'-most EST	uC-zmroteosinte022e09b1
Method	BLASTX
NCBI GI	g1709920
BLAST score	309
E value	4.0e-28
Match length	146
% identity	68
NCBI Description	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE PRECURSOR (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) >gi_1019915_emb_CAA52778_ (X74766) glycinamide ribonucleotide synthetase [Arabidopsis thaliana]

Seq. No.	283777
Contig ID	142877_1.R1011
5'-most EST	uC-zmroteosinte023a02b2
Method	BLASTX
NCBI GI	g629688
BLAST score	765
E value	2.0e-81
Match length	226
% identity	63

NCBI Description	dehydroquinase shikimate dehydrogenase - Common tobacco >gi_535771 (L32794) dehydroquinate dehydratase/shikimate dehydrogenase [Nicotiana tabacum]
Seq. No.	283778
Contig ID	142878_1.R1011
5'-most EST	uC-zmroteosinte023a03b2
Seq. No.	283779
Contig ID	142880_1.R1011
5'-most EST	uC-zmroteosinte023a05b2
Method	BLASTX
NCBI GI	g3309086
BLAST score	989
E value	1.0e-107
Match length	225
% identity	86
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]
Seq. No.	283780
Contig ID	142883_2.R1011
5'-most EST	pmx700084260.h1
Method	BLASTX
NCBI GI	g4220537
BLAST score	233
E value	1.0e-19
Match length	76
% identity	55
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
Seq. No.	283781
Contig ID	142891_1.R1011
5'-most EST	uC-zmroteosinte023b05b2
Method	BLASTX
NCBI GI	g1730621
BLAST score	597
E value	1.0e-61
Match length	292
% identity	45
NCBI Description	HYPOTHETICAL 48.1 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION >gi_630106_pir__S48817 hypothetical protein YML079w - yeast (Saccharomyces cerevisiae) >gi_587531_emb_CAA86498_ (Z46373) orf, len: 423, CAI: 0.18, 27.4% identity in 307 aa overlap with S36201 S36201 hypothetical protein 1 - Rhizobium leguminosarum [Saccharomyces cerevisiae]
Seq. No.	283782
Contig ID	142892_1.R1011
5'-most EST	uC-zmflmo17130e05a1
Seq. No.	283783
Contig ID	142941_1.R1011
5'-most EST	wyr700241738.h1
Method	BLASTX
NCBI GI	g3482914
BLAST score	546

E value	1.0e-62
Match length	263
% identity	50
NCBI Description	(AC003970) Similar to nodulins and lipase [Arabidopsis thaliana]

Seq. No.	283784
Contig ID	142943_1.R1011
5'-most EST	uC-zmroteosinte023f10b2
Method	BLASTX
NCBI GI	g2558938
BLAST score	436
E value	6.0e-43
Match length	204
% identity	47
NCBI Description	(AF024625) arm repeat containing protein [Brassica napus]

Seq. No.	283785
Contig ID	142960_1.R1011
5'-most EST	uC-zmroteosinte023h04b2

Seq. No.	283786
Contig ID	142994_1.R1011
5'-most EST	uC-zmroteosinte024c02b1
Method	BLASTN
NCBI GI	g2924733
BLAST score	42
E value	4.0e-14
Match length	134
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	283787
Contig ID	143009_1.R1011
5'-most EST	uC-zmroteosinte024d06b1
Method	BLASTX
NCBI GI	g4262167
BLAST score	327
E value	3.0e-30
Match length	141
% identity	51
NCBI Description	(AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No.	283788
Contig ID	143014_1.R1011
5'-most EST	uC-zmroteosinte085d08b1
Method	BLASTX
NCBI GI	g2642648
BLAST score	689
E value	2.0e-72
Match length	192
% identity	72
NCBI Description	(AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)

cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	283789
Contig ID	143019_1.R1011
5'-most EST	uC-zmroteosinte024e05b1

Seq. No.	283790
Contig ID	143025_1.R1011
5'-most EST	uC-zmroteosinte024e11b1
Method	BLASTX
NCBI GI	g466170
BLAST score	859
E value	2.0e-92
Match length	176
% identity	97
NCBI Description	GTP-BINDING PROTEIN YPTM1 >gi_283055_pir__A38202 ypt family - maize >gi_287833_emb_CAA44918_ (X63277) yptm1 [Zea mays]

Seq. No.	283791
Contig ID	143043_1.R1011
5'-most EST	uC-zmroteosinte024g06b1
Method	BLASTX
NCBI GI	g2335100
BLAST score	1163
E value	1.0e-128
Match length	284
% identity	74
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	283792
Contig ID	143050_1.R1011
5'-most EST	uC-zmroteosinte024h01b1
Method	BLASTX
NCBI GI	g1402878
BLAST score	353
E value	3.0e-33
Match length	159
% identity	45
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	283793
Contig ID	143062_1.R1011
5'-most EST	uC-zmroteosinte082c05b1
Method	BLASTX
NCBI GI	g2832643
BLAST score	303
E value	2.0e-27
Match length	137
% identity	52
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283794
Contig ID	143067_1.R1011
5'-most EST	uC-zmroteosinte025a06b1

Seq. No.	283795
Contig ID	143076_2.R1011

5'-most EST	rvt700550061.h1
Seq. No.	283796
Contig ID	143081_1.R1011
5'-most EST	uC-zmroteosinte025b08b1
Method	BLASTX
NCBI GI	g2252829
BLAST score	144
E value	6.0e-09
Match length	96
% identity	34
NCBI Description	(AF013293) A_IG005I10.6 gene product [Arabidopsis thaliana]
Seq. No.	283797
Contig ID	143175_1.R1011
5'-most EST	qmh700027514.f1
Method	BLASTX
NCBI GI	g1161167
BLAST score	321
E value	3.0e-29
Match length	266
% identity	30
NCBI Description	(L42466) ethylene-forming enzyme [Picea glauca]
Seq. No.	283798
Contig ID	143201_1.R1011
5'-most EST	zuv700353058.h1
Seq. No.	283799
Contig ID	143203_1.R1011
5'-most EST	uC-zmroteosinte026e04b1
Seq. No.	283800
Contig ID	143203_2.R1011
5'-most EST	wty700166350.h1
Seq. No.	283801
Contig ID	143207_1.R1011
5'-most EST	uC-zmroteosinte026e09b1
Method	BLASTX
NCBI GI	g421929
BLAST score	515
E value	1.0e-94
Match length	184
% identity	14
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]
Seq. No.	283802
Contig ID	143214_2.R1011
5'-most EST	uer700579631.h1
Seq. No.	283803
Contig ID	143218_1.R1011
5'-most EST	uC-zmroteosinte026f10b1
Seq. No.	283804

Contig ID	143225_1.R1011
5'-most EST	uC-zmroteosinte026g05b1
Method	BLASTX
NCBI GI	g2558654
BLAST score	472
E value	3.0e-47
Match length	186
% identity	55
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	283805
Contig ID	143239_1.R1011
5'-most EST	uC-zmroteosinte026h10b1
Method	BLASTX
NCBI GI	g2558664
BLAST score	344
E value	4.0e-32
Match length	212
% identity	44
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283806
Contig ID	143245_1.R1011
5'-most EST	dyk700105062.h1
Method	BLASTX
NCBI GI	g422028
BLAST score	929
E value	1.0e-100
Match length	214
% identity	87
NCBI Description	transcription factor OBF3.1, ocs element-binding - maize >gi_297020_emb_CAA48905_ (X69153) ocs-element binding factor 3.1 [Zea mays]

Seq. No.	283807
Contig ID	143246_1.R1011
5'-most EST	uC-zmroteosinte027a05b1

Seq. No.	283808
Contig ID	143256_1.R1011
5'-most EST	uC-zmroteosinte027b04b1

Seq. No.	283809
Contig ID	143293_1.R1011
5'-most EST	pmx700085817.h1
Method	BLASTX
NCBI GI	g2414618
BLAST score	301
E value	3.0e-27
Match length	119
% identity	52
NCBI Description	(Z99259) ribonuclease II RNB family protein [Schizosaccharomyces pombe]

Seq. No.	283810
Contig ID	143295_1.R1011
5'-most EST	uC-zmroteosinte027f03b1

Method	BLASTX
NCBI GI	g4049341
BLAST score	336
E value	8.0e-38
Match length	216
% identity	38
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	283811
Contig ID	143339_1.R1011
5'-most EST	xsy700217829.h1
Method	BLASTX
NCBI GI	g4102839
BLAST score	289
E value	1.0e-25
Match length	159
% identity	40
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	283812
Contig ID	143343_1.R1011
5'-most EST	rvt700549103.h1
Method	BLASTX
NCBI GI	g4056437
BLAST score	357
E value	1.0e-33
Match length	131
% identity	56
NCBI Description	(AC005990) Strong similarity to PFAM PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	283813
Contig ID	143343_2.R1011
5'-most EST	fC-zmf1700342321d4

Seq. No.	283814
Contig ID	143348_1.R1011
5'-most EST	cjh700194776.h1
Method	BLASTX
NCBI GI	g3924615
BLAST score	551
E value	1.0e-56
Match length	146
% identity	73
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283815
Contig ID	143358_1.R1011
5'-most EST	uer700578563.h1
Method	BLASTX
NCBI GI	g722377
BLAST score	575
E value	1.0e-60
Match length	146
% identity	77
NCBI Description	(U23139) highly similar to beta-ureidopropionase (SP:BUP_RAT) [Caenorhabditis elegans]

Seq. No.	283816
Contig ID	143362_1.R1011
5'-most EST	uC-zmroteosinte028d05b1
Method	BLASTX
NCBI GI	g2829918
BLAST score	384
E value	4.0e-37
Match length	121
% identity	66
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	283817
Contig ID	143378_1.R1011
5'-most EST	xsy700217057.h1

Seq. No.	283818
Contig ID	143407_1.R1011
5'-most EST	fdz701163687.h1
Method	BLASTX
NCBI GI	g1351357
BLAST score	408
E value	8.0e-40
Match length	123
% identity	65
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN (CR14) >gi_633681_emb_CAA55863_ (X79276) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	283819
Contig ID	143446_1.R1011
5'-most EST	uC-zmroteosinte092d07b2
Method	BLASTX
NCBI GI	g2506931
BLAST score	445
E value	3.0e-83
Match length	343
% identity	47
NCBI Description	APYRASE PRECURSOR (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE) >gi_2129977_pir__JC4616 apyrase (EC 3.6.1.5) - potato >gi_1381633 (U58597) ATP-diphosphohydrolase [Solanum tuberosum]

Seq. No.	283820
Contig ID	143448_1.R1011
5'-most EST	xsy700207324.h1
Method	BLASTX
NCBI GI	g3063445
BLAST score	179
E value	6.0e-13
Match length	137
% identity	24
NCBI Description	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq. No.	283821

Contig ID	143449_1.R1011
5'-most EST	afb700381871.h1
Method	BLASTX
NCBI GI	g1815666
BLAST score	159
E value	9.0e-11
Match length	54
% identity	57
NCBI Description	(U83707) farnesyl protein transferase subunit A [Lycopersicon esculentum]

Seq. No.	283822
Contig ID	143457_1.R1011
5'-most EST	ymt700220858.h1

Seq. No.	283823
Contig ID	143467_1.R1011
5'-most EST	uC-zmroteosinte029e02b1
Method	BLASTX
NCBI GI	g4512698
BLAST score	887
E value	7.0e-96
Match length	188
% identity	82
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283824
Contig ID	143512_1.R1011
5'-most EST	uC-zmroteosinte031a02b1

Seq. No.	283825
Contig ID	143536_1.R1011
5'-most EST	uC-zmroteosinte030c09b1

Seq. No.	283826
Contig ID	143598_1.R1011
5'-most EST	uC-zmroteosinte030h12b1

Seq. No.	283827
Contig ID	143604_1.R1011
5'-most EST	uC-zmroteosinte031a06b1

Seq. No.	283828
Contig ID	143621_1.R1011
5'-most EST	uwc700155810.h1

Seq. No.	283829
Contig ID	143648_1.R1011
5'-most EST	ymt700220655.h1
Method	BLASTX
NCBI GI	g4006893
BLAST score	306
E value	1.0e-27
Match length	158
% identity	39
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	283830
Contig ID	143659_1.R1011
5'-most EST	uC-zmroteosinte031f01b1

Seq. No.	283831
Contig ID	143707_1.R1011
5'-most EST	uC-zmroteosinte032b03b1
Method	BLASTX
NCBI GI	g2499946
BLAST score	612
E value	2.0e-63
Match length	181
% identity	70
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	283832
Contig ID	143710_1.R1011
5'-most EST	uC-zmroteosinte032b08b1
Method	BLASTX
NCBI GI	g2924516
BLAST score	506
E value	3.0e-51
Match length	149
% identity	58
NCBI Description	(AL022023) WD-40 repeat protein (MSI3) [Arabidopsis thaliana]

Seq. No.	283833
Contig ID	143728_1.R1011
5'-most EST	uC-zmroteosinte032d03b1

Seq. No.	283834
Contig ID	143740_1.R1011
5'-most EST	uC-zmroteosinte032e06b1

Seq. No.	283835
Contig ID	143770_1.R1011
5'-most EST	uC-zmroteosinte032h01b1
Method	BLASTX
NCBI GI	g3513726
BLAST score	170
E value	1.0e-11
Match length	70
% identity	51
NCBI Description	(AF080118) F8M12.23 gene product [Arabidopsis thaliana] >gi_4539354_emb_CAB40048.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	283836
Contig ID	143777_1.R1011
5'-most EST	uC-zmroteosinte032h11b1

Seq. No.	283837
Contig ID	143790_1.R1011

5'-most EST	fwa700101688.h1
Seq. No.	283838
Contig ID	143796_1.R1011
5'-most EST	ceu700431553.h1
Seq. No.	283839
Contig ID	143796_2.R1011
5'-most EST	uC-zmflmo17340g03a1
Seq. No.	283840
Contig ID	143802_1.R1011
5'-most EST	uC-zmflb73299g06a1
Seq. No.	283841
Contig ID	143808_1.R1011
5'-most EST	pmx700084190.h1
Seq. No.	283842
Contig ID	143808_2.R1011
5'-most EST	mwy700438817.h1
Seq. No.	283843
Contig ID	143854_2.R1011
5'-most EST	uC-zmroteosinte033h04b1
Method	BLASTX
NCBI GI	g4103635
BLAST score	215
E value	4.0e-17
Match length	82
% identity	49
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]
Seq. No.	283844
Contig ID	143857_1.R1011
5'-most EST	fwa700098272.h1
Seq. No.	283845
Contig ID	143883_1.R1011
5'-most EST	uC-zmroteosinte034c01b1
Seq. No.	283846
Contig ID	143894_1.R1011
5'-most EST	uC-zmroteosinte034c12b1
Method	BLASTX
NCBI GI	g217995
BLAST score	479
E value	5.0e-48
Match length	173
% identity	57
NCBI Description	(D13683) peroxidase [Populus kitakamiensis]
Seq. No.	283847
Contig ID	143933_1.R1011
5'-most EST	uC-zmroteosinte034g06b1
Method	BLASTX
NCBI GI	g2288969

BLAST score	494
E value	6.0e-50
Match length	98
% identity	97
NCBI Description	(Y12862) glutathione transferase [Zea mays]

Seq. No.	283848
Contig ID	143933_2.R1011
5'-most EST	ntr700075851.h1
Method	BLASTN
NCBI GI	g2288968
BLAST score	280
E value	1.0e-156
Match length	389
% identity	96
NCBI Description	Zea mays mRNA for glutathione transferase

Seq. No.	283849
Contig ID	143944_1.R1011
5'-most EST	uC-zmroteosinte034h05b1

Seq. No.	283850
Contig ID	143962_1.R1011
5'-most EST	mwy700438651.h1

Seq. No.	283851
Contig ID	143976_1.R1011
5'-most EST	uC-zmroteosinte035c01b2

Seq. No.	283852
Contig ID	144021_1.R1011
5'-most EST	tfd700572957.h1

Seq. No.	283853
Contig ID	144031_1.R1011
5'-most EST	uC-zmroteosinte035g09b2
Method	BLASTX
NCBI GI	g2281090
BLAST score	465
E value	2.0e-46
Match length	157
% identity	60
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283854
Contig ID	144093_1.R1011
5'-most EST	nwy700446528.h1

Seq. No.	283855
Contig ID	144096_1.R1011
5'-most EST	uC-zmroteosinte036g06b1

Seq. No.	283856
Contig ID	144119_1.R1011
5'-most EST	pwr700450706.h1
Method	BLASTX
NCBI GI	g4586246

BLAST score	421
E value	2.0e-41
Match length	152
% identity	49
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	283857
Contig ID	144120_1.R1011
5'-most EST	uC-zmroteosinte037b02b1
Method	BLASTX
NCBI GI	g2464901
BLAST score	344
E value	2.0e-32
Match length	99
% identity	71
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	283858
Contig ID	144149_1.R1011
5'-most EST	pmx700091683.h1

Seq. No.	283859
Contig ID	144169_1.R1011
5'-most EST	ntr700075143.h1
Method	BLASTX
NCBI GI	g550542
BLAST score	441
E value	3.0e-67
Match length	312
% identity	45
NCBI Description	(X81831) cytochrome P450 [Zea mays] >gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea mays]

Seq. No.	283860
Contig ID	144197_1.R1011
5'-most EST	uC-zmroteosinte037h10b1

Seq. No.	283861
Contig ID	144206_1.R1011
5'-most EST	uC-zmroteosinte038a07b1

Seq. No.	283862
Contig ID	144214_1.R1011
5'-most EST	uC-zmroteosinte038b03b1
Method	BLASTX
NCBI GI	g3093294
BLAST score	380
E value	1.0e-36
Match length	88
% identity	80
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	283863
Contig ID	144254_1.R1011
5'-most EST	uC-zmroteosinte038e08b1

Seq. No.	283864
Contig ID	144254_2.R1011
5'-most EST	uC-zmflb73030d12a1

Seq. No.	283865
Contig ID	144267_1.R1011
5'-most EST	uC-zmroteosinte038f09b1
Method	BLASTX
NCBI GI	g2842526
BLAST score	328
E value	4.0e-30
Match length	151
% identity	42
NCBI Description	(AL021746) hypothetical anaphase promoting factor component [Schizosaccharomyces pombe] >gi_3393013_emb_CAA20105_ (AL031174) hypothetical anaphase promoting complex component [Schizosaccharomyces pombe] >gi_3402334_dbj_BAA32157_ (AB012919) Apc10 (anaphase promoting complex) [Schizosaccharomyces pombe]

Seq. No.	283866
Contig ID	144274_1.R1011
5'-most EST	nbm700467779.h1
Method	BLASTX
NCBI GI	g4455217
BLAST score	355
E value	2.0e-33
Match length	145
% identity	51
NCBI Description	(AL035440) Avr9 elicitor response like protein [Arabidopsis thaliana]

Seq. No.	283867
Contig ID	144275_1.R1011
5'-most EST	xsy700211860.h1
Method	BLASTX
NCBI GI	g118571
BLAST score	175
E value	2.0e-12
Match length	136
% identity	32
NCBI Description	GRANATICIN POLYKETIDE SYNTHASE PUTATIVE KETOACYL REDUCTASE 1 (ORF5) >gi_80860_pir__S05397 granaticin-producing polyketide synthase chain 5 - Streptomyces violaceoruber >gi_47978_emb_CAA34263_ (X16144) ketoacyl reductase (AA 1-273) [Streptomyces violaceoruber] >gi_47992_emb_CAA34368_ (X16300) ORF 5 (AA 1-272) [Streptomyces violaceoruber] >gi_4218563_emb_CAA09652.1_ (AJ011500) polyketide ketoreductase [Streptomyces violaceoruber]

Seq. No.	283868
Contig ID	144317_1.R1011
5'-most EST	uC-zmroteosinte039b12b1

Seq. No.	283869
Contig ID	144357_1.R1011
5'-most EST	uwc700152443

Method	BLASTX
NCBI GI	g3402687
BLAST score	387
E value	4.0e-37
Match length	154
% identity	50
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	283870
Contig ID	144381_1.R1011
5'-most EST	uC-zmroteosinte039h10b1
Method	BLASTX
NCBI GI	g2289002
BLAST score	210
E value	1.0e-23
Match length	96
% identity	57
NCBI Description	(AC002335) unknown protein [Arabidopsis thaliana]

Seq. No.	283871
Contig ID	144388_1.R1011
5'-most EST	uC-zmroteosinte040a05b1

Seq. No.	283872
Contig ID	144412_1.R1011
5'-most EST	wty700165080.h1

Seq. No.	283873
Contig ID	144412_2.R1011
5'-most EST	xtj700377375.h1

Seq. No.	283874
Contig ID	144423_1.R1011
5'-most EST	uC-zmroteosinte040d06b1

Seq. No.	283875
Contig ID	144444_1.R1011
5'-most EST	xsy700214822.h1

Seq. No.	283876
Contig ID	144447_1.R1011
5'-most EST	fdz701163659.h1
Method	BLASTX
NCBI GI	g2982455
BLAST score	382
E value	7.0e-37
Match length	100
% identity	74
NCBI Description	(AL022223) putative uracil phosphoribosyl transferase [Arabidopsis thaliana]

Seq. No.	283877
Contig ID	144473_1.R1011
5'-most EST	uC-zmroteosinte040h10b1

Seq. No.	283878
Contig ID	144521_1.R1011

5'-most EST	uC-zmroteosinte041d10b1
Method	BLASTX
NCBI GI	g3219785
BLAST score	172
E value	4.0e-21
Match length	103
% identity	57
NCBI Description	PUTATIVE CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_2104433_emb_CAB08745_ (Z95395) putative cysteine synthase [Schizosaccharomyces pombe]

Seq. No.	283879
Contig ID	144524_1.R1011
5'-most EST	uC-zmroteosinte041e01b1

Seq. No.	283880
Contig ID	144536_1.R1011
5'-most EST	uC-zmflb73220g06b2

Seq. No.	283881
Contig ID	144539_1.R1011
5'-most EST	pmx700090225.h1
Method	BLASTX
NCBI GI	g2462671
BLAST score	283
E value	5.0e-25
Match length	164
% identity	41
NCBI Description	(Z98529) putative RNA-binding protein [Schizosaccharomyces pombe]

Seq. No.	283882
Contig ID	144551_1.R1011
5'-most EST	wty700166258.h1
Method	BLASTX
NCBI GI	g2739385
BLAST score	421
E value	8.0e-45
Match length	161
% identity	57
NCBI Description	(AC002505) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	283883
Contig ID	144576_1.R1011
5'-most EST	uC-zmroteosinte042b01b1

Seq. No.	283884
Contig ID	144596_1.R1011
5'-most EST	uC-zmroteosinte042c09b1
Method	BLASTX
NCBI GI	g1707980
BLAST score	393
E value	5.0e-38
Match length	98
% identity	76

NCBI Description	GLUTAREDOXIN >gi_1084458_pir__S41736 glutaredoxin thioltransferase - Rice >gi_485953_emb_CAA54397_ (X77150) glutaredoxin [Oryza sativa]

Seq. No.	283885
Contig ID	144607_1.R1011
5'-most EST	uC-zmroteosinte042d09b1
Method	BLASTX
NCBI GI	g2804465
BLAST score	168
E value	7.0e-12
Match length	124
% identity	31
NCBI Description	(AF043700) contains similarity to human RNA-binding protein FUS/TLS (SW:Q28009) [Caenorhabditis elegans]

Seq. No.	283886
Contig ID	144628_1.R1011
5'-most EST	uC-zmroteosinte042f07b1

Seq. No.	283887
Contig ID	144655_1.R1011
5'-most EST	uC-zmroteosinte042h11b1
Method	BLASTX
NCBI GI	g3355474
BLAST score	331
E value	7.0e-31
Match length	141
% identity	46
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	283888
Contig ID	144660_1.R1011
5'-most EST	uC-zmroteosinte043a05b2

Seq. No.	283889
Contig ID	144664_1.R1011
5'-most EST	uer700577692.h1

Seq. No.	283890
Contig ID	144693_1.R1011
5'-most EST	xmt700262428.h1
Method	BLASTX
NCBI GI	g2827651
BLAST score	422
E value	2.0e-41
Match length	194
% identity	20
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	283891
Contig ID	144709_1.R1011
5'-most EST	uC-zmroteosinte043f01b2

Seq. No.	283892
Contig ID	144717_1.R1011
5'-most EST	hbs701185354.h1

Seq. No.	283893
Contig ID	144720_1.R1011
5'-most EST	uC-zmroteosinte043g01b2
Method	BLASTX
NCBI GI	g4510421
BLAST score	206
E value	3.0e-16
Match length	104
% identity	45
NCBI Description	(AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	283894
Contig ID	144726_1.R1011
5'-most EST	xjt700095129.h1
Method	BLASTX
NCBI GI	g3746964
BLAST score	576
E value	2.0e-59
Match length	149
% identity	78
NCBI Description	(AF092168) signal recognition particle 54 kDa subunit precursor [Arabidopsis thaliana]

Seq. No.	283895
Contig ID	144795_1.R1011
5'-most EST	uC-zmroteosinte044g05b2

Seq. No.	283896
Contig ID	144800_1.R1011
5'-most EST	uC-zmroteosinte044g10b2
Method	BLASTX
NCBI GI	g3080400
BLAST score	176
E value	2.0e-24
Match length	120
% identity	54
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	283897
Contig ID	144808_1.R1011
5'-most EST	tfd700574789.h1
Method	BLASTX
NCBI GI	g4539459
BLAST score	577
E value	1.0e-59
Match length	159
% identity	70
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	283898
Contig ID	144869_1.R1011
5'-most EST	uC-zmroteosinte045g11b2

Seq. No.	283899

Contig ID	144900_1.R1011
5'-most EST	fwa700097070.h1
Seq. No.	283900
Contig ID	144909_1.R1011
5'-most EST	wyr700240469.h1
Method	BLASTX
NCBI GI	g4586378
BLAST score	647
E value	9.0e-97
Match length	246
% identity	71
NCBI Description	(AB021746) nicotianamine synthase 1 [Oryza sativa]
Seq. No.	283901
Contig ID	144909_2.R1011
5'-most EST	uC-zmroteosinte105a04b1
Method	BLASTX
NCBI GI	g4586378
BLAST score	264
E value	4.0e-27
Match length	124
% identity	60
NCBI Description	(AB021746) nicotianamine synthase 1 [Oryza sativa]
Seq. No.	283902
Contig ID	144953_1.R1011
5'-most EST	uC-zmflb73017c07a2
Seq. No.	283903
Contig ID	144977_1.R1011
5'-most EST	uC-zmroteosinte047a01b2
Seq. No.	283904
Contig ID	144985_1.R1011
5'-most EST	uC-zmroteosinte047a06b1
Method	BLASTX
NCBI GI	g559330
BLAST score	200
E value	3.0e-15
Match length	84
% identity	45
NCBI Description	(D38521) The ha0919 gene product is novel. [Homo sapiens]
Seq. No.	283905
Contig ID	145009_1.R1011
5'-most EST	pmx700082825.h1
Seq. No.	283906
Contig ID	145009_2.R1011
5'-most EST	yyf700351814.h1
Seq. No.	283907
Contig ID	145028_1.R1011
5'-most EST	uC-zmroteosinte047c11b2
Method	BLASTX
NCBI GI	g4572677

BLAST score 256
E value 6.0e-22
Match length 131
% identity 45
NCBI Description (AC006954) hypothetical protein [Arabidopsis thaliana]

Seq. No. 283908
Contig ID 145029_1.R1011
5'-most EST uC-zmroteosinte047c07b1

Seq. No. 283909
Contig ID 145040_1.R1011
5'-most EST wyr700242037.h1
Method BLASTX
NCBI GI g1871187
BLAST score 787
E value 5.0e-84
Match length 232
% identity 64
NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 283910
Contig ID 145044_1.R1011
5'-most EST gct701175810.h1
Method BLASTX
NCBI GI g4544412
BLAST score 294
E value 2.0e-26
Match length 98
% identity 53
NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 283911
Contig ID 145062_1.R1011
5'-most EST nbm700465319.h1
Method BLASTX
NCBI GI g4097587
BLAST score 249
E value 5.0e-21
Match length 76
% identity 58
NCBI Description (U64926) NTGP5 [Nicotiana tabacum]

Seq. No. 283912
Contig ID 145069_1.R1011
5'-most EST uC-zmroteosinte047e08b2

Seq. No. 283913
Contig ID 145110_1.R1011
5'-most EST cyk700050256.f1
Method BLASTX
NCBI GI g2696221
BLAST score 407
E value 1.0e-39
Match length 142
% identity 57
NCBI Description (D55708) chitinase [Oryza sativa]

Seq. No.	283914
Contig ID	145126_1.R1011
5'-most EST	uC-zmroteosinte048a12b1
Method	BLASTX
NCBI GI	g2129635
BLAST score	207
E value	5.0e-28
Match length	151
% identity	49
NCBI Description	light repressible receptor protein kinase - Arabidopsis thaliana >gi_1321686_emb_CAA66376_ (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No.	283915
Contig ID	145128_1.R1011
5'-most EST	nwy700444566.h1

Seq. No.	283916
Contig ID	145141_1.R1011
5'-most EST	uC-zmroteosinte048c05b1
Method	BLASTX
NCBI GI	g4510348
BLAST score	288
E value	1.0e-25
Match length	134
% identity	47
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	283917
Contig ID	145154_1.R1011
5'-most EST	uC-zmroteosinte048d07b1

Seq. No.	283918
Contig ID	145161_1.R1011
5'-most EST	wty700170004.h1

Seq. No.	283919
Contig ID	145198_1.R1011
5'-most EST	uC-zmroteosinte049b01b1
Method	BLASTX
NCBI GI	g3702324
BLAST score	185
E value	1.0e-13
Match length	98
% identity	37
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283920
Contig ID	145223_1.R1011
5'-most EST	uC-zmroteosinte049d09b1
Method	BLASTX
NCBI GI	g4454051
BLAST score	641
E value	6.0e-67
Match length	240
% identity	52

NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	283921
Contig ID	145235_1.R1011
5'-most EST	uC-zmroteosinte049e10b1

Seq. No.	283922
Contig ID	145251_1.R1011
5'-most EST	rvt700552989.h1
Method	BLASTX
NCBI GI	g1449336
BLAST score	210
E value	2.0e-16
Match length	222
% identity	32
NCBI Description	(Z77163) lipM [Mycobacterium tuberculosis]

Seq. No.	283923
Contig ID	145254_1.R1011
5'-most EST	ymt700219992.h1
Method	BLASTX
NCBI GI	g2506379
BLAST score	716
E value	1.0e-75
Match length	271
% identity	53
NCBI Description	GTP-BINDING PROTEIN GUF1 (GTPASE GUF1) >gi_1077352_pir__S50374 GTP-binding protein GUF1 - yeast (Saccharomyces cerevisiae) >gi_596037 (U17243) Similar to GTP binding proteins [Saccharomyces cerevisiae]

Seq. No.	283924
Contig ID	145299_2.R1011
5'-most EST	pmx700082148.h1
Method	BLASTX
NCBI GI	g3063706
BLAST score	620
E value	1.0e-64
Match length	175
% identity	66
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	283925
Contig ID	145307_1.R1011
5'-most EST	ymt700222317.h1
Method	BLASTX
NCBI GI	g3914502
BLAST score	674
E value	1.0e-86
Match length	200
% identity	84
NCBI Description	ASPARTATE CARBAMOYLTRANSFERASE 1 PRECURSOR (ASPARTATE TRANSCARBAMYLASE 1) (ATCASE 1) >gi_495659 (M96981) aspartate carbamoyltransferase [Pisum sativum]

Seq. No.	283926

Contig ID	145384_1.R1011
5'-most EST	uC-zmroteosinte053g12b2
Method	BLASTX
NCBI GI	g2829910
BLAST score	391
E value	8.0e-38
Match length	157
% identity	46
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	283927
Contig ID	145420_1.R1011
5'-most EST	uC-zmroteosinte057d05b1

Seq. No.	283928
Contig ID	145454_1.R1011
5'-most EST	uC-zmroteosinte057g08b1
Method	BLASTX
NCBI GI	g3482977
BLAST score	548
E value	2.0e-56
Match length	122
% identity	84
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	283929
Contig ID	145455_1.R1011
5'-most EST	pmx700083239.h1
Method	BLASTX
NCBI GI	g3834629
BLAST score	311
E value	4.0e-28
Match length	260
% identity	26
NCBI Description	(AF094519) diaphanous-related formin; p134 mDia2 [Mus musculus]

Seq. No.	283930
Contig ID	145455_2.R1011
5'-most EST	pmx700091716.h1

Seq. No.	283931
Contig ID	145506_1.R1011
5'-most EST	qmh700030501.f1
Method	BLASTX
NCBI GI	g3522950
BLAST score	381
E value	1.0e-36
Match length	175
% identity	49
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283932
Contig ID	145558_1.R1011
5'-most EST	cat700019122.r1
Method	BLASTX

NCBI GI	g2316016
BLAST score	557
E value	3.0e-57
Match length	190
% identity	59
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	283933
Contig ID	145560_1.R1011
5'-most EST	uC-zmroteosinte058h12b2
Method	BLASTX
NCBI GI	g1171691
BLAST score	397
E value	2.0e-38
Match length	208
% identity	37
NCBI Description	NEUROLYSIN PRECURSOR (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) >gi_987087_emb_CAA60630_ (X87157) neurolysin [Rattus norvegicus]

Seq. No.	283934
Contig ID	145568_1.R1011
5'-most EST	fC-zmf1700552771f3

Seq. No.	283935
Contig ID	145622_1.R1011
5'-most EST	ntr700073133.h1
Method	BLASTX
NCBI GI	g2623304
BLAST score	197
E value	5.0e-15
Match length	159
% identity	30
NCBI Description	(AC002409) similar to Medicago nodulin N21 [Arabidopsis thaliana]

Seq. No.	283936
Contig ID	145635_1.R1011
5'-most EST	dyk700102872.h1
Method	BLASTX
NCBI GI	g1346104
BLAST score	1066
E value	1.0e-117
Match length	226
% identity	88
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT (GP-ALPHA-1) >gi_540533_dbj_BAA07405_ (D38232) G protein alpha subunit [Oryza sativa]

Seq. No.	283937
Contig ID	145655_1.R1011
5'-most EST	uC-zmroteosinte060b05b1

Seq. No.	283938
Contig ID	145656_1.R1011
5'-most EST	tfd700576610.h1

Method	BLASTX
NCBI GI	g1323742
BLAST score	150
E value	2.0e-09
Match length	112
% identity	35
NCBI Description	(U32427) unknown [Triticum aestivum]

Seq. No.	283939
Contig ID	145674_1.R1011
5'-most EST	ymt700224550.h1
Method	BLASTX
NCBI GI	g4539452
BLAST score	1029
E value	1.0e-112
Match length	247
% identity	74
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	283940
Contig ID	145678_1.R1011
5'-most EST	ypc700799057.h1
Method	BLASTN
NCBI GI	g3510345
BLAST score	48
E value	1.0e-17
Match length	208
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	283941
Contig ID	145705_1.R1011
5'-most EST	xmt700262067.h1
Method	BLASTX
NCBI GI	g4455309
BLAST score	253
E value	2.0e-27
Match length	133
% identity	51
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283942
Contig ID	145754_1.R1011
5'-most EST	uC-zmroteosinte061b11b2
Method	BLASTX
NCBI GI	g4160292
BLAST score	521
E value	7.0e-53
Match length	203
% identity	49
NCBI Description	(Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]

Seq. No.	283943
Contig ID	145770_1.R1011
5'-most EST	uC-zmroteosinte061d03b2

Method	BLASTX
NCBI GI	g4249403
BLAST score	239
E value	5.0e-20
Match length	83
% identity	58
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	283944
Contig ID	145782_2.R1011
5'-most EST	uC-zmroteosinte120h08b2
Method	BLASTX
NCBI GI	g4467124
BLAST score	220
E value	9.0e-18
Match length	165
% identity	32
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283945
Contig ID	145788_1.R1011
5'-most EST	uC-zmroteosinte061e11b2

Seq. No.	283946
Contig ID	145808_1.R1011
5'-most EST	ymt700222406.h1

Seq. No.	283947
Contig ID	145815_1.R1011
5'-most EST	cyk700047690.f1
Method	BLASTX
NCBI GI	g1168470
BLAST score	472
E value	1.0e-47
Match length	112
% identity	79
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	283948
Contig ID	145819_1.R1011
5'-most EST	uC-zmroteosinte061h06b2

Seq. No.	283949
Contig ID	145846_1.R1011
5'-most EST	uC-zmroteosinte062b11b1
Method	BLASTX
NCBI GI	g4559380
BLAST score	492
E value	9.0e-50
Match length	144
% identity	62
NCBI Description	(AC006526) putative auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	283950
Contig ID	145859_1.R1011
5'-most EST	xyt700344750.h1
Method	BLASTX
NCBI GI	g549736
BLAST score	168
E value	1.0e-11
Match length	89
% identity	45
NCBI Description	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION >gi_539212_pir__S38002 hypothetical protein YKL172w - yeast (Saccharomyces cerevisiae) >gi_407510_emb_CAA81515_ (Z26878) unknown [Saccharomyces cerevisiae] >gi_486302_emb_CAA82014_ (Z28172) ORF YKL172w [Saccharomyces cerevisiae] >gi_1582533_prf__2118403G ORF [Saccharomyces cerevisiae]

Seq. No.	283951
Contig ID	145863_1.R1011
5'-most EST	uC-zmroteosinte062d08b1
Method	BLASTX
NCBI GI	g3643598
BLAST score	309
E value	3.0e-28
Match length	96
% identity	59
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	283952
Contig ID	145918_1.R1011
5'-most EST	mwy700442380.h1
Method	BLASTX
NCBI GI	g2459441
BLAST score	142
E value	3.0e-09
Match length	93
% identity	35
NCBI Description	(AC002332) putative SWI/SNF complex subunit BAF170 [Arabidopsis thaliana]

Seq. No.	283953
Contig ID	145923_1.R1011
5'-most EST	uC-zmroteosinte074b10b1
Method	BLASTX
NCBI GI	g2252831
BLAST score	439
E value	3.0e-43
Match length	218
% identity	40
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	283954
Contig ID	145941_1.R1011
5'-most EST	uC-zmroteosinte063c06b1
Method	BLASTX

NCBI GI	g3341694
BLAST score	257
E value	4.0e-22
Match length	108
% identity	50
NCBI Description	(AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No.	283955
Contig ID	145950_1.R1011
5'-most EST	uC-zmroteosinte063d03b1

Seq. No.	283956
Contig ID	145966_1.R1011
5'-most EST	wyr700235221.h1
Method	BLASTX
NCBI GI	g4512659
BLAST score	855
E value	6.0e-92
Match length	263
% identity	65
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	283957
Contig ID	145981_1.R1011
5'-most EST	uC-zmflb73246b07b3
Method	BLASTX
NCBI GI	g4587560
BLAST score	390
E value	2.0e-37
Match length	185
% identity	50
NCBI Description	(AC006577) F15I1.27 [Arabidopsis thaliana]

Seq. No.	283958
Contig ID	146059_1.R1011
5'-most EST	rvl700457553.h1

Seq. No.	283959
Contig ID	146081_1.R1011
5'-most EST	ymt700220938.h1
Method	BLASTX
NCBI GI	g1350680
BLAST score	363
E value	6.0e-35
Match length	94
% identity	69
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	283960
Contig ID	146086_1.R1011
5'-most EST	pmx700084301.h1
Method	BLASTX
NCBI GI	g2582971
BLAST score	432
E value	5.0e-67

Match length	139
% identity	88
NCBI Description	(D83711) TKRP125 [Nicotiana tabacum]

Seq. No.	283961
Contig ID	146111_1.R1011
5'-most EST	cyk700048388.f1

Seq. No.	283962
Contig ID	146120_1.R1011
5'-most EST	qmh700029404.f1
Method	BLASTX
NCBI GI	g3702332
BLAST score	182
E value	3.0e-13
Match length	141
% identity	31
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	283963
Contig ID	146126_1.R1011
5'-most EST	uC-zmroteosinte066c07b1
Method	BLASTX
NCBI GI	g3170178
BLAST score	181
E value	4.0e-13
Match length	58
% identity	53
NCBI Description	(AF039689) antigen NY-CO-7 [Homo sapiens]

Seq. No.	283964
Contig ID	146130_1.R1011
5'-most EST	uC-zmroteosinte066c11b1
Method	BLASTX
NCBI GI	g3075392
BLAST score	418
E value	6.0e-41
Match length	175
% identity	45
NCBI Description	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]

Seq. No.	283965
Contig ID	146131_1.R1011
5'-most EST	uC-zmroteosinte066c12b1

Seq. No.	283966
Contig ID	146146_1.R1011
5'-most EST	ceu700430218.h1
Method	BLASTX
NCBI GI	g3135271
BLAST score	447
E value	4.0e-44
Match length	146
% identity	54
NCBI Description	(AC003058) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	283967
Contig ID	146157_1.R1011
5'-most EST	tfd700575845.h1
Method	BLASTX
NCBI GI	g3559805
BLAST score	413
E value	2.0e-62
Match length	141
% identity	76
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	283968
Contig ID	146159_1.R1011
5'-most EST	mwy700440372.h1

Seq. No.	283969
Contig ID	146175_1.R1011
5'-most EST	fC-zmle700433352a4
Method	BLASTX
NCBI GI	g4585908
BLAST score	650
E value	6.0e-68
Match length	258
% identity	50
NCBI Description	(AC006298) putative lysosomal acid lipase [Arabidopsis thaliana]

Seq. No.	283970
Contig ID	146192_1.R1011
5'-most EST	wyr700239751.h1

Seq. No.	283971
Contig ID	146215_1.R1011
5'-most EST	uC-zmroteosinte067c06b1
Method	BLASTX
NCBI GI	g4490325
BLAST score	378
E value	1.0e-41
Match length	139
% identity	60
NCBI Description	(AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283972
Contig ID	146237_1.R1011
5'-most EST	uC-zmroteosinte067e04b1
Method	BLASTX
NCBI GI	g4490316
BLAST score	447
E value	3.0e-44
Match length	225
% identity	46
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	283973
Contig ID	146243_1.R1011

5'-most EST	uC-zmflb73241f08b2
Seq. No.	283974
Contig ID	146251_1.R1011
5'-most EST	uC-zmroteosinte067f07b1
Seq. No.	283975
Contig ID	146328_1.R1011
5'-most EST	uC-zmroteosinte068e05b1
Method	BLASTX
NCBI GI	g4505235
BLAST score	309
E value	3.0e-28
Match length	164
% identity	41
NCBI Description	mannose phosphate isomerase >gi_462567_sp_P34949_MANA_HUMAN MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) >gi_631328_pir__S41122 mannose-6-phosphate isomerase (EC 5.3.1.8) - human >gi_416017_emb_CAA53657_ (X76057) phosphomannose isomerase [Homo sapiens] >gi_740967_prf__2006245A phosphomannose isomerase [Homo sapiens]
Seq. No.	283976
Contig ID	146338_1.R1011
5'-most EST	dhd700197920.h1
Method	BLASTX
NCBI GI	g3885336
BLAST score	340
E value	1.0e-31
Match length	210
% identity	30
NCBI Description	(AC005623) receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	283977
Contig ID	146339_1.R1011
5'-most EST	nbm700471011.h1
Seq. No.	283978
Contig ID	146397_2.R1011
5'-most EST	kem700611456.h1
Method	BLASTX
NCBI GI	g4539347
BLAST score	350
E value	2.0e-33
Match length	87
% identity	76
NCBI Description	(AL035539) putative growth regulator protein [Arabidopsis thaliana]
Seq. No.	283979
Contig ID	146421_1.R1011
5'-most EST	uC-zmroteosinte069f02b1
Seq. No.	283980
Contig ID	146455_1.R1011

5'-most EST	uC-zmroteosinte070a01b1
Seq. No.	283981
Contig ID	146471_1.R1011
5'-most EST	uC-zmroteosinte070b05b1
Method	BLASTX
NCBI GI	g3850588
BLAST score	515
E value	3.0e-52
Match length	209
% identity	48
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]
Seq. No.	283982
Contig ID	146481_1.R1011
5'-most EST	uC-zmroteosinte070c03b1
Seq. No.	283983
Contig ID	146488_1.R1011
5'-most EST	ymt700224150.h1
Method	BLASTX
NCBI GI	g4220474
BLAST score	443
E value	1.0e-43
Match length	230
% identity	48
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]
Seq. No.	283984
Contig ID	146519_1.R1011
5'-most EST	fwa700097948.h1
Method	BLASTX
NCBI GI	g2829889
BLAST score	285
E value	4.0e-25
Match length	150
% identity	41
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	283985
Contig ID	146570_1.R1011
5'-most EST	uC-zmroteosinte072c04b2
Method	BLASTX
NCBI GI	g4544440
BLAST score	283
E value	5.0e-25
Match length	178
% identity	37
NCBI Description	(AC006592) unknown protein [Arabidopsis thaliana]
Seq. No.	283986
Contig ID	146581_1.R1011
5'-most EST	pmx700083494.h1

Method	BLASTX
NCBI GI	g2501242
BLAST score	268
E value	3.0e-23
Match length	176
% identity	34
NCBI Description	DNA TOPOISOMERASE III >gi_1292912 (U43431) DNA topoisomerase III [Homo sapiens]

Seq. No.	283987
Contig ID	146602_1.R1011
5'-most EST	uC-zmflmo17154a09a1
Method	BLASTX
NCBI GI	g2342676
BLAST score	391
E value	9.0e-38
Match length	95
% identity	75
NCBI Description	(AC000106) Strong similarity to Oryza NADPH oxidase (gb_X93301). [Arabidopsis thaliana]

Seq. No.	283988
Contig ID	146611_2.R1011
5'-most EST	cat700021214.r1

Seq. No.	283989
Contig ID	146613_1.R1011
5'-most EST	uC-zmroteosinte072g10b2

Seq. No.	283990
Contig ID	146615_1.R1011
5'-most EST	uC-zmroteosinte072g12b2

Seq. No.	283991
Contig ID	146627_1.R1011
5'-most EST	uC-zmroteosinte072h12b2
Method	BLASTX
NCBI GI	g4432861
BLAST score	237
E value	9.0e-20
Match length	85
% identity	56
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283992
Contig ID	146674_1.R1011
5'-most EST	tzu700203127.h1
Method	BLASTX
NCBI GI	g1724112
BLAST score	171
E value	5.0e-12
Match length	68
% identity	53
NCBI Description	(U80037) ABA induced plasma membrane protein PM 19 [Triticum aestivum]

Seq. No.	283993

Contig ID	146677_1.R1011
5'-most EST	uC-zmroteosinte073e05b1
Method	BLASTX
NCBI GI	g3860051
BLAST score	177
E value	8.0e-18
Match length	165
% identity	42
NCBI Description	(AF096868) transcytosis associated protein p115 [Mus musculus]

Seq. No.	283994
Contig ID	146680_1.R1011
5'-most EST	uC-zmroteosinte073e08b1
Method	BLASTX
NCBI GI	g4314388
BLAST score	533
E value	1.0e-55
Match length	198
% identity	59
NCBI Description	(AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	283995
Contig ID	146733_1.R1011
5'-most EST	cjh700193449.h1
Method	BLASTX
NCBI GI	g1172557
BLAST score	579
E value	9.0e-60
Match length	112
% identity	100
NCBI Description	OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_422030_pir__S34146 porin por1 - maize >gi_626044_pir__A55017 porin, plastid - maize >gi_313136_emb_CAA51828_ (X73429) porin [Zea mays]

Seq. No.	283996
Contig ID	146737_1.R1011
5'-most EST	uC-zmroteosinte074b06b1

Seq. No.	283997
Contig ID	146744_1.R1011
5'-most EST	dyk700106239.h1
Method	BLASTX
NCBI GI	g2589162
BLAST score	494
E value	1.0e-60
Match length	194
% identity	61
NCBI Description	(D88451) aldehyde oxidase [Zea mays]

Seq. No.	283998
Contig ID	146773_1.R1011
5'-most EST	uC-zmroteosinte074e12b1

Seq. No.	283999

Contig ID	146775_1.R1011
5'-most EST	yyf700347701.h1
Seq. No.	284000
Contig ID	146785_1.R1011
5'-most EST	wyr700239104.h1
Method	BLASTX
NCBI GI	g4432841
BLAST score	180
E value	1.0e-12
Match length	166
% identity	36
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.	284001
Contig ID	146791_1.R1011
5'-most EST	qmh700028951.f1
Method	BLASTX
NCBI GI	g2632019
BLAST score	282
E value	9.0e-25
Match length	212
% identity	36
NCBI Description	(AJ002571) YkfB [Bacillus subtilis] >gi_2633652_emb_CAB13155_ (Z99110) similar to chloromuconate cycloisomerase [Bacillus subtilis]
Seq. No.	284002
Contig ID	146820_1.R1011
5'-most EST	uC-zmroteosinte075a12b1
Method	BLASTX
NCBI GI	g2246380
BLAST score	437
E value	3.0e-43
Match length	147
% identity	59
NCBI Description	(Z86095) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]
Seq. No.	284003
Contig ID	146843_1.R1011
5'-most EST	wyr700243620.h1
Method	BLASTN
NCBI GI	g559535
BLAST score	69
E value	3.0e-30
Match length	178
% identity	91
NCBI Description	Z.mays mRNA for metallothionein
Seq. No.	284004
Contig ID	146853_1.R1011
5'-most EST	wyr700242766.h1
Seq. No.	284005
Contig ID	146855_1.R1011
5'-most EST	uC-zmflb73362g04a2

Seq. No.	284006
Contig ID	146865_1.R1011
5'-most EST	pwr700450624.h1
Method	BLASTX
NCBI GI	g1076715
BLAST score	456
E value	2.0e-45
Match length	104
% identity	75
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	284007
Contig ID	146865_2.R1011
5'-most EST	fdz701158843.h1
Method	BLASTX
NCBI GI	g1076715
BLAST score	232
E value	2.0e-19
Match length	50
% identity	82
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	284008
Contig ID	146884_1.R1011
5'-most EST	uC-zmroteosinte075g07b1

Seq. No.	284009
Contig ID	146884_2.R1011
5'-most EST	uC-zmflb73062d04a1

Seq. No.	284010
Contig ID	146894_1.R1011
5'-most EST	dyk700104745.h1
Method	BLASTX
NCBI GI	g4539302
BLAST score	203
E value	8.0e-16
Match length	71
% identity	59
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	284011
Contig ID	146904_1.R1011
5'-most EST	pmx700083466.h1

Seq. No.	284012
Contig ID	146913_1.R1011
5'-most EST	uC-zmroteosinte076b02b2
Method	BLASTX
NCBI GI	g3522957
BLAST score	433
E value	1.0e-42
Match length	129
% identity	67

NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	284013
Contig ID	146998_1.R1011
5'-most EST	uC-zmroteosinte077b01b1
Method	BLASTX
NCBI GI	g4467121
BLAST score	441
E value	8.0e-44
Match length	112
% identity	76
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	284014
Contig ID	146999_1.R1011
5'-most EST	uC-zmroteosinte077b02b1
Method	BLASTX
NCBI GI	g3169173
BLAST score	176
E value	2.0e-13
Match length	57
% identity	53
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	284015
Contig ID	147002_1.R1011
5'-most EST	xyt700346565.h1
Method	BLASTX
NCBI GI	g4056490
BLAST score	293
E value	1.0e-26
Match length	113
% identity	55
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284016
Contig ID	147007_1.R1011
5'-most EST	uwc700149825.h1
Method	BLASTX
NCBI GI	g585452
BLAST score	711
E value	3.0e-88
Match length	268
% identity	66
NCBI Description	MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi_1076666_pir__A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor, mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002) precursor of the 59kDa subunit of the mitochondrial NAD+-dependent malic enzyme [Solanum tuberosum]

Seq. No.	284017
Contig ID	147022_1.R1011
5'-most EST	pmx700082067.h1

Seq. No.	284018
Contig ID	147038_1.R1011
5'-most EST	uC-zmroteosinte077g01b1

Seq. No.	284019
Contig ID	147049_1.R1011
5'-most EST	nbm700465271.h1

Seq. No.	284020
Contig ID	147105_1.R1011
5'-most EST	uC-zmflb73242a10a1

Seq. No.	284021
Contig ID	147133_1.R1011
5'-most EST	uC-zmflb73162d07b2
Method	BLASTX
NCBI GI	g465898
BLAST score	267
E value	3.0e-23
Match length	136
% identity	43
NCBI Description	HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III >gi_630692_pir__S44849 K12H4.8 protein - Caenorhabditis elegans >gi_289703 (L14331) homology with eukaryotic initiation factor-4A (eIF-4A) and E. coli Ribonuclease III; coded for by C. elegans cDNA GenBank:T02268; putative [Caenorhabditis elegans]

Seq. No.	284022
Contig ID	147144_1.R1011
5'-most EST	uC-zmroteosinte080e04b1
Method	BLASTX
NCBI GI	g125578
BLAST score	560
E value	8.0e-58
Match length	127
% identity	86
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	284023
Contig ID	147177_1.R1011
5'-most EST	uC-zmroteosinte080h05b1
Method	BLASTX
NCBI GI	g2146739
BLAST score	427
E value	2.0e-79
Match length	216
% identity	71
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No.	284024
Contig ID	147210_1.R1011
5'-most EST	uC-zmroteosinte082b10b2

Seq. No.	284025
Contig ID	147212_1.R1011
5'-most EST	uC-zmroteosinte082b11b2

Seq. No.	284026
Contig ID	147232_1.R1011
5'-most EST	nbm700467409.h1

Seq. No.	284027
Contig ID	147232_2.R1011
5'-most EST	uC-zmroteosinte082c11b2

Seq. No.	284028
Contig ID	147235_1.R1011
5'-most EST	uC-zmroteosinte082d09b1

Seq. No.	284029
Contig ID	147253_1.R1011
5'-most EST	uC-zmroteosinte082d08b1
Method	BLASTX
NCBI GI	g3377507
BLAST score	298
E value	6.0e-27
Match length	68
% identity	85
NCBI Description	(AF056026) auxin transport protein EIR1 [Arabidopsis thaliana] >gi_3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No.	284030
Contig ID	147262_1.R1011
5'-most EST	uC-zmroteosinte082e03b2

Seq. No.	284031
Contig ID	147292_2.R1011
5'-most EST	cat700019559.r1

Seq. No.	284032
Contig ID	147296_1.R1011
5'-most EST	uC-zmflb73262d11b3

Seq. No.	284033
Contig ID	147331_1.R1011
5'-most EST	uC-zmflb73301c10b2
Method	BLASTX
NCBI GI	g4587518
BLAST score	955
E value	1.0e-104
Match length	214
% identity	84
NCBI Description	(AC007060) Strong similarity to F19I3.8 gi_3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb_AC004238 and is a member of PF_01370 the NAD dependent

epimerase/dehydratase family. EST gb_AA59

Seq. No.	284034
Contig ID	147333_1.R1011
5'-most EST	uC-zmroteosinte083b12b1

Seq. No.	284035
Contig ID	147353_1.R1011
5'-most EST	vux700157894.h1
Method	BLASTX
NCBI GI	g1001631
BLAST score	293
E value	4.0e-26
Match length	170
% identity	38
NCBI Description	(D64002) integral membrane protein [Synechocystis sp.]

Seq. No.	284036
Contig ID	147393_1.R1011
5'-most EST	uC-zmroteosinte083h02b1

Seq. No.	284037
Contig ID	147445_1.R1011
5'-most EST	uC-zmroteosinte084d07b1
Method	BLASTX
NCBI GI	g3522956
BLAST score	389
E value	1.0e-37
Match length	141
% identity	51
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	284038
Contig ID	147474_1.R1011
5'-most EST	pmx700083688.h1
Method	BLASTX
NCBI GI	g2501102
BLAST score	298
E value	2.0e-27
Match length	88
% identity	69
NCBI Description	SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi_1184167 (U39452) syntaxin-related [Arabidopsis thaliana] >gi_3063443 (AC003981) F22O13.4 [Arabidopsis thaliana] >gi_1587182_prf__2206310A syntaxin-related protein [Arabidopsis thaliana]

Seq. No.	284039
Contig ID	147501_1.R1011
5'-most EST	uC-zmroteosinte088a08b1

Seq. No.	284040
Contig ID	147510_1.R1011
5'-most EST	uC-zmroteosinte088b05b1
Method	BLASTN

NCBI GI	g3925238
BLAST score	96
E value	2.0e-46
Match length	220
% identity	88
NCBI Description	Zea mays 6-phosphogluconate dehydrogenase isoenzyme A gene, partial cds

Seq. No.	284041
Contig ID	147518_1.R1011
5'-most EST	uC-zmroteosinte088c01b1
Method	BLASTX
NCBI GI	g2465021
BLAST score	290
E value	8.0e-26
Match length	198
% identity	33
NCBI Description	(AJ001452) sesquiterpene cyclase [Fragaria vesca]

Seq. No.	284042
Contig ID	147519_1.R1011
5'-most EST	uC-zmroteosinte088c02b1
Method	BLASTX
NCBI GI	g3688598
BLAST score	474
E value	2.0e-47
Match length	158
% identity	59
NCBI Description	(AB009029) Cycloartenol Synthase [Panax ginseng]

Seq. No.	284043
Contig ID	147555_1.R1011
5'-most EST	uC-zmroteosinte088f07b1
Method	BLASTX
NCBI GI	g2739044
BLAST score	161
E value	7.0e-11
Match length	52
% identity	56
NCBI Description	(AF024651) polyphosphoinositide binding protein Sshlp [Glycine max]

Seq. No.	284044
Contig ID	147555_2.R1011
5'-most EST	xmt700257002.h1
Method	BLASTX
NCBI GI	g2739044
BLAST score	297
E value	6.0e-27
Match length	81
% identity	62
NCBI Description	(AF024651) polyphosphoinositide binding protein Sshlp [Glycine max]

Seq. No.	284045
Contig ID	147562_1.R1011
5'-most EST	uC-zmroteosinte085g02b1

Seq. No.	284046
Contig ID	147564_1.R1011
5'-most EST	uC-zmroteosinte085g04b1
Method	BLASTX
NCBI GI	g1707046
BLAST score	253
E value	1.0e-21
Match length	175
% identity	39
NCBI Description	(U80447) strong similarity to 'DEAD' box family of helicases (PS:PS00039) [Caenorhabditis elegans]

Seq. No.	284047
Contig ID	147566_1.R1011
5'-most EST	uC-zmroteosinte085g07b1

Seq. No.	284048
Contig ID	147577_1.R1011
5'-most EST	uC-zmroteosinte085h06b1

Seq. No.	284049
Contig ID	147587_1.R1011
5'-most EST	wyr700240986.h1
Method	BLASTX
NCBI GI	g2746335
BLAST score	169
E value	2.0e-11
Match length	150
% identity	30
NCBI Description	(AF037205) RING zinc finger protein [Mus musculus]

Seq. No.	284050
Contig ID	147598_1.R1011
5'-most EST	uC-zmroteosinte086b05b1

Seq. No.	284051
Contig ID	147612_1.R1011
5'-most EST	uC-zmroteosinte086c07b1
Method	BLASTX
NCBI GI	g3157941
BLAST score	145
E value	6.0e-09
Match length	52
% identity	50
NCBI Description	(AC002131) Contains similarity to hypothetical protein gb_U95973 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	284052
Contig ID	147623_1.R1011
5'-most EST	mwy700440618.h1

Seq. No.	284053
Contig ID	147625_1.R1011
5'-most EST	uC-zmroteosinte086d09b1
Method	BLASTX
NCBI GI	g4467137

BLAST score	329
E value	1.0e-30
Match length	145
% identity	47
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	284054
Contig ID	147648_1.R1011
5'-most EST	uC-zmroteosinte086f08b1

Seq. No.	284055
Contig ID	147730_1.R1011
5'-most EST	uC-zmroteosinte087f03b2

Seq. No.	284056
Contig ID	147731_1.R1011
5'-most EST	uC-zmroteosinte087f05b2
Method	BLASTX
NCBI GI	g2252863
BLAST score	458
E value	1.0e-45
Match length	179
% identity	54
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]

Seq. No.	284057
Contig ID	147742_1.R1011
5'-most EST	cjh700193632.h1
Method	BLASTX
NCBI GI	g3201616
BLAST score	253
E value	1.0e-21
Match length	90
% identity	47
NCBI Description	(AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284058
Contig ID	147850_1.R1011
5'-most EST	uC-zmroteosinte090a08b2
Method	BLASTX
NCBI GI	g3763932
BLAST score	1184
E value	1.0e-130
Match length	286
% identity	78
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	284059
Contig ID	147891_1.R1011
5'-most EST	tzu700205436.h1
Method	BLASTX
NCBI GI	g404690
BLAST score	529
E value	6.0e-54
Match length	185
% identity	57

NCBI Description	(L19075) cytochrome P450 [Catharanthus roseus]

Seq. No.	284060
Contig ID	147905_1.R1011
5'-most EST	uC-zmroteosinte090g04b2

Seq. No.	284061
Contig ID	147942_1.R1011
5'-most EST	uC-zmroteosinte091b12b2
Method	BLASTX
NCBI GI	g3287834
BLAST score	566
E value	6.0e-58
Match length	334
% identity	38
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME XC14 (D-CADINENE SYNTHASE) >gi_2147016_pir__S68366 (+)-delta-cadinene synthase isozyme XC14 - Gossypium arboreum >gi_1045314 (U23205) (+)-delta-cadinene synthase isozyme XC14 [Gossypium arboreum]

Seq. No.	284062
Contig ID	147952_1.R1011
5'-most EST	uC-zmroteosinte091c10b2
Method	BLASTX
NCBI GI	g3763940
BLAST score	209
E value	2.0e-16
Match length	60
% identity	62
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284063
Contig ID	147955_1.R1011
5'-most EST	uC-zmroteosinte091d01b2
Method	BLASTX
NCBI GI	g2344889
BLAST score	265
E value	7.0e-23
Match length	195
% identity	31
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	284064
Contig ID	147961_1.R1011
5'-most EST	tzu700202417.h1
Method	BLASTX
NCBI GI	g1621461
BLAST score	484
E value	1.0e-48
Match length	106
% identity	76
NCBI Description	(U73103) laccase [Liriodendron tulipifera]

Seq. No.	284065
Contig ID	147967_1.R1011
5'-most EST	uC-zmroteosinte091e03b2

Method	BLASTX
NCBI GI	g4006848
BLAST score	500
E value	2.0e-50
Match length	190
% identity	48
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	284066
Contig ID	147981_1.R1011
5'-most EST	mwy700441302.h1

Seq. No.	284067
Contig ID	147986_1.R1011
5'-most EST	pmx700089651.h1
Method	BLASTX
NCBI GI	g3738295
BLAST score	456
E value	3.0e-45
Match length	161
% identity	57
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	284068
Contig ID	148016_1.R1011
5'-most EST	gct701178423.h1
Method	BLASTX
NCBI GI	g4586113
BLAST score	331
E value	8.0e-34
Match length	117
% identity	71
NCBI Description	(AL049638) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	284069
Contig ID	148019_1.R1011
5'-most EST	ymt700223552.h1
Method	BLASTX
NCBI GI	g2213611
BLAST score	147
E value	1.0e-14
Match length	93
% identity	44
NCBI Description	(AC000103) F21J9.5 [Arabidopsis thaliana]

Seq. No.	284070
Contig ID	148040_1.R1011
5'-most EST	xsy700208818.h1
Method	BLASTX
NCBI GI	g3287826
BLAST score	435
E value	1.0e-47
Match length	340
% identity	36
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME C2 (D-CADINENE

SYNTHASE) >gi_2879841_emb_CAA76223.1_ (Y16432)
(+)-delta-cadinene synthase [Gossypium arboreum]

Seq. No.	284071
Contig ID	148040_2.R1011
5'-most EST	xsy700208189.h1
Method	BLASTX
NCBI GI	g3287835
BLAST score	481
E value	6.0e-48
Match length	299
% identity	34
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME A (D-CADINENE SYNTHASE) >gi_1002523 (U27535) (+)-delta-cadinene synthase isozyme A [Gossypium arboreum] >gi_1217956_emb_CAA65289_ (X96429) (+)-delta-cadinene synthase [Gossypium arboreum]

Seq. No.	284072
Contig ID	148048_2.R1011
5'-most EST	gwl700616421.h1
Method	BLASTX
NCBI GI	g3860010
BLAST score	245
E value	1.0e-20
Match length	110
% identity	63
NCBI Description	(AF091086) unknown [Homo sapiens]

Seq. No.	284073
Contig ID	148056_1.R1011
5'-most EST	uC-zmroteosinte092e04b2

Seq. No.	284074
Contig ID	148058_1.R1011
5'-most EST	uC-zmroteosinte092e06b2

Seq. No.	284075
Contig ID	148089_1.R1011
5'-most EST	uC-zmroteosinte092h03b2

Seq. No.	284076
Contig ID	148158_1.R1011
5'-most EST	uC-zmflb73356b11a2

Seq. No.	284077
Contig ID	148184_1.R1011
5'-most EST	uC-zmroteosinte094a05b2

Seq. No.	284078
Contig ID	148186_1.R1011
5'-most EST	uC-zmroteosinte094a07b2

Seq. No.	284079
Contig ID	148206_1.R1011
5'-most EST	uC-zmroteosinte101b07b2
Method	BLASTX
NCBI GI	g1483218

BLAST score 497
E value 6.0e-50
Match length 201
% identity 53
NCBI Description (X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No. 284080
Contig ID 148215_1.R1011
5'-most EST uC-zmroteosinte094d01b2

Seq. No. 284081
Contig ID 148217_1.R1011
5'-most EST wyr700239348.h1

Seq. No. 284082
Contig ID 148246_1.R1011
5'-most EST uC-zmroteosinte094f09b2

Seq. No. 284083
Contig ID 148261_1.R1011
5'-most EST uC-zmroteosinte094h01b2
Method BLASTX
NCBI GI g2370253
BLAST score 219
E value 1.0e-17
Match length 114
% identity 65
NCBI Description (Y13273) putative protein kinase [Lycopersicon esculentum]

Seq. No. 284084
Contig ID 148355_1.R1011
5'-most EST uC-zmroteosinte096a04b2
Method BLASTX
NCBI GI g2529707
BLAST score 336
E value 7.0e-33
Match length 161
% identity 46
NCBI Description (AF001434) Hpast [Homo sapiens]

Seq. No. 284085
Contig ID 148389_1.R1011
5'-most EST pmx700085854.h1
Method BLASTX
NCBI GI g3393022
BLAST score 417
E value 1.0e-40
Match length 217
% identity 45
NCBI Description (AL031174) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 284086
Contig ID 148393_1.R1011
5'-most EST uC-zmroteosinte096d08b2
Method BLASTX
NCBI GI g1707019

BLAST score	259
E value	3.0e-22
Match length	124
% identity	44
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284087
Contig ID	148437_1.R1011
5'-most EST	vqh700053205.r1

Seq. No.	284088
Contig ID	148469_1.R1011
5'-most EST	uC-zmroteosinte097g01b1

Seq. No.	284089
Contig ID	148478_1.R1011
5'-most EST	uC-zmflmo17044a08a1

Seq. No.	284090
Contig ID	148503_1.R1011
5'-most EST	uC-zmflb73257h08b3

Seq. No.	284091
Contig ID	148504_1.R1011
5'-most EST	uC-zmroteosinte098b11b2

Seq. No.	284092
Contig ID	148512_1.R1011
5'-most EST	wyr700239036.h1
Method	BLASTX
NCBI GI	g1872521
BLAST score	282
E value	2.0e-25
Match length	144
% identity	51
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	284093
Contig ID	148534_1.R1011
5'-most EST	uC-zmroteosinte098e04b2
Method	BLASTX
NCBI GI	g282994
BLAST score	448
E value	2.0e-44
Match length	170
% identity	51
NCBI Description	Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No.	284094
Contig ID	148572_1.R1011
5'-most EST	uC-zmroteosinte098h08b2

Seq. No.	284095
Contig ID	148574_1.R1011

5'-most EST	uC-zmroteosinte098h10b2
Method	BLASTX
NCBI GI	g4377180
BLAST score	516
E value	4.0e-52
Match length	193
% identity	51
NCBI Description	(AE001667) Phosphoglycerate Mutase [Chlamydia pneumoniae]

Seq. No.	284096
Contig ID	148578_1.R1011
5'-most EST	wyr700241449.h1
Method	BLASTX
NCBI GI	g294845
BLAST score	272
E value	6.0e-24
Match length	122
% identity	41
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	284097
Contig ID	148588_1.R1011
5'-most EST	uC-zmroteosinte099b01b2

Seq. No.	284098
Contig ID	148613_1.R1011
5'-most EST	uC-zmroteosinte099d04b2
Method	BLASTX
NCBI GI	g1304227
BLAST score	298
E value	1.0e-26
Match length	161
% identity	42
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	284099
Contig ID	148623_1.R1011
5'-most EST	uC-zmroteosinte099e02b2

Seq. No.	284100
Contig ID	148629_1.R1011
5'-most EST	uC-zmroteosinte106f02b2

Seq. No.	284101
Contig ID	148629_2.R1011
5'-most EST	uC-zmflb73031b08a1

Seq. No.	284102
Contig ID	148637_1.R1011
5'-most EST	yyf700348262.h1

Seq. No.	284103
Contig ID	148683_1.R1011
5'-most EST	uC-zmroteosinte100b06b2

Method	BLASTX
NCBI GI	g2244799
BLAST score	181
E value	4.0e-13
Match length	84
% identity	48
NCBI Description	(Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No.	284104
Contig ID	148761_1.R1011
5'-most EST	uwc700150812.h1
Method	BLASTX
NCBI GI	g4006868
BLAST score	230
E value	9.0e-19
Match length	114
% identity	43
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	284105
Contig ID	148764_1.R1011
5'-most EST	nbm700474347.h1
Method	BLASTX
NCBI GI	g1147632
BLAST score	619
E value	2.0e-64
Match length	190
% identity	72
NCBI Description	(U42208) OSBZ8 [Oryza sativa]

Seq. No.	284106
Contig ID	148768_1.R1011
5'-most EST	fwa700100380.h1
Method	BLASTX
NCBI GI	g1698582
BLAST score	837
E value	6.0e-95
Match length	248
% identity	79
NCBI Description	(U60767) integral membrane protein OsNramp3 [Oryza sativa]

Seq. No.	284107
Contig ID	148778_1.R1011
5'-most EST	uC-zmroteosinte101h01b2
Method	BLASTX
NCBI GI	g1351630
BLAST score	293
E value	2.0e-26
Match length	155
% identity	44
NCBI Description	PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE) >gi_2130253_pir__S62537 hypothetical protein SPAC12G12.06c - fission yeast (Schizosaccharomyces pombe) >gi_1052524_emb_CAA91501_ (Z66568) SPAC12G12.06c, unknown, len: 363 [Schizosaccharomyces pombe]

Seq. No.	284108
Contig ID	148782_1.R1011
5'-most EST	uC-zmroteosinte101h05b2
Method	BLASTX
NCBI GI	g3041855
BLAST score	225
E value	2.0e-18
Match length	45
% identity	78
NCBI Description	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]

Seq. No.	284109
Contig ID	148786_1.R1011
5'-most EST	rvl700454243.h1
Method	BLASTX
NCBI GI	g461899
BLAST score	728
E value	4.0e-77
Match length	171
% identity	78
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No.	284110
Contig ID	148787_1.R1011
5'-most EST	uC-zmroteosinte101h11b2

Seq. No.	284111
Contig ID	148794_1.R1011
5'-most EST	uC-zmroteosinte102a08b2

Seq. No.	284112
Contig ID	148840_1.R1011
5'-most EST	uC-zmflb73372f09a1
Method	BLASTX
NCBI GI	g4539302
BLAST score	188
E value	4.0e-14
Match length	50
% identity	72
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	284113
Contig ID	148848_1.R1011
5'-most EST	uC-zmroteosinte102h09b2
Method	BLASTX
NCBI GI	g3935157
BLAST score	589
E value	6.0e-61
Match length	158
% identity	68
NCBI Description	(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No. 284114
Contig ID 148862_1.R1011
5'-most EST uC-zmroteosinte103c01b2

Seq. No. 284115
Contig ID 148888_1.R1011
5'-most EST xjt700096266.h1

Seq. No. 284116
Contig ID 148939_1.R1011
5'-most EST uC-zmroteosinte118h04b1
Method BLASTX
NCBI GI g2921304
BLAST score 400
E value 8.0e-39
Match length 163
% identity 51
NCBI Description (AF033496) herbicide safener binding protein [Zea mays]

Seq. No. 284117
Contig ID 148945_1.R1011
5'-most EST uC-zmroteosinte104a06b2

Seq. No. 284118
Contig ID 148948_1.R1011
5'-most EST uC-zmroteosinte104a09b2

Seq. No. 284119
Contig ID 148956_1.R1011
5'-most EST gct701175803.h1
Method BLASTX
NCBI GI g3341443
BLAST score 511
E value 8.0e-52
Match length 175
% identity 58
NCBI Description (AJ223074) acid phosphatase [Glycine max]

Seq. No. 284120
Contig ID 148959_1.R1011
5'-most EST uC-zmroteosinte104b08b2
Method BLASTX
NCBI GI g2108252
BLAST score 195
E value 7.0e-15
Match length 58
% identity 32
NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 284121
Contig ID 148962_1.R1011
5'-most EST uC-zmroteosinte104b11b2

Seq. No.	284122
Contig ID	149006_1.R1011
5'-most EST	dyk700104515.h1
Seq. No.	284123
Contig ID	149028_1.R1011
5'-most EST	uC-zmroteosinte104h10b2
Seq. No.	284124
Contig ID	149090_1.R1011
5'-most EST	uC-zmroteosinte105f04b1
Seq. No.	284125
Contig ID	149103_1.R1011
5'-most EST	uC-zmroteosinte105g06b1
Method	BLASTX
NCBI GI	g2921304
BLAST score	436
E value	4.0e-43
Match length	171
% identity	54
NCBI Description	(AF033496) herbicide safener binding protein [Zea mays]
Seq. No.	284126
Contig ID	149116_1.R1011
5'-most EST	dyk700104633.h1
Method	BLASTX
NCBI GI	g3522961
BLAST score	159
E value	5.0e-21
Match length	122
% identity	47
NCBI Description	(AC004411) putative pto kinase [Arabidopsis thaliana]
Seq. No.	284127
Contig ID	149168_1.R1011
5'-most EST	nbm700468783.h1
Method	BLASTX
NCBI GI	g3287695
BLAST score	314
E value	7.0e-29
Match length	144
% identity	42
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]
Seq. No.	284128
Contig ID	149171_1.R1011
5'-most EST	uC-zmroteosinte106e12b2
Seq. No.	284129
Contig ID	149174_1.R1011
5'-most EST	uC-zmroteosinte106f03b2
Method	BLASTX
NCBI GI	g4415933
BLAST score	452

E value	7.0e-45
Match length	180
% identity	51
NCBI Description	(AC006418) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana]

Seq. No.	284130
Contig ID	149181_1.R1011
5'-most EST	wyr700237765.h1

Seq. No.	284131
Contig ID	149250_1.R1011
5'-most EST	dyk700104479.h1
Method	BLASTX
NCBI GI	g4468798
BLAST score	311
E value	2.0e-28
Match length	90
% identity	61
NCBI Description	(AJ010440) GST7 protein [Zea mays]

Seq. No.	284132
Contig ID	149342_1.R1011
5'-most EST	uC-zmroteosinte109c09b3
Method	BLASTX
NCBI GI	g1402916
BLAST score	239
E value	1.0e-20
Match length	109
% identity	56
NCBI Description	(X98319) peroxidase [Arabidopsis thaliana] >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a [Arabidopsis thaliana]

Seq. No.	284133
Contig ID	149347_1.R1011
5'-most EST	uC-zmroteosinte109c02b3

Seq. No.	284134
Contig ID	149350_1.R1011
5'-most EST	uC-zmroteosinte109c05b3
Method	BLASTX
NCBI GI	g3451069
BLAST score	659
E value	6.0e-69
Match length	247
% identity	55
NCBI Description	(AL031326) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284135
Contig ID	149360_1.R1011
5'-most EST	tfd700571126.h1

Seq. No.	284136

Contig ID	149368_1.R1011
5'-most EST	uC-zmflmo17428e02a1
Seq. No.	284137
Contig ID	149372_1.R1011
5'-most EST	xjt700095418.h1
Seq. No.	284138
Contig ID	149436_1.R1011
5'-most EST	uC-zmroteosinte115b10b1
Seq. No.	284139
Contig ID	149469_1.R1011
5'-most EST	uC-zmroteosinte115e10b1
Seq. No.	284140
Contig ID	149502_1.R1011
5'-most EST	uC-zmroteosinte115h07b1
Seq. No.	284141
Contig ID	149526_2.R1011
5'-most EST	sem700930122.h1
Seq. No.	284142
Contig ID	149541_1.R1011
5'-most EST	pmx700085785.h1
Seq. No.	284143
Contig ID	149575_1.R1011
5'-most EST	uC-zmroteosinte117b05b2
Method	BLASTX
NCBI GI	g4567304
BLAST score	485
E value	9.0e-49
Match length	162
% identity	57
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.	284144
Contig ID	149581_1.R1011
5'-most EST	uC-zmroteosinte117a07b2
Method	BLASTX
NCBI GI	g3878874
BLAST score	319
E value	3.0e-29
Match length	156
% identity	46
NCBI Description	(Z69793) R03A10.3 [Caenorhabditis elegans]
Seq. No.	284145
Contig ID	149614_1.R1011
5'-most EST	uC-zmroteosinte117c02b2
Seq. No.	284146
Contig ID	149720_1.R1011
5'-most EST	pmx700082196.h1
Method	BLASTX

NCBI GI	g3860251
BLAST score	404
E value	3.0e-39
Match length	153
% identity	54
NCBI Description	(AC005824) putative permease [Arabidopsis thaliana]

Seq. No.	284147
Contig ID	149784_1.R1011
5'-most EST	uC-zmroteosinte120a07b2
Method	BLASTX
NCBI GI	g4220541
BLAST score	459
E value	2.0e-45
Match length	171
% identity	55
NCBI Description	(AL035356) Rab geranylgeranyl transferase like protein [Arabidopsis thaliana]

Seq. No.	284148
Contig ID	149825_1.R1011
5'-most EST	uC-zmroteosinte119b12b1

Seq. No.	284149
Contig ID	149842_1.R1011
5'-most EST	uC-zmroteosinte119c09b2
Method	BLASTN
NCBI GI	g507844
BLAST score	55
E value	7.0e-22
Match length	190
% identity	83
NCBI Description	Zea mays A188 retrotransposon gag gene, complete cds

Seq. No.	284150
Contig ID	149846_1.R1011
5'-most EST	uC-zmroteosinte119c11b2

Seq. No.	284151
Contig ID	149849_1.R1011
5'-most EST	uC-zmroteosinte120d03b2

Seq. No.	284152
Contig ID	149861_1.R1011
5'-most EST	uC-zmroteosinte119d09b2
Method	BLASTX
NCBI GI	g4504369
BLAST score	299
E value	5.0e-27
Match length	164
% identity	42
NCBI Description	rad2 nuclease family member, homolog of S. cerevisiae exonuclease 1 >gi_3170238 (AF042282) Hex1 [Homo sapiens] >gi_3703096 (AF091740) exonuclease 1a [Homo sapiens]

Seq. No.	284153
Contig ID	149866_1.R1011

5'-most EST	uC-zmroteosinte120c10b1
Seq. No.	284154
Contig ID	149867_1.R1011
5'-most EST	uC-zmroteosinte120e07b2
Seq. No.	284155
Contig ID	149879_1.R1011
5'-most EST	uC-zmroteosinte119e07b2
Method	BLASTN
NCBI GI	g3851004
BLAST score	40
E value	5.0e-13
Match length	68
% identity	90
NCBI Description	Zea mays pyruvate dehydrogenase E1 alpha subunit RNA, nuclear gene encoding mitochondrial protein, complete cds
Seq. No.	284156
Contig ID	149884_1.R1011
5'-most EST	wyr700240244.h1
Method	BLASTX
NCBI GI	g2465430
BLAST score	190
E value	5.0e-17
Match length	137
% identity	38
NCBI Description	(AF021258) 32 kDa protein [Hordeum vulgare]
Seq. No.	284157
Contig ID	149924_1.R1011
5'-most EST	uC-zmroteosinte119g08b2
Method	BLASTX
NCBI GI	g3152595
BLAST score	526
E value	1.0e-53
Match length	134
% identity	78
NCBI Description	(AC002986) Similar to D. melanogaster sno gene gb_U95760. EST gb_N97148 and gb_Z26221 come from this gene. [Arabidopsis thaliana]
Seq. No.	284158
Contig ID	149949_1.R1011
5'-most EST	uC-zmroteosinte119h11b1
Seq. No.	284159
Contig ID	149950_1.R1011
5'-most EST	uC-zmroteosinte120h11b1
Seq. No.	284160
Contig ID	150166_1.R1011
5'-most EST	uC-zmflmo17302a10a1
Method	BLASTX
NCBI GI	g3142300
BLAST score	285
E value	2.0e-25

Match length	90
% identity	60
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	284161
Contig ID	150175_1.R1011
5'-most EST	fC-zmfl1700342151f1
Method	BLASTN
NCBI GI	g2832242
BLAST score	233
E value	1.0e-128
Match length	328
% identity	47
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	284162
Contig ID	150181_1.R1011
5'-most EST	fC-zmfl700342321a5

Seq. No.	284163
Contig ID	150195_1.R1011
5'-most EST	fC-zmfl700342738f4
Method	BLASTX
NCBI GI	g3913240
BLAST score	897
E value	6.0e-97
Match length	200
% identity	89
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi_2239151_emb_CAA71128_ (Y10022) CHLD magnesium chelatase subunit [Nicotiana tabacum]

Seq. No.	284164
Contig ID	150213_1.R1011
5'-most EST	uC-zmflb73122h12a1

Seq. No.	284165
Contig ID	150221_1.R1011
5'-most EST	fC-zmfl700343101a1
Method	BLASTX
NCBI GI	g3790188
BLAST score	383
E value	8.0e-37
Match length	103
% identity	76
NCBI Description	(Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana tabacum]

Seq. No.	284166
Contig ID	150229_1.R1011
5'-most EST	fC-zmfl700343353a4

Seq. No. 284167

Contig ID	150231_1.R1011
5'-most EST	pmx700087532.h1

Seq. No.	284168
Contig ID	150372_1.R1011
5'-most EST	fC-zmro700830206r3

Seq. No.	284169
Contig ID	150394_1.R1011
5'-most EST	fC-zmst700335976h1
Method	BLASTX
NCBI GI	g4126403
BLAST score	529
E value	9.0e-54
Match length	142
% identity	66
NCBI Description	(AB011796) flavonol synthase [Citrus unshiu]

Seq. No.	284170
Contig ID	150396_1.R1011
5'-most EST	fC-zmfl700342745z1
Method	BLASTX
NCBI GI	g3668091
BLAST score	217
E value	2.0e-17
Match length	157
% identity	7
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284171
Contig ID	150461_1.R1011
5'-most EST	fC-zmfl700343407g1
Method	BLASTX
NCBI GI	g4544445
BLAST score	485
E value	2.0e-48
Match length	120
% identity	74
NCBI Description	(AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]

Seq. No.	284172
Contig ID	150467_1.R1011
5'-most EST	fC-zmfl700343788r3
Method	BLASTX
NCBI GI	g4056437
BLAST score	152
E value	1.0e-09
Match length	68
% identity	47
NCBI Description	(AC005990) Strong similarity to PFAM PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	284173
Contig ID	150481_1.R1011
5'-most EST	fC-zmro700569159a1

Seq. No.	284174
Contig ID	150521_1.R1011
5'-most EST	fC-zmfl700345340z1
Method	BLASTX
NCBI GI	g4204849
BLAST score	524
E value	2.0e-53
Match length	122
% identity	80
NCBI Description	(U55875) protein kinase [Arabidopsis thaliana]

Seq. No.	284175
Contig ID	150571_1.R1011
5'-most EST	nbm700470515.h1
Method	BLASTX
NCBI GI	g2464864
BLAST score	779
E value	2.0e-82
Match length	520
% identity	33
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	284176
Contig ID	150585_1.R1011
5'-most EST	pwr700450602.h1
Method	BLASTX
NCBI GI	g2529229
BLAST score	618
E value	2.0e-64
Match length	183
% identity	67
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	284177
Contig ID	150656_1.R1011
5'-most EST	fC-zmfl700349349r3

Seq. No.	284178
Contig ID	150677_1.R1011
5'-most EST	fC-zmfl700350418z1
Method	BLASTX
NCBI GI	g2414579
BLAST score	162
E value	3.0e-11
Match length	46
% identity	63
NCBI Description	(Z99292) flavoprotein [Schizosaccharomyces pombe]

Seq. No.	284179
Contig ID	150682_1.R1011
5'-most EST	fC-zmfl700350123g1
Method	BLASTX
NCBI GI	g4559351
BLAST score	262
E value	4.0e-22
Match length	248
% identity	30

NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284180
Contig ID	150702_1.R1011
5'-most EST	fC-zmro700833740a5
Method	BLASTX
NCBI GI	g1362078
BLAST score	1034
E value	1.0e-112
Match length	258
% identity	70
NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi_311835_emb_CAA48324_ (X68254) cellulase [Tropaeolum majus]

Seq. No.	284181
Contig ID	150710_1.R1011
5'-most EST	fC-zmfl700350656a3

Seq. No.	284182
Contig ID	150797_1.R1011
5'-most EST	tfd700570411.h1

Seq. No.	284183
Contig ID	150818_1.R1011
5'-most EST	fC-zmst700620948d1

Seq. No.	284184
Contig ID	150872_1.R1011
5'-most EST	fC-zmst700621688d1
Method	BLASTX
NCBI GI	g4210330
BLAST score	581
E value	6.0e-60
Match length	139
% identity	76
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	284185
Contig ID	150875_1.R1011
5'-most EST	wen700334889.h1
Method	BLASTX
NCBI GI	g1171429
BLAST score	387
E value	5.0e-37
Match length	131
% identity	56
NCBI Description	(U44028) CKC [Arabidopsis thaliana]

Seq. No.	284186
Contig ID	150876_1.R1011
5'-most EST	fC-zmfl700352302b1

Seq. No.	284187
Contig ID	150894_1.R1011
5'-most EST	fC-zmst700455785f1

Method	BLASTX
NCBI GI	g134804
BLAST score	1094
E value	1.0e-120
Match length	324
% identity	69
NCBI Description	ARGININE DECARBOXYLASE (ARGDC) (ADC) >gi_100543_pir__S12265 arginine decarboxylase - oat >gi_16120_emb_CAA40137_ (X56802) arginine decarboxylase [Avena sativa]

Seq. No.	284188
Contig ID	150940_1.R1011
5'-most EST	fC-zmfl700354316f1

Seq. No.	284189
Contig ID	150941_1.R1011
5'-most EST	fC-zmfl700354316b1

Seq. No.	284190
Contig ID	150945_1.R1011
5'-most EST	fC-zmfl700354316i1
Method	BLASTX
NCBI GI	g2982462
BLAST score	248
E value	6.0e-21
Match length	82
% identity	60
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	284191
Contig ID	151025_1.R1011
5'-most EST	pmx700083186.h1

Seq. No.	284192
Contig ID	151128_1.R1011
5'-most EST	fC-zmfl700380180f2
Method	BLASTX
NCBI GI	g3738328
BLAST score	612
E value	2.0e-63
Match length	151
% identity	72
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	284193
Contig ID	151143_1.R1011
5'-most EST	fC-zmfl700381110d2

Seq. No.	284194
Contig ID	151184_1.R1011
5'-most EST	nbm700473306.h1
Method	BLASTX
NCBI GI	g4107003
BLAST score	596
E value	8.0e-62
Match length	124

% identity	91
NCBI Description	(D82036) OSK5 [Oryza sativa] >gi_4107007_dbj_BAA36297_ (D82038) OSK3 [Oryza sativa]

Seq. No.	284195
Contig ID	151188_1.R1011
5'-most EST	fC-zmst700454849r1
Method	BLASTX
NCBI GI	g1477684
BLAST score	265
E value	5.0e-23
Match length	59
% identity	86
NCBI Description	(U55768) SNF1-related protein kinase [Oryza sativa]

Seq. No.	284196
Contig ID	151215_1.R1011
5'-most EST	qmh700029330.f1

Seq. No.	284197
Contig ID	151234_1.R1011
5'-most EST	fC-zmfl700382427r5

Seq. No.	284198
Contig ID	151285_1.R1011
5'-most EST	fC-zmfl700383036r3

Seq. No.	284199
Contig ID	151292_1.R1011
5'-most EST	fC-zmfl700464948a2
Method	BLASTX
NCBI GI	g2191182
BLAST score	374
E value	7.0e-36
Match length	154
% identity	27
NCBI Description	(AF007271) similar to N. tabacum membrane-associated salt-inducible protein (PID:g473874) [Arabidopsis thaliana]

Seq. No.	284200
Contig ID	151296_1.R1011
5'-most EST	fC-zmfl700465148a2
Method	BLASTX
NCBI GI	g1710124
BLAST score	560
E value	1.0e-57
Match length	121
% identity	83
NCBI Description	(U62279) leucine-rich repeat-containing extracellular glycoprotein; contains six N-glycosylation sites [NX(S/T)] [Sorghum bicolor]

Seq. No.	284201
Contig ID	151298_1.R1011
5'-most EST	fC-zmfl700465282a2
Method	BLASTX
NCBI GI	g2654870

BLAST score	746
E value	2.0e-79
Match length	157
% identity	86
NCBI Description	(AF015302) RbohAOsp [Oryza sativa]

Seq. No.	284202
Contig ID	151305_1.R1011
5'-most EST	fdz701167007.h1

Seq. No.	284203
Contig ID	151315_1.R1011
5'-most EST	fC-zmfl700467714a2

Seq. No.	284204
Contig ID	151320_1.R1011
5'-most EST	fC-zmfl700467913a2
Method	BLASTX
NCBI GI	g1931651
BLAST score	194
E value	9.0e-15
Match length	62
% identity	66
NCBI Description	(U95973) membrane-associated salt-inducible protein isolog [Arabidopsis thaliana]

Seq. No.	284205
Contig ID	151325_1.R1011
5'-most EST	cyk700049131.f1

Seq. No.	284206
Contig ID	151330_1.R1011
5'-most EST	fC-zmfl700468220a2
Method	BLASTN
NCBI GI	g886741
BLAST score	373
E value	0.0e+00
Match length	442
% identity	96
NCBI Description	Z.mays mRNA for heat shock factor

Seq. No.	284207
Contig ID	151357_1.R1011
5'-most EST	fC-zmfl700469566a2
Method	BLASTX
NCBI GI	g2224911
BLAST score	289
E value	5.0e-26
Match length	127
% identity	53
NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No.	284208
Contig ID	151372_1.R1011
5'-most EST	uC-zmflb73228b01a1
Method	BLASTX

NCBI GI	g3885334
BLAST score	615
E value	6.0e-64
Match length	154
% identity	72
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	284209
Contig ID	151372_2.R1011
5'-most EST	fC-zmfl700470902r9

Seq. No.	284210
Contig ID	151373_1.R1011
5'-most EST	fC-zmfl700470945b1
Method	BLASTX
NCBI GI	g1703201
BLAST score	323
E value	6.0e-30
Match length	95
% identity	64
NCBI Description	PROTEIN KINASE AFC3 >gi_601791 (U16178) protein kinase [Arabidopsis thaliana]

Seq. No.	284211
Contig ID	151391_1.R1011
5'-most EST	fC-zmfl700472680d4

Seq. No.	284212
Contig ID	151416_1.R1011
5'-most EST	fC-zmfl700548428r3

Seq. No.	284213
Contig ID	151427_1.R1011
5'-most EST	fC-zmfl700549224a1
Method	BLASTX
NCBI GI	g2851577
BLAST score	784
E value	7.0e-84
Match length	180
% identity	78
NCBI Description	SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-MIII) >gi_1877219_emb_CAA70817_ (Y09604) serine carboxypeptidase III, CP-MIII [Hordeum vulgare]

Seq. No.	284214
Contig ID	151439_1.R1011
5'-most EST	fC-zmfl700550135a1
Method	BLASTX
NCBI GI	g1076315
BLAST score	220
E value	8.0e-18
Match length	157
% identity	32
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)

CYP90 protein [Arabidopsis thaliana]

Seq. No.	284215
Contig ID	151440_1.R1011
5'-most EST	fC-zmfl700550135d4
Method	BLASTX
NCBI GI	g2935342
BLAST score	224
E value	3.0e-18
Match length	74
% identity	55
NCBI Description	(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 [Arabidopsis thaliana]

Seq. No.	284216
Contig ID	151441_1.R1011
5'-most EST	fC-zmfl700550149r3

Seq. No.	284217
Contig ID	151447_1.R1011
5'-most EST	fC-zmfl700550363f3
Method	BLASTX
NCBI GI	g1431870
BLAST score	248
E value	3.0e-21
Match length	116
% identity	41
NCBI Description	(U43904) ent-kaurene synthase B [Cucurbita maxima]

Seq. No.	284218
Contig ID	151449_1.R1011
5'-most EST	fC-zmfl700550537r3

Seq. No.	284219
Contig ID	151450_1.R1011
5'-most EST	fC-zmfl700550602a1
Method	BLASTX
NCBI GI	g3056725
BLAST score	186
E value	1.0e-13
Match length	122
% identity	39
NCBI Description	(AF034774) ent-kaurene synthase [Arabidopsis thaliana]

Seq. No.	284220
Contig ID	151466_1.R1011
5'-most EST	fC-zmfl700551429a1
Method	BLASTX
NCBI GI	g417073
BLAST score	316
E value	5.0e-29
Match length	94
% identity	72
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	284221
Contig ID	151467_1.R1011
5'-most EST	fC-zmfl700551429b1

Seq. No.	284222
Contig ID	151477_1.R1011
5'-most EST	fC-zmfl700552263a1
Method	BLASTX
NCBI GI	g4512659
BLAST score	572
E value	5.0e-59
Match length	156
% identity	69
NCBI Description	(AC006931) putative protein kinase [Arabidopsis thaliana] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No.	284223
Contig ID	151478_1.R1011
5'-most EST	uC-zmflmo17382f07a1

Seq. No.	284224
Contig ID	151481_1.R1011
5'-most EST	fC-zmfl700552479b1

Seq. No.	284225
Contig ID	151484_1.R1011
5'-most EST	rvt700552544.h1
Method	BLASTN
NCBI GI	g22430
BLAST score	128
E value	1.0e-65
Match length	469
% identity	48
NCBI Description	Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate dehydrogenase subunit A

Seq. No.	284226
Contig ID	151495_1.R1011
5'-most EST	fC-zmfl700552735d4

Seq. No.	284227
Contig ID	151498_1.R1011
5'-most EST	fC-zmfl700552755r3

Seq. No.	284228
Contig ID	151501_1.R1011
5'-most EST	fC-zmfl700552771d4

Seq. No.	284229
Contig ID	151504_1.R1011
5'-most EST	fC-zmfl700552895a1
Method	BLASTX
NCBI GI	g1220453
BLAST score	391
E value	4.0e-46

Match length	150
% identity	57
NCBI Description	(M79328) alpha-amylase [Solanum tuberosum]

Seq. No.	284230
Contig ID	151507_1.R1011
5'-most EST	fC-zmfl700552946f3
Method	BLASTX
NCBI GI	g642134
BLAST score	223
E value	4.0e-21
Match length	94
% identity	64
NCBI Description	(D45355) protein kinase [Arabidopsis thaliana] >gi_3063704_emb_CAA18595.1_ (AL022537) protein kinase AME3 [Arabidopsis thaliana]

Seq. No.	284231
Contig ID	151533_1.R1011
5'-most EST	fC-zmfl700553382b1
Method	BLASTX
NCBI GI	g4376158
BLAST score	406
E value	2.0e-39
Match length	117
% identity	71
NCBI Description	(X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No.	284232
Contig ID	151534_1.R1011
5'-most EST	kem700610753.h1

Seq. No.	284233
Contig ID	151535_1.R1011
5'-most EST	fC-zmfl700610753r1

Seq. No.	284234
Contig ID	151541_1.R1011
5'-most EST	fC-zmfl700612166r1
Method	BLASTX
NCBI GI	g4544445
BLAST score	408
E value	1.0e-39
Match length	90
% identity	82
NCBI Description	(AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]

Seq. No.	284235
Contig ID	151542_1.R1011
5'-most EST	fC-zmst700619081a1
Method	BLASTX
NCBI GI	g2462749
BLAST score	361
E value	2.0e-34
Match length	112
% identity	65

NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	284236
Contig ID	151545_1.R1011
5'-most EST	fC-zmfl700610957a1
Method	BLASTN
NCBI GI	g2198852
BLAST score	39
E value	2.0e-12
Match length	67
% identity	90
NCBI Description	Zea mays cystathionine gamma-synthase (CGS1) gene, complete cds

Seq. No.	284237
Contig ID	151566_1.R1011
5'-most EST	fC-zmfl700611267a1
Method	BLASTX
NCBI GI	g3355308
BLAST score	263
E value	4.0e-28
Match length	157
% identity	50
NCBI Description	(AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]

Seq. No.	284238
Contig ID	151568_1.R1011
5'-most EST	fC-zmfl700611718a1
Method	BLASTX
NCBI GI	g282882
BLAST score	198
E value	5.0e-15
Match length	110
% identity	39
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166848 (M84659) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	284239
Contig ID	151600_1.R1011
5'-most EST	fC-zmfl700905152g1
Method	BLASTX
NCBI GI	g4126403
BLAST score	507
E value	2.0e-74
Match length	250
% identity	53
NCBI Description	(AB011796) flavonol synthase [Citrus unshiu]

Seq. No.	284240
Contig ID	151635_1.R1011
5'-most EST	wyr700243248.h1

Seq. No.	284241
Contig ID	151646_1.R1011
5'-most EST	fC-zmle700207342a1

Method	BLASTX
NCBI GI	g2213614
BLAST score	144
E value	6.0e-09
Match length	119
% identity	37
NCBI Description	(AC000103) F21J9.8 [Arabidopsis thaliana]

Seq. No.	284242
Contig ID	151666_1.R1011
5'-most EST	fC-zmle700421686f2
Method	BLASTX
NCBI GI	g282882
BLAST score	166
E value	2.0e-11
Match length	80
% identity	45
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166848 (M84659) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	284243
Contig ID	151723_1.R1011
5'-most EST	nwy700447087.h1
Method	BLASTX
NCBI GI	g4510424
BLAST score	462
E value	1.0e-45
Match length	200
% identity	47
NCBI Description	(AC006929) putative carboxypeptidase [Arabidopsis thaliana]

Seq. No.	284244
Contig ID	151731_1.R1011
5'-most EST	fC-zmle700423591f2
Method	BLASTX
NCBI GI	g2499708
BLAST score	381
E value	2.0e-39
Match length	131
% identity	66
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea mays]

Seq. No.	284245
Contig ID	151738_1.R1011
5'-most EST	fC-zmle700423687d2

Seq. No.	284246
Contig ID	151766_1.R1011
5'-most EST	fC-zmle700424174a1

Seq. No.	284247
Contig ID	151772_1.R1011
5'-most EST	fC-zmle700424186r3

Method	BLASTX
NCBI GI	g2129552
BLAST score	245
E value	9.0e-21
Match length	55
% identity	84
NCBI Description	calcium-dependent protein kinase 19 - Arabidopsis thaliana (fragment)

Seq. No.	284248
Contig ID	151786_1.R1011
5'-most EST	fC-zmle700424546f2
Method	BLASTX
NCBI GI	g2586087
BLAST score	293
E value	2.0e-26
Match length	145
% identity	46
NCBI Description	(U72724) receptor kinase-like protein [Oryza sativa]

Seq. No.	284249
Contig ID	151787_1.R1011
5'-most EST	fC-zmle700424546r3

Seq. No.	284250
Contig ID	151807_1.R1011
5'-most EST	fC-zmle700425046f2
Method	BLASTX
NCBI GI	g3063445
BLAST score	173
E value	3.0e-12
Match length	103
% identity	39
NCBI Description	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq. No.	284251
Contig ID	151848_1.R1011
5'-most EST	fC-zmle700426833f2

Seq. No.	284252
Contig ID	151862_1.R1011
5'-most EST	fC-zmle700426995a1

Seq. No.	284253
Contig ID	151915_1.R1011
5'-most EST	fC-zmle700427941a1
Method	BLASTN
NCBI GI	g4416300
BLAST score	47
E value	2.0e-17
Match length	87
% identity	48
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	284254
Contig ID	151916_1.R1011

5'-most EST	zla700380701.h1
Method	BLASTX
NCBI GI	g2342860
BLAST score	261
E value	2.0e-22
Match length	136
% identity	40
NCBI Description	(U67168) E4/E8 binding protein-1 [Lycopersicon esculentum]

Seq. No.	284255
Contig ID	151921_1.R1011
5'-most EST	uC-zmflmo17418b11a1
Method	BLASTX
NCBI GI	g2801536
BLAST score	241
E value	4.0e-20
Match length	62
% identity	68
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	284256
Contig ID	151923_1.R1011
5'-most EST	tfd700570035.h1
Method	BLASTX
NCBI GI	g3914365
BLAST score	1270
E value	1.0e-140
Match length	278
% identity	84
NCBI Description	PHOSPHOLIPASE D 2 PRECURSOR (PLD 2) (CHOLINE PHOSPHATASE 2) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 2) >gi_1902901_dbj_BAA19466_ (AB001919) phospholipase D [Oryza sativa]

Seq. No.	284257
Contig ID	151929_1.R1011
5'-most EST	fC-zmle700432434d3

Seq. No.	284258
Contig ID	151930_1.R1011
5'-most EST	fC-zmle700428130r6

Seq. No.	284259
Contig ID	151942_1.R1011
5'-most EST	fC-zmle700428147r2
Method	BLASTX
NCBI GI	g4585908
BLAST score	291
E value	2.0e-35
Match length	111
% identity	68
NCBI Description	(AC006298) putative lysosomal acid lipase [Arabidopsis thaliana]

Seq. No.	284260
Contig ID	151963_1.R1011
5'-most EST	fC-zmro700451154f1

Method	BLASTX
NCBI GI	g113951
BLAST score	419
E value	5.0e-41
Match length	80
% identity	100
NCBI Description	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi_71763_pir__LUMS36 annexin II - mouse >gi_220555_dbj_BAA00914_ (D10024) protein-tyrosine kinase substrate p36 [Mus musculus] >gi_309133 (M14044) calpactin I heavy chain (p36) [Mus musculus]

Seq. No.	284261
Contig ID	151972_1.R1011
5'-most EST	fC-zmro700451040r1

Seq. No.	284262
Contig ID	151992_1.R1011
5'-most EST	fC-zmle700428888a1
Method	BLASTN
NCBI GI	g22302
BLAST score	119
E value	2.0e-60
Match length	264
% identity	76
NCBI Description	Maize Gpc1 gene for glyceraldehyde-3-phosphate dehydrogenase (GADPH) subunit C

Seq. No.	284263
Contig ID	151993_1.R1011
5'-most EST	fC-zmle700428888d3
Method	BLASTX
NCBI GI	g4587987
BLAST score	179
E value	5.0e-13
Match length	62
% identity	55
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No.	284264
Contig ID	152008_1.R1011
5'-most EST	qmh700029529.f1
Method	BLASTX
NCBI GI	g3860264
BLAST score	578
E value	1.0e-59
Match length	142
% identity	73
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	284265
Contig ID	152009_1.R1011
5'-most EST	uer700580536.h1
Method	BLASTX
NCBI GI	g3860264

BLAST score	341
E value	6.0e-32
Match length	92
% identity	67
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	284266
Contig ID	152016_1.R1011
5'-most EST	fC-zmle700434272r2
Method	BLASTX
NCBI GI	g2252860
BLAST score	153
E value	5.0e-10
Match length	134
% identity	35
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	284267
Contig ID	152017_1.R1011
5'-most EST	nwy700444171.h1
Method	BLASTX
NCBI GI	g2832304
BLAST score	417
E value	8.0e-41
Match length	101
% identity	77
NCBI Description	(AF044489) receptor-like protein kinase [Oryza sativa]

Seq. No.	284268
Contig ID	152027_1.R1011
5'-most EST	fC-zmle700429434r4

Seq. No.	284269
Contig ID	152034_1.R1011
5'-most EST	fC-zmle700429795b1

Seq. No.	284270
Contig ID	152040_1.R1011
5'-most EST	fC-zmle700429868a1
Method	BLASTX
NCBI GI	g3135274
BLAST score	350
E value	4.0e-33
Match length	131
% identity	50
NCBI Description	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	284271
Contig ID	152048_1.R1011
5'-most EST	ceu700429881.h1
Method	BLASTX
NCBI GI	g1076634
BLAST score	310
E value	1.0e-28
Match length	94
% identity	69

NCBI Description	protein-serine/threonine kinase NPK15 - common tobacco >gi_505146_dbj_BAA06538_ (D31737) protein-serine/threonine kinase [Nicotiana tabacum]

Seq. No.	284272
Contig ID	152050_1.R1011
5'-most EST	fC-zmle700429881b1
Method	BLASTX
NCBI GI	g1076634
BLAST score	164
E value	3.0e-11
Match length	74
% identity	41
NCBI Description	protein-serine/threonine kinase NPK15 - common tobacco >gi_505146_dbj_BAA06538_ (D31737) protein-serine/threonine kinase [Nicotiana tabacum]

Seq. No.	284273
Contig ID	152075_1.R1011
5'-most EST	fC-zmle700430083r4

Seq. No.	284274
Contig ID	152084_1.R1011
5'-most EST	fC-zmro700452322f1
Method	BLASTX
NCBI GI	g1888357
BLAST score	296
E value	1.0e-26
Match length	120
% identity	53
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	284275
Contig ID	152091_1.R1011
5'-most EST	fC-zmle700445574b1

Seq. No.	284276
Contig ID	152102_1.R1011
5'-most EST	fC-zmle700439325r3
Method	BLASTX
NCBI GI	g2494089
BLAST score	401
E value	6.0e-39
Match length	87
% identity	90
NCBI Description	DIHYDRODIPICOLINATE SYNTHASE PRECURSOR (DHDPS) >gi_1432156 (U61730) dihydrodipicolinate synthase [Coix lacryma-jobi]

Seq. No.	284277
Contig ID	152112_1.R1011
5'-most EST	cat700017177.r1
Method	BLASTX
NCBI GI	g2244993
BLAST score	394
E value	4.0e-38

Match length	133
% identity	51
NCBI Description	(Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No.	284278
Contig ID	152118_1.R1011
5'-most EST	fC-zmro700452607f1

Seq. No.	284279
Contig ID	152127_1.R1011
5'-most EST	fC-zmle700431109a4
Method	BLASTX
NCBI GI	g2781357
BLAST score	550
E value	4.0e-56
Match length	146
% identity	68
NCBI Description	(AC003113) F24O1.13 [Arabidopsis thaliana]

Seq. No.	284280
Contig ID	152157_1.R1011
5'-most EST	fC-zmle700431563a4
Method	BLASTX
NCBI GI	g3236253
BLAST score	794
E value	5.0e-85
Match length	192
% identity	76
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	284281
Contig ID	152159_1.R1011
5'-most EST	fC-zmle700431563r3
Method	BLASTX
NCBI GI	g3236253
BLAST score	278
E value	1.0e-24
Match length	136
% identity	46
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	284282
Contig ID	152187_1.R1011
5'-most EST	fC-zmle700431965d3
Method	BLASTX
NCBI GI	g4455218
BLAST score	146
E value	3.0e-09
Match length	88
% identity	47
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	284283
Contig ID	152215_1.R1011

5'-most EST	rvl700455261.h1
Method	BLASTX
NCBI GI	g4091008
BLAST score	372
E value	1.0e-43
Match length	158
% identity	59
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	284284
Contig ID	152217_1.R1011
5'-most EST	fC-zmle700432191r3
Method	BLASTX
NCBI GI	g4091008
BLAST score	343
E value	3.0e-32
Match length	82
% identity	79
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	284285
Contig ID	152237_1.R1011
5'-most EST	fC-zmle700432434a4
Method	BLASTX
NCBI GI	g2792155
BLAST score	511
E value	7.0e-52
Match length	158
% identity	58
NCBI Description	(AJ223291) chalcone reductase [Sesbania rostrata]

Seq. No.	284286
Contig ID	152250_1.R1011
5'-most EST	uC-zmflmo17135c02a1
Method	BLASTN
NCBI GI	g1568532
BLAST score	63
E value	7.0e-27
Match length	91
% identity	95
NCBI Description	T.aestivum gene for transfer RNA-Tyr (pTty4)

Seq. No.	284287
Contig ID	152318_1.R1011
5'-most EST	uC-zmflb73300a05a1

Seq. No.	284288
Contig ID	152323_1.R1011
5'-most EST	fC-zmst700455187f1

Seq. No.	284289
Contig ID	152325_1.R1011
5'-most EST	fC-zmle700434174b1

Seq. No.	284290
Contig ID	152333_1.R1011
5'-most EST	fC-zmle700434272a3

Method	BLASTX
NCBI GI	g1076755
BLAST score	582
E value	3.0e-60
Match length	168
% identity	68
NCBI Description	protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]

Seq. No.	284291
Contig ID	152339_1.R1011
5'-most EST	uC-zmflmo17037g07a1
Method	BLASTX
NCBI GI	g1076755
BLAST score	300
E value	2.0e-27
Match length	79
% identity	75
NCBI Description	protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]

Seq. No.	284292
Contig ID	152340_1.R1011
5'-most EST	fC-zmst700455422f1
Method	BLASTX
NCBI GI	g2493494
BLAST score	222
E value	6.0e-18
Match length	92
% identity	48
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa]

Seq. No.	284293
Contig ID	152372_1.R1011
5'-most EST	uer700578255.h1

Seq. No.	284294
Contig ID	152392_1.R1011
5'-most EST	fC-zmst700456113f1

Seq. No.	284295
Contig ID	152402_1.R1011
5'-most EST	fC-zmle700439325a4
Method	BLASTX
NCBI GI	g118237
BLAST score	177
E value	9.0e-22
Match length	102
% identity	57
NCBI Description	DIHYDRODIPICOLINATE SYNTHASE 2 PRECURSOR (DHDPS) >gi_68225_pir__WZWTH6 dihydrodipicolinate synthase (EC 4.2.1.52) precursor (clone pDA26) - wheat >gi_170682 (M60599) dihydrodipicolinate synthase [Triticum aestivum]

Seq. No.	284296
Contig ID	152428_1.R1011
5'-most EST	fC-zmle700440270r4

Seq. No.	284297
Contig ID	152431_1.R1011
5'-most EST	fC-zmle700440385a3
Method	BLASTX
NCBI GI	g1017706
BLAST score	262
E value	9.0e-23
Match length	148
% identity	40
NCBI Description	(U17901) PLAP [Rattus norvegicus]

Seq. No.	284298
Contig ID	152441_1.R1011
5'-most EST	uC-zmrob73044g02a1
Method	BLASTX
NCBI GI	g4490297
BLAST score	260
E value	1.0e-22
Match length	96
% identity	48
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	284299
Contig ID	152479_1.R1011
5'-most EST	fC-zmle700442181a1
Method	BLASTX
NCBI GI	g1362190
BLAST score	1389
E value	1.0e-160
Match length	310
% identity	94
NCBI Description	calcium-dependent protein kinase - maize (fragment) >gi_506413 (L15390) calcium-dependent protein kinase [Zea mays]

Seq. No.	284300
Contig ID	152482_1.R1011
5'-most EST	fC-zmle700441534b1

Seq. No.	284301
Contig ID	152485_1.R1011
5'-most EST	fC-zmle700441428f6
Method	BLASTX
NCBI GI	g1350778
BLAST score	516
E value	2.0e-52
Match length	137
% identity	71
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi_2119118_pir__I50151 acidic ribosomal phosphoprotein - chicken >gi_453474 (L28704) acidic ribosomal phosphoprotein [Gallus gallus]

Seq. No.	284302
Contig ID	152514_1.R1011
5'-most EST	mwy700441811.h1
Method	BLASTX
NCBI GI	g629561
BLAST score	192
E value	1.0e-14
Match length	90
% identity	39
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	284303
Contig ID	152523_1.R1011
5'-most EST	fC-zmle700442386f8
Method	BLASTX
NCBI GI	g3925370
BLAST score	314
E value	1.0e-28
Match length	178
% identity	39
NCBI Description	(Z75714) similar to 40S ribosomal protein S7; cDNA EST EMBL:T00854 comes from this gene; cDNA EST EMBL:T00855 comes from this gene; cDNA EST EMBL:D70956 comes from this gene; cDNA EST EMBL:D71012 comes from this gene; cDNA EST

Seq. No.	284304
Contig ID	152523_2.R1011
5'-most EST	fC-zmro700449739f5
Method	BLASTX
NCBI GI	g3851636
BLAST score	244
E value	1.0e-20
Match length	130
% identity	43
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	284305
Contig ID	152524_1.R1011
5'-most EST	uC-zmflb73005c05a1
Method	BLASTX
NCBI GI	g1680686
BLAST score	337
E value	2.0e-31
Match length	132
% identity	47
NCBI Description	(U51330) rust resistance kinase Lr10 [Triticum aestivum]

Seq. No.	284306
Contig ID	152556_1.R1011
5'-most EST	fC-zmle700442181b1
Method	BLASTX
NCBI GI	g1504052
BLAST score	599
E value	5.0e-62

Match length	120
% identity	96
NCBI Description	(D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No.	284307
Contig ID	152593_1.R1011
5'-most EST	cyk700047663.f1
Method	BLASTX
NCBI GI	g731806
BLAST score	403
E value	4.0e-39
Match length	177
% identity	49
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 7 >gi_626344_pir__S48431 probable membrane protein YIL048w - yeast (Saccharomyces cerevisiae) >gi_557820_emb_CAA86174_ (Z38060) orf, len: 1151, CAI: 0.17, similar to S30768 S30768 PROBABLE ATPASE - YEAST (SACCHAROMYCES CEREVISIAE) [Saccharomyces cerevisiae]

Seq. No.	284308
Contig ID	152600_1.R1011
5'-most EST	fC-zmle700443881f8
Method	BLASTX
NCBI GI	g4101473
BLAST score	445
E value	4.0e-44
Match length	96
% identity	92
NCBI Description	(AF003382) KEA1 [Arabidopsis thaliana]

Seq. No.	284309
Contig ID	152625_1.R1011
5'-most EST	fC-zmle700444419d6
Method	BLASTN
NCBI GI	g998429
BLAST score	60
E value	5.0e-25
Match length	84
% identity	93
NCBI Description	GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]

Seq. No.	284310
Contig ID	152630_1.R1011
5'-most EST	fC-zmle700444433d4

Seq. No.	284311
Contig ID	152660_1.R1011
5'-most EST	fC-zmle700444583f7
Method	BLASTX
NCBI GI	g3402758
BLAST score	707
E value	1.0e-74
Match length	250
% identity	56
NCBI Description	(AL031187) serine/threonine kinase - like protein

[Arabidopsis thaliana]

Seq. No.	284312
Contig ID	152662_1.R1011
5'-most EST	uC-zmflmo17355e11a1
Method	BLASTX
NCBI GI	g3047117
BLAST score	155
E value	4.0e-10
Match length	34
% identity	85
NCBI Description	(AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana]

Seq. No.	284313
Contig ID	152666_1.R1011
5'-most EST	cyk700047731.f1
Method	BLASTX
NCBI GI	g3560168
BLAST score	531
E value	6.0e-54
Match length	160
% identity	64
NCBI Description	(AL031525) 60S ribosomal protein L19 [Schizosaccharomyces pombe]

Seq. No.	284314
Contig ID	152667_1.R1011
5'-most EST	fC-zmle700445151f7

Seq. No.	284315
Contig ID	152693_1.R1011
5'-most EST	fC-zmle700445074b1

Seq. No.	284316
Contig ID	152719_1.R1011
5'-most EST	fC-zmle700445302a1

Seq. No.	284317
Contig ID	152736_1.R1011
5'-most EST	fC-zmle700445470a4

Seq. No.	284318
Contig ID	152737_1.R1011
5'-most EST	fC-zmle700445470d4

Seq. No.	284319
Contig ID	152747_1.R1011
5'-most EST	fC-zmro700448566r2

Seq. No.	284320
Contig ID	152749_1.R1011
5'-most EST	uC-zmromo17049f12a1
Method	BLASTX
NCBI GI	g2760839
BLAST score	177
E value	2.0e-12

Match length	85
% identity	44
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	284321
Contig ID	152782_1.R1011
5'-most EST	cat700021779.r1

Seq. No.	284322
Contig ID	152782_2.R1011
5'-most EST	fC-zmle700446531d3

Seq. No.	284323
Contig ID	152791_1.R1011
5'-most EST	fC-zmle700446611d4

Seq. No.	284324
Contig ID	152796_1.R1011
5'-most EST	uC-zmflmo17421h06a1

Seq. No.	284325
Contig ID	152799_1.R1011
5'-most EST	wyr700243281.h1

Seq. No.	284326
Contig ID	152810_1.R1011
5'-most EST	nwy700446705.h1
Method	BLASTX
NCBI GI	g3914372
BLAST score	149
E value	2.0e-09
Match length	111
% identity	37
NCBI Description	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE ALPHA (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-ALPHA) (LPAAT-ALPHA) >gi_2155238 (U56417) lysophosphatidic acid acyltransferase-alpha [Homo sapiens] >gi_2253613 (U75971) putative lysophospholipid acyltransferase [Homo sapiens] >gi_2894090_emb_CAA70758_ (Y09565) 1-acylglycerol-3-phosphate O-acyltransferase [Homo sapiens]

Seq. No.	284327
Contig ID	152824_1.R1011
5'-most EST	cat700020370.r1

Seq. No.	284328
Contig ID	152845_1.R1011
5'-most EST	fC-zmle700447121b1

Seq. No.	284329
Contig ID	152851_1.R1011
5'-most EST	ceu700426579.h1
Method	BLASTX
NCBI GI	g3785998
BLAST score	427
E value	6.0e-42

Match length	176
% identity	47
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	284330
Contig ID	152851_2.R1011
5'-most EST	uer700577821.h1

Seq. No.	284331
Contig ID	152862_1.R1011
5'-most EST	fC-zmle700447381r3

Seq. No.	284332
Contig ID	152873_1.R1011
5'-most EST	fC-zmle700447417r3

Seq. No.	284333
Contig ID	152882_1.R1011
5'-most EST	cyk700049203.f1
Method	BLASTX
NCBI GI	g3641845
BLAST score	769
E value	5.0e-82
Match length	206
% identity	73
NCBI Description	(AJ223358) stelar K+ outward rectifying channel [Arabidopsis thaliana]

Seq. No.	284334
Contig ID	152899_1.R1011
5'-most EST	fC-zmle700447968r6

Seq. No.	284335
Contig ID	152902_1.R1011
5'-most EST	fC-zmle700448206a3

Seq. No.	284336
Contig ID	152915_1.R1011
5'-most EST	fC-zmle700448273d6
Method	BLASTX
NCBI GI	g3810676
BLAST score	642
E value	3.0e-67
Match length	184
% identity	42
NCBI Description	(AJ223357) SKOR [Arabidopsis thaliana]

Seq. No.	284337
Contig ID	152934_1.R1011
5'-most EST	fC-zmle700559868i1
Method	BLASTX
NCBI GI	g1709449
BLAST score	823
E value	2.0e-88
Match length	169
% identity	91
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT

PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate dehydrogenase E1 alpha subunit [Pisum sativum]

Seq. No.	284338
Contig ID	152961_1.R1011
5'-most EST	fC-zmle700577847f1
Method	BLASTX
NCBI GI	g2130082
BLAST score	416
E value	8.0e-41
Match length	144
% identity	55
NCBI Description	protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] >gi_1586408_prf__2203451A receptor kinase-like protein [Oryza sativa]

Seq. No.	284339
Contig ID	152963_1.R1011
5'-most EST	fC-zmle700582420a2
Method	BLASTX
NCBI GI	g3834350
BLAST score	214
E value	2.0e-17
Match length	88
% identity	49
NCBI Description	(AB010991) 3b-hydroxylase [Lycopersicon esculentum]

Seq. No.	284340
Contig ID	152977_1.R1011
5'-most EST	uer700582230.h1
Method	BLASTX
NCBI GI	g4314401
BLAST score	334
E value	1.0e-31
Match length	93
% identity	65
NCBI Description	(AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	284341
Contig ID	152997_1.R1011
5'-most EST	fC-zmle700583118f1
Method	BLASTX
NCBI GI	g1731990
BLAST score	509
E value	9.0e-52
Match length	135
% identity	72
NCBI Description	(Y09602) serine carboxypeptidase II, CP-MII [Hordeum vulgare]

Seq. No.	284342
Contig ID	153004_1.R1011
5'-most EST	fC-zmle700579561f1
Method	BLASTX

NCBI GI	g4206122
BLAST score	543
E value	2.0e-55
Match length	150
% identity	69
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	284343
Contig ID	153015_1.R1011
5'-most EST	fC-zmle700579741a2

Seq. No.	284344
Contig ID	153059_1.R1011
5'-most EST	fC-zmle700582230f4
Method	BLASTX
NCBI GI	g3402751
BLAST score	270
E value	9.0e-24
Match length	70
% identity	70
NCBI Description	(AL031187) putative protein [Arabidopsis thaliana]

Seq. No.	284345
Contig ID	153075_1.R1011
5'-most EST	fC-zmle700582462r1

Seq. No.	284346
Contig ID	153089_1.R1011
5'-most EST	vfk700404809.h1

Seq. No.	284347
Contig ID	153096_1.R1011
5'-most EST	xsy700208431.h1

Seq. No.	284348
Contig ID	153138_1.R1011
5'-most EST	cyk700049504.f1

Seq. No.	284349
Contig ID	153155_1.R1011
5'-most EST	fC-zmro700449558f7
Method	BLASTX
NCBI GI	g2130024
BLAST score	346
E value	1.0e-36
Match length	112
% identity	73
NCBI Description	DNA-binding protein ABF2 - wild oat >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No.	284350
Contig ID	153155_2.R1011
5'-most EST	uC-zmrob73060g04a1
Method	BLASTX
NCBI GI	g2130024

BLAST score	308
E value	1.0e-30
Match length	114
% identity	66
NCBI Description	DNA-binding protein ABF2 - wild oat >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No.	284351
Contig ID	153155_3.R1011
5'-most EST	dyk700103077.h1
Method	BLASTX
NCBI GI	g2130024
BLAST score	283
E value	5.0e-37
Match length	98
% identity	83
NCBI Description	DNA-binding protein ABF2 - wild oat >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No.	284352
Contig ID	153168_1.R1011
5'-most EST	dyk700106614.h1
Method	BLASTN
NCBI GI	g4514723
BLAST score	37
E value	3.0e-11
Match length	72
% identity	90
NCBI Description	Oryza sativa OsENOD40 gene, complete cds

Seq. No.	284353
Contig ID	153224_1.R1011
5'-most EST	cyk700049432.f1
Method	BLASTN
NCBI GI	g1420923
BLAST score	35
E value	3.0e-10
Match length	87
% identity	85
NCBI Description	Zea mays repressor-like protein (in1) gene, complete cds

Seq. No.	284354
Contig ID	153226_1.R1011
5'-most EST	fC-zmro700450116a1
Method	BLASTX
NCBI GI	g2245077
BLAST score	646
E value	9.0e-68
Match length	152
% identity	80
NCBI Description	(Z97343) glucanase homolog [Arabidopsis thaliana]

Seq. No.	284355
Contig ID	153250_1.R1011
5'-most EST	ceu700428430.h1

Seq. No.	284356
Contig ID	153283_1.R1011
5'-most EST	fC-zmro700451924r1

Seq. No.	284357
Contig ID	153295_1.R1011
5'-most EST	uC-zmrob73060e06a1

Seq. No.	284358
Contig ID	153317_1.R1011
5'-most EST	fC-zmro700453242f1
Method	BLASTX
NCBI GI	g4314401
BLAST score	393
E value	3.0e-38
Match length	134
% identity	57
NCBI Description	(AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	284359
Contig ID	153334_1.R1011
5'-most EST	fC-zmro700569167a1
Method	BLASTX
NCBI GI	g2500197
BLAST score	417
E value	8.0e-41
Match length	106
% identity	78
NCBI Description	RAC-LIKE GTP BINDING PROTEIN RAC13 >gi_1361976_pir__S57325 GTP-binding protein Rac 13 - upland cotton >gi_1087111_bbs_170156 (S79308) 21.8 kda GTP-binding protein=Rac13 [Gossypium hirsutum=cotton plants, cv. Acala SJ-2, boll fibers, Peptide, 196 aa] [Gossypium hirsutum]

Seq. No.	284360
Contig ID	153362_1.R1011
5'-most EST	fC-zmro700570160a1
Method	BLASTX
NCBI GI	g3411266
BLAST score	2774
E value	0.0e+00
Match length	532
% identity	100
NCBI Description	(AF080567) pullulanase-type starch debranching enzyme [Zea mays]

Seq. No.	284361
Contig ID	153366_1.R1011
5'-most EST	fC-zmro700570435a1
Method	BLASTX
NCBI GI	g1109699
BLAST score	401
E value	9.0e-39
Match length	170
% identity	49

NCBI Description	(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
Seq. No.	284362
Contig ID	153403_1.R1011
5'-most EST	fC-zmro700571573a1
Seq. No.	284363
Contig ID	153473_1.R1011
5'-most EST	uC-zmflmo17393e06a1
Seq. No.	284364
Contig ID	153535_1.R1011
5'-most EST	fC-zmst700620205a1
Method	BLASTX
NCBI GI	g3282250
BLAST score	786
E value	5.0e-84
Match length	210
% identity	70
NCBI Description	(AF009337) CDPK-related protein kinase [Tradescantia virginiana]
Seq. No.	284365
Contig ID	153671_1.R1011
5'-most EST	fC-zmro700833812f1
Method	BLASTN
NCBI GI	g662929
BLAST score	40
E value	4.0e-13
Match length	84
% identity	87
NCBI Description	G.max mRNA for heat shock transcription factor
Seq. No.	284366
Contig ID	153674_1.R1011
5'-most EST	fC-zmro700829571d1
Method	BLASTX
NCBI GI	g3096935
BLAST score	667
E value	7.0e-70
Match length	220
% identity	65
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]
Seq. No.	284367
Contig ID	153686_1.R1011
5'-most EST	fC-zmro700829816a1
Method	BLASTX
NCBI GI	g462147
BLAST score	622
E value	6.0e-65
Match length	158
% identity	73
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase (EC 5.3.1.9) - Arabidopsis thaliana

>gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	284368
Contig ID	153690_1.R1011
5'-most EST	fC-zmro700829816r6

Seq. No.	284369
Contig ID	153694_1.R1011
5'-most EST	fC-zmro700829824d1
Method	BLASTX
NCBI GI	g3892712
BLAST score	504
E value	4.0e-51
Match length	116
% identity	81
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein [Arabidopsis thaliana]

Seq. No.	284370
Contig ID	153696_1.R1011
5'-most EST	fC-zmro700829944f1
Method	BLASTX
NCBI GI	g4581146
BLAST score	534
E value	4.0e-62
Match length	141
% identity	87
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	284371
Contig ID	153700_1.R1011
5'-most EST	fC-zmro700831628d4
Method	BLASTX
NCBI GI	g541816
BLAST score	354
E value	3.0e-33
Match length	109
% identity	69
NCBI Description	protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	284372
Contig ID	153701_1.R1011
5'-most EST	fC-zmro700829958a6
Method	BLASTX
NCBI GI	g1076632
BLAST score	712
E value	2.0e-75
Match length	153
% identity	85
NCBI Description	protein kinase - common tobacco >gi_506534_emb_CAA50374_ (X71057) protein kinase [Nicotiana tabacum]

Seq. No.	284373
Contig ID	153710_1.R1011

5'-most EST	fC-zmro700832903d6
Seq. No.	284374
Contig ID	153722_1.R1011
5'-most EST	fC-zmro700830732d4
Method	BLASTX
NCBI GI	g349379
BLAST score	164
E value	3.0e-11
Match length	76
% identity	61
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]
Seq. No.	284375
Contig ID	153723_1.R1011
5'-most EST	fC-zmro700830015f1
Method	BLASTX
NCBI GI	g349379
BLAST score	552
E value	8.0e-57
Match length	133
% identity	84
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]
Seq. No.	284376
Contig ID	153727_1.R1011
5'-most EST	fC-zmro700830206f1
Method	BLASTX
NCBI GI	g4432856
BLAST score	270
E value	1.0e-23
Match length	106
% identity	51
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.	284377
Contig ID	153728_1.R1011
5'-most EST	fC-zmro700833336r1
Seq. No.	284378
Contig ID	153736_2.R1011
5'-most EST	fC-zmro700830872f1
Method	BLASTX
NCBI GI	g2213581
BLAST score	217
E value	2.0e-17
Match length	43
% identity	95
NCBI Description	(AC000348) T7N9.1 [Arabidopsis thaliana]
Seq. No.	284379
Contig ID	153738_1.R1011
5'-most EST	fC-zmro700830206d6
Method	BLASTX
NCBI GI	g1903357
BLAST score	706
E value	2.0e-74

Match length	202
% identity	62
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	284380
Contig ID	153754_1.R1011
5'-most EST	fC-zmro700830313a2
Method	BLASTX
NCBI GI	g3805849
BLAST score	691
E value	9.0e-73
Match length	250
% identity	80
NCBI Description	(AL031986) cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana]

Seq. No.	284381
Contig ID	153755_1.R1011
5'-most EST	fC-zmro700830313d1
Method	BLASTX
NCBI GI	g4092771
BLAST score	167
E value	1.0e-11
Match length	87
% identity	36
NCBI Description	(AF105139) disease resistance gene homolog 1A [Brassica napus]

Seq. No.	284382
Contig ID	153759_1.R1011
5'-most EST	fC-zmro700833817d4

Seq. No.	284383
Contig ID	153762_1.R1011
5'-most EST	fC-zmro700834004d4
Method	BLASTX
NCBI GI	g4006829
BLAST score	497
E value	7.0e-50
Match length	191
% identity	53
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	284384
Contig ID	153763_1.R1011
5'-most EST	fC-zmro700830314f1
Method	BLASTX
NCBI GI	g4006829
BLAST score	159
E value	5.0e-11
Match length	44
% identity	70
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	284385
Contig ID	153763_2.R1011

5'-most EST	fC-zmro700830314i1
Method	BLASTX
NCBI GI	g2852447
BLAST score	185
E value	1.0e-27
Match length	91
% identity	71
NCBI Description	(D88206) protein kinase [Arabidopsis thaliana]

Seq. No.	284386
Contig ID	153772_1.R1011
5'-most EST	fC-zmro700832904r1
Method	BLASTX
NCBI GI	g3421413
BLAST score	605
E value	1.0e-62
Match length	130
% identity	87
NCBI Description	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No.	284387
Contig ID	153779_1.R1011
5'-most EST	fC-zmro700830431a2
Method	BLASTX
NCBI GI	g3282092
BLAST score	172
E value	3.0e-12
Match length	113
% identity	42
NCBI Description	(AJ007446) hypothetical protein [Thermotoga neapolitana]

Seq. No.	284388
Contig ID	153781_1.R1011
5'-most EST	fC-zmro700830431f1
Method	BLASTX
NCBI GI	g399427
BLAST score	441
E value	6.0e-48
Match length	129
% identity	66
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_99392_pir__S24996 phosphopyruvate hydratase (EC 4.2.1.11) - Chlamydomonas reinhardtii >gi_18143_emb_CAA47043_ (X66412) enolase [Chlamydomonas reinhardtii]

Seq. No.	284389
Contig ID	153792_1.R1011
5'-most EST	fC-zmro700830687f1

Seq. No.	284390
Contig ID	153793_1.R1011
5'-most EST	fC-zmro700830845d4

Seq. No.	284391

Contig ID	153794_1.R1011
5'-most EST	fC-zmro700830732f1
Method	BLASTX
NCBI GI	g3881381
BLAST score	382
E value	8.0e-37
Match length	141
% identity	52
NCBI Description	(Z68270) Similarity to Yeast Man(0)-alpha-mannosidase (SW:MNS1_YEAST); cDNA EST EMBL:D71247 comes from this gene; cDNA EST EMBL:D73896 comes from this gene [Caenorhabditis elegans]

Seq. No.	284392
Contig ID	153800_1.R1011
5'-most EST	fC-zmro700830845r1
Method	BLASTX
NCBI GI	g130185
BLAST score	226
E value	2.0e-18
Match length	81
% identity	62
NCBI Description	PHYTOCHROME A >gi_65877_pir__FKPUZ phytochrome - zucchini >gi_167501 (M15265) phytochrome [Cucurbita pepo] >gi_225435_prf__1303260A phytochrome [Cucurbita pepo]

Seq. No.	284393
Contig ID	153809_1.R1011
5'-most EST	fC-zmro700833022a1
Method	BLASTX
NCBI GI	g2065531
BLAST score	458
E value	2.0e-45
Match length	107
% identity	77
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	284394
Contig ID	153810_1.R1011
5'-most EST	fC-zmro700830873r1

Seq. No.	284395
Contig ID	153814_1.R1011
5'-most EST	fC-zmro700833677r1
Method	BLASTX
NCBI GI	g4567279
BLAST score	353
E value	4.0e-33
Match length	142
% identity	52
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	284396
Contig ID	153820_1.R1011
5'-most EST	fC-zmro700830949r1
Method	BLASTX

NCBI GI	g4220476
BLAST score	877
E value	2.0e-94
Match length	240
% identity	69
NCBI Description	(AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No.	284397
Contig ID	153822_1.R1011
5'-most EST	fC-zmro700830949d4

Seq. No.	284398
Contig ID	153823_1.R1011
5'-most EST	fC-zmro700830949f1
Method	BLASTX
NCBI GI	g4220476
BLAST score	429
E value	3.0e-42
Match length	149
% identity	62
NCBI Description	(AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No.	284399
Contig ID	153831_1.R1011
5'-most EST	fC-zmro700830969d4
Method	BLASTX
NCBI GI	g4587547
BLAST score	211
E value	3.0e-16
Match length	260
% identity	28
NCBI Description	(AC006577) Contains similarity to DNA-binding protein Gt-2 gb_X68261 from Oryza sativa. [Arabidopsis thaliana]

Seq. No.	284400
Contig ID	153834_1.R1011
5'-most EST	fC-zmro700831112a2
Method	BLASTX
NCBI GI	g4033431
BLAST score	473
E value	6.0e-50
Match length	118
% identity	86
NCBI Description	PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK) >gi_2982467_emb_CAA18231_ (AL022223) pyruvate kinase like protein [Arabidopsis thaliana]

Seq. No.	284401
Contig ID	153835_1.R1011
5'-most EST	fC-zmro700831112d4

Seq. No.	284402
Contig ID	153837_1.R1011
5'-most EST	fC-zmro700833834d4
Method	BLASTX
NCBI GI	g2497543
BLAST score	1416

E value	1.0e-157
Match length	308
% identity	91
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	284403
Contig ID	153845_1.R1011
5'-most EST	fC-zmro700833881r1

Seq. No.	284404
Contig ID	153848_1.R1011
5'-most EST	fC-zmro700831516f1
Method	BLASTX
NCBI GI	g4512667
BLAST score	753
E value	2.0e-80
Match length	147
% identity	92
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	284405
Contig ID	153850_1.R1011
5'-most EST	fC-zmro700831226f1
Method	BLASTX
NCBI GI	g3077640
BLAST score	169
E value	4.0e-12
Match length	44
% identity	70
NCBI Description	(AJ223151) O-methyltransferase [Prunus dulcis]

Seq. No.	284406
Contig ID	153857_1.R1011
5'-most EST	fC-zmro700831372a5

Seq. No.	284407
Contig ID	153862_1.R1011
5'-most EST	fC-zmro700831491a2
Method	BLASTX
NCBI GI	g3947735
BLAST score	397
E value	1.0e-38
Match length	119
% identity	63
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	284408
Contig ID	153863_1.R1011
5'-most EST	fC-zmro700832291r1

Seq. No.	284409
Contig ID	153868_1.R1011
5'-most EST	fC-zmro700832290d4

Seq. No. 284410

Contig ID	153886_1.R1011
5'-most EST	fC-zmro700831625r1
Method	BLASTX
NCBI GI	g1169199
BLAST score	269
E value	8.0e-24
Match length	64
% identity	75
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT102 >gi_479739_pir__S35271 hypothetical protein - Arabidopsis thaliana >gi_166928 (L11368) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	284411
Contig ID	153902_1.R1011
5'-most EST	fC-zmro700831777f1
Method	BLASTX
NCBI GI	g3482967
BLAST score	208
E value	4.0e-17
Match length	57
% identity	86
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	284412
Contig ID	153907_1.R1011
5'-most EST	fC-zmro700833194a1
Method	BLASTX
NCBI GI	g3834302
BLAST score	1327
E value	1.0e-147
Match length	335
% identity	81
NCBI Description	(AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis thaliana]

Seq. No.	284413
Contig ID	153909_1.R1011
5'-most EST	fC-zmro700831855f1
Method	BLASTX
NCBI GI	g310563
BLAST score	193
E value	9.0e-15
Match length	42
% identity	93
NCBI Description	(L19359) calmodulin [Glycine max] >gi_1583771_prf__2121384E calmodulin [Glycine max]

Seq. No.	284414
Contig ID	153910_1.R1011
5'-most EST	fC-zmro700831873a2
Method	BLASTX
NCBI GI	g2983600

BLAST score	271
E value	4.0e-24
Match length	95
% identity	56
NCBI Description	(AE000725) argininosuccinate synthase [Aquifex aeolicus]

Seq. No.	284415
Contig ID	153912_1.R1011
5'-most EST	fC-zmro700832036a2
Method	BLASTX
NCBI GI	g4249391
BLAST score	278
E value	9.0e-25
Match length	80
% identity	64
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	284416
Contig ID	153914_1.R1011
5'-most EST	fC-zmro700831916f1
Method	BLASTX
NCBI GI	g4454472
BLAST score	493
E value	3.0e-49
Match length	236
% identity	48
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	284417
Contig ID	153922_1.R1011
5'-most EST	fC-zmro700833080d7
Method	BLASTX
NCBI GI	g2462749
BLAST score	731
E value	2.0e-77
Match length	180
% identity	82
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	284418
Contig ID	153935_1.R1011
5'-most EST	fC-zmro700834123d4
Method	BLASTX
NCBI GI	g2499488
BLAST score	239
E value	5.0e-20
Match length	59
% identity	83
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	284419
Contig ID	153936_1.R1011
5'-most EST	fC-zmro700831993d4
Method	BLASTX
NCBI GI	g2499946
BLAST score	1500
E value	1.0e-167
Match length	393
% identity	75
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	284420
Contig ID	153939_1.R1011
5'-most EST	fC-zmro700833207f1
Method	BLASTX
NCBI GI	g1421730
BLAST score	239
E value	3.0e-20
Match length	113
% identity	42
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	284421
Contig ID	153954_1.R1011
5'-most EST	fC-zmro700832291d4
Method	BLASTX
NCBI GI	g2983600
BLAST score	166
E value	2.0e-11
Match length	76
% identity	43
NCBI Description	(AE000725) argininosuccinate synthase [Aquifex aeolicus]

Seq. No.	284422
Contig ID	153963_1.R1011
5'-most EST	fC-zmro700832290f1
Method	BLASTX
NCBI GI	g3766299
BLAST score	366
E value	2.0e-43
Match length	103
% identity	100
NCBI Description	(AJ012080) sucrose synthase [Pisum sativum]

Seq. No.	284423
Contig ID	153964_1.R1011
5'-most EST	fC-zmro700832291a5
Method	BLASTX
NCBI GI	g4371296
BLAST score	788
E value	4.0e-84
Match length	240
% identity	62

NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	284424
Contig ID	153996_1.R1011
5'-most EST	fC-zmro700833812d7

Seq. No.	284425
Contig ID	154007_1.R1011
5'-most EST	fC-zmro700832664a5
Method	BLASTX
NCBI GI	g2970447
BLAST score	604
E value	2.0e-81
Match length	155
% identity	99
NCBI Description	(AF049706) aspartokinase-homoserine dehydrogenase [Glycine max]

Seq. No.	284426
Contig ID	154010_1.R1011
5'-most EST	fC-zmro700833374d4
Method	BLASTN
NCBI GI	g2970446
BLAST score	417
E value	0.0e+00
Match length	425
% identity	100
NCBI Description	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) mRNA, complete cds

Seq. No.	284427
Contig ID	154014_1.R1011
5'-most EST	fC-zmro700832792a2
Method	BLASTX
NCBI GI	g3915873
BLAST score	490
E value	8.0e-50
Match length	97
% identity	94
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) (NODULIN-100) >gi_2606081 (AF030231) sucrose synthase [Glycine max]

Seq. No.	284428
Contig ID	154018_1.R1011
5'-most EST	fC-zmro700832904a5
Method	BLASTX
NCBI GI	g1408460
BLAST score	887
E value	1.0e-95
Match length	251
% identity	73
NCBI Description	(U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]

Seq. No. 284429

Contig ID	154020_1.R1011
5'-most EST	fC-zmro700833022a2
Method	BLASTN
NCBI GI	g20738
BLAST score	46
E value	7.0e-17
Match length	62
% identity	94
NCBI Description	P.sativum gdcP gene for P-protein of glycine decarboxylase enzyme complex

Seq. No.	284430
Contig ID	154021_1.R1011
5'-most EST	fC-zmro700832864a2
Method	BLASTX
NCBI GI	g3021270
BLAST score	329
E value	1.0e-30
Match length	122
% identity	59
NCBI Description	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq. No.	284431
Contig ID	154022_1.R1011
5'-most EST	fC-zmro700832864d4
Method	BLASTX
NCBI GI	g3776082
BLAST score	185
E value	6.0e-14
Match length	43
% identity	88
NCBI Description	(Y18250) MtN30 [Medicago truncatula]

Seq. No.	284432
Contig ID	154024_1.R1011
5'-most EST	fC-zmro700832903a2
Method	BLASTX
NCBI GI	g4262226
BLAST score	355
E value	4.0e-33
Match length	150
% identity	52
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	284433
Contig ID	154049_1.R1011
5'-most EST	fC-zmro700833080a3
Method	BLASTX
NCBI GI	g2462749
BLAST score	1080
E value	1.0e-118
Match length	308
% identity	69
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	284434
Contig ID	154055_1.R1011
5'-most EST	fC-zmro700833080f3

Seq. No.	284435
Contig ID	154058_1.R1011
5'-most EST	fC-zmro700833080r4

Seq. No.	284436
Contig ID	154059_1.R1011
5'-most EST	fC-zmro700833139a2
Method	BLASTX
NCBI GI	g3738339
BLAST score	678
E value	2.0e-71
Match length	158
% identity	83
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	284437
Contig ID	154062_1.R1011
5'-most EST	fC-zmro700834080r1

Seq. No.	284438
Contig ID	154077_1.R1011
5'-most EST	fC-zmro700833222a2
Method	BLASTX
NCBI GI	g2499115
BLAST score	742
E value	5.0e-79
Match length	147
% identity	93
NCBI Description	VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1835788 (U86662) VPS41 [Lycopersicon esculentum]

Seq. No.	284439
Contig ID	154080_1.R1011
5'-most EST	fC-zmro700833677d4
Method	BLASTX
NCBI GI	g2499115
BLAST score	219
E value	8.0e-18
Match length	85
% identity	58
NCBI Description	VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1835788 (U86662) VPS41 [Lycopersicon esculentum]

Seq. No.	284440
Contig ID	154085_1.R1011
5'-most EST	fC-zmro700833238a2
Method	BLASTX
NCBI GI	g3913366
BLAST score	206
E value	2.0e-16
Match length	115
% identity	42
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR

>gi_1597723 (U67422) CRINKLY4 precursor [Zea mays]

Seq. No.	284441
Contig ID	154099_1.R1011
5'-most EST	fC-zmro700833336a5
Method	BLASTX
NCBI GI	g3549626
BLAST score	1030
E value	1.0e-112
Match length	331
% identity	61
NCBI Description	(AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No.	284442
Contig ID	154106_1.R1011
5'-most EST	fC-zmro700833336r3

Seq. No.	284443
Contig ID	154114_1.R1011
5'-most EST	fC-zmro700833411a2
Method	BLASTX
NCBI GI	g2852449
BLAST score	637
E value	1.0e-66
Match length	143
% identity	85
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No.	284444
Contig ID	154116_1.R1011
5'-most EST	fC-zmro700833616a2
Method	BLASTX
NCBI GI	g3176072
BLAST score	357
E value	7.0e-34
Match length	77
% identity	88
NCBI Description	(AJ002485) protein phosphatase 1, catalytic beta subunit [Medicago sativa]

Seq. No.	284445
Contig ID	154118_1.R1011
5'-most EST	fC-zmro700833639a5

Seq. No.	284446
Contig ID	154121_1.R1011
5'-most EST	fC-zmro700833881d4

Seq. No.	284447
Contig ID	154135_1.R1011
5'-most EST	fC-zmro700834165d4

Seq. No.	284448
Contig ID	154136_1.R1011
5'-most EST	fC-zmro700833775a2

Seq. No.	284449
Contig ID	154145_1.R1011
5'-most EST	fC-zmro700833834r1
Method	BLASTX
NCBI GI	g129584
BLAST score	535
E value	1.0e-54
Match length	104
% identity	99
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_99944_pir__S22991 phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - soybean >gi_18377_emb_CAA37129_ (X52953) phenylalanine ammonia-lyase [Glycine max]

Seq. No.	284450
Contig ID	154159_1.R1011
5'-most EST	fC-zmro700833834a5
Method	BLASTX
NCBI GI	g129584
BLAST score	597
E value	5.0e-62
Match length	121
% identity	96
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_99944_pir__S22991 phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - soybean >gi_18377_emb_CAA37129_ (X52953) phenylalanine ammonia-lyase [Glycine max]

Seq. No.	284451
Contig ID	154165_1.R1011
5'-most EST	fC-zmro700833881a5
Method	BLASTX
NCBI GI	g4544389
BLAST score	604
E value	8.0e-63
Match length	157
% identity	76
NCBI Description	(AC007047) putative homeodomain protein [Arabidopsis thaliana]

Seq. No.	284452
Contig ID	154224_1.R1011
5'-most EST	fC-zmro700834292f1
Method	BLASTX
NCBI GI	g3947733
BLAST score	308
E value	3.0e-28
Match length	97
% identity	63
NCBI Description	(AJ009719) NL25 [Solanum tuberosum]

Seq. No.	284453
Contig ID	154227_1.R1011
5'-most EST	fC-zmro700834313a1
Method	BLASTX
NCBI GI	g4539330
BLAST score	398

E value	7.0e-39
Match length	112
% identity	69
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	284454
Contig ID	154230_1.R1011
5'-most EST	fC-zmro700835567d1

Seq. No.	284455
Contig ID	154236_1.R1011
5'-most EST	fC-zmro700834391a1
Method	BLASTX
NCBI GI	g2982253
BLAST score	224
E value	3.0e-18
Match length	56
% identity	71
NCBI Description	(AF051209) CROC-1-like protein [Picea mariana]

Seq. No.	284456
Contig ID	154245_1.R1011
5'-most EST	fC-zmro700834671a4
Method	BLASTX
NCBI GI	g421843
BLAST score	966
E value	1.0e-105
Match length	217
% identity	85
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	284457
Contig ID	154247_1.R1011
5'-most EST	fC-zmro700834671d1
Method	BLASTX
NCBI GI	g421843
BLAST score	409
E value	6.0e-40
Match length	106
% identity	76
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	284458
Contig ID	154257_1.R1011
5'-most EST	fC-zmro700834842a4
Method	BLASTX
NCBI GI	g2642154
BLAST score	310
E value	5.0e-28
Match length	112
% identity	54
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana]

>gi_3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana]

Seq. No.	284459
Contig ID	154263_1.R1011
5'-most EST	fC-zmro700834874a4
Method	BLASTX
NCBI GI	g4587513
BLAST score	515
E value	2.0e-52
Match length	156
% identity	65
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	284460
Contig ID	154265_1.R1011
5'-most EST	fC-zmro700834874d1

Seq. No.	284461
Contig ID	154276_1.R1011
5'-most EST	fC-zmro700835120a1

Seq. No.	284462
Contig ID	154278_1.R1011
5'-most EST	fC-zmro700835120d1
Method	BLASTX
NCBI GI	g4585973
BLAST score	273
E value	4.0e-24
Match length	59
% identity	88
NCBI Description	(AC005287) translation initiation factor [Arabidopsis thaliana]

Seq. No.	284463
Contig ID	154283_1.R1011
5'-most EST	fC-zmro700835214a1
Method	BLASTX
NCBI GI	g1170626
BLAST score	655
E value	8.0e-69
Match length	155
% identity	82
NCBI Description	CALCIUM/CALMODULIN-DEPENDENT SERINE/THREONINE PROTEIN KINASE >gi_478408_pir__JQ2251 calcium/calmodulin-binding protein kinase - apple tree >gi_311320_emb_CAA78961_ (Z17313) calcium/calmodulin-dependent serine/threonine protein kinase [Malus domestica] >gi_984160_emb_CAA86286_ (Z38126) calmodulin-binding protein kinase [Malus domestica]

Seq. No.	284464
Contig ID	154292_1.R1011
5'-most EST	fC-zmro700835521f1
Method	BLASTX
NCBI GI	g3947735

BLAST score	174
E value	5.0e-13
Match length	59
% identity	58
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	284465
Contig ID	154293_1.R1011
5'-most EST	fC-zmro700835521r1

Seq. No.	284466
Contig ID	154296_1.R1011
5'-most EST	fC-zmro700835534f1
Method	BLASTX
NCBI GI	g404026
BLAST score	606
E value	4.0e-63
Match length	139
% identity	81
NCBI Description	(M96568) oleoyl-acyl carrier protein thioesterase [Carthamus tinctorius]

Seq. No.	284467
Contig ID	154298_1.R1011
5'-most EST	fC-zmro700835567a2
Method	BLASTX
NCBI GI	g4454018
BLAST score	145
E value	6.0e-09
Match length	111
% identity	33
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.	284468
Contig ID	154309_1.R1011
5'-most EST	fC-zmro700835579a1
Method	BLASTX
NCBI GI	g2129830
BLAST score	1525
E value	1.0e-170
Match length	307
% identity	95
NCBI Description	heat shock transcription factor 31 - soybean (fragment) >gi_671867_emb_CAA87079_ (Z46955) heat shock transcription factor 31 [Glycine max]

Seq. No.	284469
Contig ID	154330_1.R1011
5'-most EST	fC-zmro700835729a1
Method	BLASTX
NCBI GI	g3341695
BLAST score	542
E value	2.0e-55
Match length	153
% identity	67
NCBI Description	(AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	284470
Contig ID	154350_1.R1011
5'-most EST	fC-zmro700835986f1
Method	BLASTX
NCBI GI	g2911280
BLAST score	482
E value	1.0e-74
Match length	158
% identity	85
NCBI Description	(U73937) PK12 protein kinase [Nicotiana tabacum]

Seq. No.	284471
Contig ID	154354_1.R1011
5'-most EST	fC-zmro700836155f1
Method	BLASTX
NCBI GI	g2462834
BLAST score	149
E value	1.0e-09
Match length	77
% identity	39
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284472
Contig ID	154355_1.R1011
5'-most EST	fC-zmro700836155d1

Seq. No.	284473
Contig ID	154367_1.R1011
5'-most EST	fC-zmse700159774a1

Seq. No.	284474
Contig ID	154369_1.R1011
5'-most EST	fC-zmse700160578a1

Seq. No.	284475
Contig ID	154370_1.R1011
5'-most EST	ceu700427152.h1

Seq. No.	284476
Contig ID	154374_1.R1011
5'-most EST	fC-zmse700161738a1

Seq. No.	284477
Contig ID	154379_1.R1011
5'-most EST	ceu700421864.h1
Method	BLASTX
NCBI GI	g1652892
BLAST score	366
E value	1.0e-34
Match length	119
% identity	29
NCBI Description	(D90909) ABC transporter [Synechocystis sp.]

Seq. No.	284478
Contig ID	154385_1.R1011
5'-most EST	fC-zmse700196812a1

Seq. No.	284479
Contig ID	154387_1.R1011
5'-most EST	fC-zmse700197203a1
Method	BLASTX
NCBI GI	g3929647
BLAST score	330
E value	9.0e-31
Match length	128
% identity	52
NCBI Description	(AJ004881) Immutans protein [Arabidopsis thaliana]

Seq. No.	284480
Contig ID	154396_1.R1011
5'-most EST	gwl700612747.h1
Method	BLASTX
NCBI GI	g2583120
BLAST score	339
E value	3.0e-39
Match length	142
% identity	58
NCBI Description	(AC002387) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	284481
Contig ID	154402_1.R1011
5'-most EST	fC-zmse700612684a1

Seq. No.	284482
Contig ID	154410_1.R1011
5'-most EST	fC-zmse700613130r1

Seq. No.	284483
Contig ID	154423_1.R1011
5'-most EST	fC-zmse700613867a1

Seq. No.	284484
Contig ID	154427_1.R1011
5'-most EST	uC-zmflb73228f07a1

Seq. No.	284485
Contig ID	154448_1.R1011
5'-most EST	fC-zmse700614946a1
Method	BLASTX
NCBI GI	g1688233
BLAST score	380
E value	3.0e-36
Match length	187
% identity	55
NCBI Description	(U77655) DNA binding protein homolog [Solanum tuberosum]

Seq. No.	284486
Contig ID	154455_1.R1011
5'-most EST	fC-zmse700616908f1

Seq. No.	284487
Contig ID	154473_1.R1011

5'-most EST	xyt700347345.h1
Seq. No.	284488
Contig ID	154510_1.R1011
5'-most EST	fC-zmse700616992a1
Seq. No.	284489
Contig ID	154553_1.R1011
5'-most EST	fC-zmse700798807r6
Seq. No.	284490
Contig ID	154568_1.R1011
5'-most EST	fC-zmse700801387a1
Method	BLASTX
NCBI GI	g4063742
BLAST score	173
E value	2.0e-12
Match length	64
% identity	52
NCBI Description	(AC005851) putative phaseolin G-box binding protein [Arabidopsis thaliana]
Seq. No.	284491
Contig ID	154574_1.R1011
5'-most EST	fC-zmse700803335a1
Method	BLASTN
NCBI GI	g168436
BLAST score	67
E value	3.0e-29
Match length	137
% identity	88
NCBI Description	Zea mays catalase (Cat3) gene, complete cds
Seq. No.	284492
Contig ID	154612_1.R1011
5'-most EST	fC-zmse700836407r1
Seq. No.	284493
Contig ID	154621_1.R1011
5'-most EST	fC-zmse700836619a1
Method	BLASTX
NCBI GI	g4455158
BLAST score	167
E value	2.0e-11
Match length	42
% identity	74
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]
Seq. No.	284494
Contig ID	154631_1.R1011
5'-most EST	fC-zmse700836747f1
Seq. No.	284495
Contig ID	154632_1.R1011
5'-most EST	fC-zmse700836747d1
Method	BLASTX
NCBI GI	g2462754

BLAST score	145
E value	4.0e-09
Match length	79
% identity	39
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	284496
Contig ID	154635_1.R1011
5'-most EST	fC-zmse700836776a1
Method	BLASTX
NCBI GI	g1220178
BLAST score	479
E value	5.0e-48
Match length	136
% identity	71
NCBI Description	(Z69995) dormancy related protein [Trollius ledebourii]

Seq. No.	284497
Contig ID	154662_1.R1011
5'-most EST	fC-zmse700836955a1
Method	BLASTX
NCBI GI	g1046278
BLAST score	498
E value	3.0e-50
Match length	96
% identity	97
NCBI Description	(U28645) PvAlf [Phaseolus vulgaris]

Seq. No.	284498
Contig ID	154664_1.R1011
5'-most EST	fC-zmse700837058d1

Seq. No.	284499
Contig ID	154667_1.R1011
5'-most EST	fC-zmse700837068a4
Method	BLASTX
NCBI GI	g2244814
BLAST score	408
E value	5.0e-58
Match length	159
% identity	72
NCBI Description	(Z97336) protein kinase [Arabidopsis thaliana]

Seq. No.	284500
Contig ID	154668_1.R1011
5'-most EST	fC-zmse700837068r1

Seq. No.	284501
Contig ID	154674_1.R1011
5'-most EST	fC-zmse700837418a1
Method	BLASTX
NCBI GI	g3980401
BLAST score	211
E value	1.0e-16
Match length	47
% identity	85
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No.	284502
Contig ID	154678_1.R1011
5'-most EST	fC-zmse700837458a1
Method	BLASTX
NCBI GI	g2632252
BLAST score	179
E value	4.0e-13
Match length	114
% identity	39
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	284503
Contig ID	154686_1.R1011
5'-most EST	fC-zmse700837706d1
Method	BLASTX
NCBI GI	g3581917
BLAST score	193
E value	1.0e-14
Match length	87
% identity	45
NCBI Description	(AL031545) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	284504
Contig ID	154691_1.R1011
5'-most EST	fC-zmse700837777a1
Method	BLASTX
NCBI GI	g3980406
BLAST score	344
E value	3.0e-32
Match length	101
% identity	58
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	284505
Contig ID	154693_1.R1011
5'-most EST	fC-zmse700837891a1
Method	BLASTX
NCBI GI	g133438
BLAST score	425
E value	4.0e-42
Match length	114
% identity	72
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA' CHAIN >gi_81504_pir__B29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - spinach chloroplast >gi_295120 (M55297) RNA polymerase [Spinacia oleracea]

Seq. No.	284506
Contig ID	154695_1.R1011
5'-most EST	fC-zmse700837891d3
Method	BLASTX
NCBI GI	g2924258
BLAST score	176
E value	1.0e-26

Match length	111
% identity	65
NCBI Description	(Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No.	284507
Contig ID	154702_1.R1011
5'-most EST	fC-zmse700838314y1
Method	BLASTX
NCBI GI	g2980770
BLAST score	523
E value	2.0e-53
Match length	134
% identity	76
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	284508
Contig ID	154703_1.R1011
5'-most EST	fC-zmse700838314r1

Seq. No.	284509
Contig ID	154705_1.R1011
5'-most EST	fC-zmse700838314g1
Method	BLASTX
NCBI GI	g2980770
BLAST score	760
E value	6.0e-81
Match length	195
% identity	74
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	284510
Contig ID	154714_1.R1011
5'-most EST	fC-zmse700838540f1
Method	BLASTX
NCBI GI	g3915037
BLAST score	577
E value	2.0e-59
Match length	114
% identity	91
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No.	284511
Contig ID	154726_1.R1011
5'-most EST	fC-zmse700838708a4
Method	BLASTX
NCBI GI	g3201623
BLAST score	737
E value	1.0e-114
Match length	262
% identity	79
NCBI Description	(AC004669) shaggy-like kinase dzeta [Arabidopsis thaliana]

Seq. No.	284512
Contig ID	154728_1.R1011
5'-most EST	fC-zmse700838708r1

Seq. No.	284513
Contig ID	154750_1.R1011
5'-most EST	fC-zmse700838914f1

Seq. No.	284514
Contig ID	154754_1.R1011
5'-most EST	fC-zmse700839180a4
Method	BLASTX
NCBI GI	g3850070
BLAST score	669
E value	1.0e-72
Match length	209
% identity	65
NCBI Description	(AL033385) transketolase [Schizosaccharomyces pombe]

Seq. No.	284515
Contig ID	154760_1.R1011
5'-most EST	fC-zmse700839356f1
Method	BLASTX
NCBI GI	g3256035
BLAST score	899
E value	4.0e-97
Match length	280
% identity	60
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No.	284516
Contig ID	154769_1.R1011
5'-most EST	fC-zmse700839369r1

Seq. No.	284517
Contig ID	154776_1.R1011
5'-most EST	fC-zmse700839445a1
Method	BLASTX
NCBI GI	g632736
BLAST score	581
E value	7.0e-68
Match length	186
% identity	67
NCBI Description	(S72424) CBP20=pathogen- and wound-inducible antifungal protein {clone cbp20-44, pathogen- and wound-inducible} [Nicotiana tabacum=tobacco, Samsun NN, leaves, Peptide Partial, 208 aa] [Nicotiana tabacum]

Seq. No.	284518
Contig ID	154788_1.R1011
5'-most EST	fC-zmst1700331867a1
Method	BLASTX
NCBI GI	g2501215
BLAST score	144
E value	8.0e-09
Match length	74
% identity	35
NCBI Description	THIOL:DISULFIDE INTERCHANGE PROTEIN TXLA HOMOLOG >gi_1653069_dbj_BAA17986_ (D90910) thiol:disulfide

interchange protein TrxA [Synechocystis sp.]

Seq. No.	284519
Contig ID	154789_1.R1011
5'-most EST	fC-zmst1700331867d1
Seq. No.	284520
Contig ID	154829_1.R1011
5'-most EST	wyr700240470.h1
Seq. No.	284521
Contig ID	154838_1.R1011
5'-most EST	fC-zmst1700334018r1
Seq. No.	284522
Contig ID	154880_1.R1011
5'-most EST	fC-zmst700335861r5
Seq. No.	284523
Contig ID	154886_1.R1011
5'-most EST	fC-zmst700335931b1
Seq. No.	284524
Contig ID	154899_1.R1011
5'-most EST	fC-zmst1700336269a1
Method	BLASTX
NCBI GI	g3242728
BLAST score	402
E value	3.0e-45
Match length	227
% identity	50
NCBI Description	(AC003040) unknown protein [Arabidopsis thaliana]
Seq. No.	284525
Contig ID	154914_1.R1011
5'-most EST	xmt700263365.h1
Method	BLASTX
NCBI GI	g3641836
BLAST score	803
E value	6.0e-86
Match length	227
% identity	67
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	284526
Contig ID	154918_1.R1011
5'-most EST	fC-zmst700336672f4
Method	BLASTX
NCBI GI	g1817584
BLAST score	331
E value	1.0e-30
Match length	185
% identity	42
NCBI Description	(Y08991) adaptor protein [Homo sapiens]
Seq. No.	284527

Contig ID	154925_1.R1011
5'-most EST	fC-zmst1700336683a1
Method	BLASTX
NCBI GI	g2129662
BLAST score	297
E value	7.0e-27
Match length	147
% identity	42
NCBI Description	ovule-specific homeotic protein homolog A20 - Arabidopsis thaliana >gi_1881536 (U37589) A20 [Arabidopsis thaliana]

Seq. No.	284528
Contig ID	154926_1.R1011
5'-most EST	uC-zmflb73240g08a2

Seq. No.	284529
Contig ID	154929_1.R1011
5'-most EST	fC-zmst700336806f4
Method	BLASTX
NCBI GI	g4191774
BLAST score	492
E value	9.0e-50
Match length	138
% identity	62
NCBI Description	(AC005917) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	284530
Contig ID	155253_1.R1011
5'-most EST	fC-zmst700455051f1
Method	BLASTX
NCBI GI	g735882
BLAST score	433
E value	6.0e-43
Match length	119
% identity	75
NCBI Description	(L40176) lycopene cyclase [Arabidopsis thaliana]

Seq. No.	284531
Contig ID	155261_1.R1011
5'-most EST	fC-zmst700455559d2

Seq. No.	284532
Contig ID	155305_1.R1011
5'-most EST	tzu700206201.h1
Method	BLASTX
NCBI GI	g2465925
BLAST score	322
E value	4.0e-41
Match length	145
% identity	61
NCBI Description	(AF024649) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	284533
Contig ID	155328_1.R1011
5'-most EST	fC-zmst700458854d4

Seq. No.	284534
Contig ID	155382_1.R1011
5'-most EST	fC-zmst700620845a1
Method	BLASTX
NCBI GI	g1352077
BLAST score	216
E value	3.0e-17
Match length	83
% identity	46
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (EXO-(1-->4)-BETA-D-GALACTANASE) >gi_971485_emb_CAA58734_ (X83854) putative beta-galactosidase/galactanase [Lycopersicon esculentum] >gi_4138139_emb_CAA10174_ (AJ012797) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	284535
Contig ID	155388_1.R1011
5'-most EST	fC-zmst700620908a1

Seq. No.	284536
Contig ID	155404_1.R1011
5'-most EST	fC-zmst700621333a1

Seq. No.	284537
Contig ID	155422_1.R1011
5'-most EST	fC-zmst700621924a1
Method	BLASTX
NCBI GI	g3201554
BLAST score	169
E value	5.0e-12
Match length	47
% identity	66
NCBI Description	(AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.	284538
Contig ID	155438_1.R1011
5'-most EST	fC-zmst700621982a1
Method	BLASTX
NCBI GI	g3914371
BLAST score	487
E value	4.0e-49
Match length	103
% identity	91
NCBI Description	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) >gi_791098_emb_CAA56159_ (X79722) glycerol-3-phosphate O-acyltransferase [Phaseolus vulgaris]

Seq. No.	284539
Contig ID	155441_1.R1011
5'-most EST	fC-zmst700624316a1

Seq. No.	284540
Contig ID	155454_1.R1011
5'-most EST	fC-zmst700622579a1
Method	BLASTX
NCBI GI	g3979665

BLAST score	306
E value	1.0e-27
Match length	128
% identity	49
NCBI Description	(X66482) orf [Arabidopsis thaliana]

Seq. No.	284541
Contig ID	155466_1.R1011
5'-most EST	fC-zmst700623156d1
Method	BLASTX
NCBI GI	g3820648
BLAST score	473
E value	2.0e-47
Match length	112
% identity	76
NCBI Description	(Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	284542
Contig ID	155495_1.R1011
5'-most EST	fC-zmst700624501a1

Seq. No.	284543
Contig ID	155502_1.R1011
5'-most EST	fC-zmst700808322a1

Seq. No.	284544
Contig ID	155506_1.R1011
5'-most EST	fC-zmst700808322r6

Seq. No.	284545
Contig ID	155536_1.R1011
5'-most EST	uC-zmflb73122g05a1

Seq. No.	284546
Contig ID	155559_1.R1011
5'-most EST	uC-zmflmo17043b09a1

Seq. No.	284547
Contig ID	155589_1.R1011
5'-most EST	uC-zmflb73260g09a1
Method	BLASTN
NCBI GI	g2642323
BLAST score	48
E value	9.0e-18
Match length	76
% identity	91
NCBI Description	Zea mays profilin (PRO4) mRNA, complete cds

Seq. No.	284548
Contig ID	155591_1.R1011
5'-most EST	uC-zmflb73337c10a1
Method	BLASTX
NCBI GI	g1730502
BLAST score	288
E value	2.0e-25
Match length	144
% identity	45

NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	284549
Contig ID	155591_2.R1011
5'-most EST	uC-zmflb731237d08a1
Method	BLASTX
NCBI GI	g1730502
BLAST score	227
E value	1.0e-18
Match length	73
% identity	58
NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	284550
Contig ID	155592_1.R1011
5'-most EST	pmx700088534.h1
Method	BLASTX
NCBI GI	g4581108
BLAST score	178
E value	1.0e-12
Match length	95
% identity	36
NCBI Description	(AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea (GB:L36857) [Arabidopsis thaliana]

Seq. No.	284551
Contig ID	155599_1.R1011
5'-most EST	uC-zmflb73004c06a1

Seq. No.	284552
Contig ID	155605_1.R1011
5'-most EST	uC-zmflb73004d03a1

Seq. No.	284553
Contig ID	155614_1.R1011
5'-most EST	uC-zmflb73189g06a1

Seq. No.	284554
Contig ID	155614_2.R1011
5'-most EST	hvj700624628.h1

Seq. No.	284555
Contig ID	155627_1.R1011
5'-most EST	uC-zmflb73004g02a1

Seq. No.	284556
Contig ID	155647_1.R1011
5'-most EST	uC-zmflb73148e12a1

Seq. No.	284557
Contig ID	155652_1.R1011
5'-most EST	uC-zmflb73062g04a1

Seq. No.	284558
Contig ID	155660_1.R1011
5'-most EST	kem700612242.h1

Seq. No.	284559
Contig ID	155662_1.R1011
5'-most EST	uC-zmflmo17404b04a1

Seq. No.	284560
Contig ID	155668_1.R1011
5'-most EST	uC-zmflb73005c09a1
Method	BLASTX
NCBI GI	g3643596
BLAST score	334
E value	4.0e-41
Match length	119
% identity	68
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284561
Contig ID	155697_1.R1011
5'-most EST	uC-zmflmo17357b10a1

Seq. No.	284562
Contig ID	155705_1.R1011
5'-most EST	uC-zmflb73005g08a1
Method	BLASTN
NCBI GI	g3169011
BLAST score	34
E value	2.0e-09
Match length	54
% identity	91
NCBI Description	Hordeum vulgare mRNA for putative calmodulin binding transporter protein

Seq. No.	284563
Contig ID	155711_1.R1011
5'-most EST	uC-zmflmo17391h02a1

Seq. No.	284564
Contig ID	155712_1.R1011
5'-most EST	uC-zmflb73134d06a2
Method	BLASTX
NCBI GI	g3063710
BLAST score	348
E value	1.0e-32
Match length	108
% identity	63
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	284565
Contig ID	155755_1.R1011
5'-most EST	uC-zmflmo17028d09a1

Seq. No.	284566
Contig ID	155763_1.R1011

5'-most EST	uC-zmflb73006g02a1
Seq. No.	284567
Contig ID	155787_1.R1011
5'-most EST	uC-zmflb73106d01a1
Seq. No.	284568
Contig ID	155797_1.R1011
5'-most EST	uC-zmflmo17189b05a1
Method	BLASTX
NCBI GI	g1346107
BLAST score	281
E value	3.0e-38
Match length	83
% identity	99
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi_557696 (U12233) GTP binding protein beta subunit [Zea mays]
Seq. No.	284569
Contig ID	155802_1.R1011
5'-most EST	uC-zmflb73008c11a1
Seq. No.	284570
Contig ID	155805_1.R1011
5'-most EST	uC-zmflb73082g05a2
Seq. No.	284571
Contig ID	155817_1.R1011
5'-most EST	uC-zmflmo17319g07a1
Seq. No.	284572
Contig ID	155817_2.R1011
5'-most EST	uC-zmflmo17395e05a1
Seq. No.	284573
Contig ID	155836_1.R1011
5'-most EST	uC-zmflmo17016c06a1
Seq. No.	284574
Contig ID	155848_1.R1011
5'-most EST	cat700016446.r1
Seq. No.	284575
Contig ID	155849_1.R1011
5'-most EST	uC-zmflb73010a05a1
Seq. No.	284576
Contig ID	155869_1.R1011
5'-most EST	uC-zmflmo17056e11a1
Seq. No.	284577
Contig ID	155873_1.R1011
5'-most EST	uC-zmrob73044e04a1
Seq. No.	284578
Contig ID	155891_1.R1011
5'-most EST	uC-zmflb73091a10a1

Seq. No.	284579
Contig ID	155893_1.R1011
5'-most EST	uC-zmflb73236b09a1

Seq. No.	284580
Contig ID	155905_1.R1011
5'-most EST	uC-zmflb73009g08a2
Method	BLASTX
NCBI GI	g3875381
BLAST score	407
E value	1.0e-39
Match length	193
% identity	43
NCBI Description	(Z47808) cDNA EST EMBL:C10289 comes from this gene; cDNA EST EMBL:C11909 comes from this gene [Caenorhabditis elegans] >gi_3876933_emb_CAA87783_ (Z47809) cDNA EST EMBL:C10289 comes from this gene; cDNA EST EMBL:C11909 comes from this gene [Caenorhabditis elegans]

Seq. No.	284581
Contig ID	155910_1.R1011
5'-most EST	uC-zmflb73010h01a1

Seq. No.	284582
Contig ID	155911_1.R1011
5'-most EST	uC-zmflb73009h05a2

Seq. No.	284583
Contig ID	155913_1.R1011
5'-most EST	uC-zmflb73009h07a2

Seq. No.	284584
Contig ID	155979_1.R1011
5'-most EST	tzu700206612.h1

Seq. No.	284585
Contig ID	155986_1.R1011
5'-most EST	uC-zmflmo17001b09a1

Seq. No.	284586
Contig ID	155989_1.R1011
5'-most EST	uC-zmrob73037d08a1

Seq. No.	284587
Contig ID	155990_1.R1011
5'-most EST	uC-zmflb73011b09a1

Seq. No.	284588
Contig ID	156005_1.R1011
5'-most EST	uC-zmflb73011d06a1

Seq. No.	284589
Contig ID	156011_1.R1011
5'-most EST	uC-zmflb73338e04a1

Seq. No.	284590

Contig ID	156028_1.R1011
5'-most EST	uC-zmflb73011f10a1
Seq. No.	284591
Contig ID	156029_1.R1011
5'-most EST	uC-zmflb73065h11a1
Method	BLASTX
NCBI GI	g3063457
BLAST score	176
E value	1.0e-12
Match length	43
% identity	81
NCBI Description	(AC003981) F22O13.19 [Arabidopsis thaliana]
Seq. No.	284592
Contig ID	156030_1.R1011
5'-most EST	yne700378508.h1
Seq. No.	284593
Contig ID	156035_1.R1011
5'-most EST	uC-zmflb73011g07a1
Seq. No.	284594
Contig ID	156041_1.R1011
5'-most EST	uC-zmflb73011h03a1
Seq. No.	284595
Contig ID	156050_1.R1011
5'-most EST	uC-zmflb73012a11a2
Method	BLASTX
NCBI GI	g2262151
BLAST score	377
E value	6.0e-36
Match length	129
% identity	61
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]
Seq. No.	284596
Contig ID	156052_1.R1011
5'-most EST	uC-zmrob73058d03a1
Seq. No.	284597
Contig ID	156101_1.R1011
5'-most EST	uC-zmromo17071b11a1
Seq. No.	284598
Contig ID	156106_1.R1011
5'-most EST	uC-zmflb73013d02a2
Seq. No.	284599
Contig ID	156130_1.R1011
5'-most EST	uC-zmflb73013g06a2
Seq. No.	284600
Contig ID	156135_1.R1011
5'-most EST	uC-zmflb73168a03a1

Method	BLASTN
NCBI GI	g168535
BLAST score	64
E value	2.0e-27
Match length	72
% identity	97
NCBI Description	Zea mays putative thiol protease homolog mRNA, partial cds

Seq. No.	284601
Contig ID	156152_1.R1011
5'-most EST	uC-zmflb73014b03a1
Method	BLASTX
NCBI GI	g2191127
BLAST score	396
E value	2.0e-38
Match length	96
% identity	77
NCBI Description	(AF007269) A_IG002N01.1 gene product [Arabidopsis thaliana]

Seq. No.	284602
Contig ID	156163_1.R1011
5'-most EST	qmh700030330.f1

Seq. No.	284603
Contig ID	156168_1.R1011
5'-most EST	uC-zmflmo17321f10a1

Seq. No.	284604
Contig ID	156170_1.R1011
5'-most EST	uC-zmflmo17204e02a1

Seq. No.	284605
Contig ID	156181_1.R1011
5'-most EST	uC-zmflmo17418a05a1

Seq. No.	284606
Contig ID	156203_1.R1011
5'-most EST	uC-zmflb73302f07a1
Method	BLASTN
NCBI GI	g3511235
BLAST score	36
E value	1.0e-10
Match length	60
% identity	90
NCBI Description	Zea mays starch branching enzyme IIb (ae) gene, complete cds

Seq. No.	284607
Contig ID	156215_1.R1011
5'-most EST	uC-zmflmo17241a08a1

Seq. No.	284608
Contig ID	156227_1.R1011
5'-most EST	uC-zmflb73015c08a2

Seq. No.	284609
Contig ID	156229_1.R1011

5'-most EST	ceu700422430.h1
Seq. No.	284610
Contig ID	156230_1.R1011
5'-most EST	uC-zmromo17089f08a1
Method	BLASTX
NCBI GI	g3176661
BLAST score	233
E value	2.0e-19
Match length	68
% identity	66
NCBI Description	(AC004393) Similar to putative DNA polymerase gb_M29683 from S. cerevisiae. [Arabidopsis thaliana]
Seq. No.	284611
Contig ID	156257_1.R1011
5'-most EST	uC-zmflmo17420g03a1
Seq. No.	284612
Contig ID	156263_1.R1011
5'-most EST	uC-zmflb73015h05a2
Method	BLASTX
NCBI GI	g3355486
BLAST score	148
E value	1.0e-09
Match length	59
% identity	56
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.	284613
Contig ID	156267_1.R1011
5'-most EST	xdb700338251.h1
Seq. No.	284614
Contig ID	156280_1.R1011
5'-most EST	uC-zmflmo17104c02a1
Method	BLASTX
NCBI GI	g3695388
BLAST score	231
E value	4.0e-19
Match length	92
% identity	49
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]
Seq. No.	284615
Contig ID	156302_1.R1011
5'-most EST	uC-zmflb73238g10a1
Seq. No.	284616
Contig ID	156303_1.R1011
5'-most EST	uC-zmromo17026d10a1
Seq. No.	284617
Contig ID	156306_1.R1011
5'-most EST	uC-zmflb73016e05a1
Seq. No.	284618

Contig ID	156309_1.R1011
5'-most EST	uC-zmflb73030b04a1
Seq. No.	284619
Contig ID	156325_1.R1011
5'-most EST	uC-zmflb73299a04a1
Method	BLASTX
NCBI GI	g3925363
BLAST score	258
E value	1.0e-23
Match length	120
% identity	55
NCBI Description	(AF067961) homeodomain protein [Malus domestica]
Seq. No.	284620
Contig ID	156330_1.R1011
5'-most EST	uC-zmflb73240d02a2
Seq. No.	284621
Contig ID	156333_1.R1011
5'-most EST	uC-zmflb73017a03a2
Seq. No.	284622
Contig ID	156337_1.R1011
5'-most EST	uC-zmflb73017a11a2
Seq. No.	284623
Contig ID	156339_1.R1011
5'-most EST	uC-zmflmo17054b01a1
Seq. No.	284624
Contig ID	156358_1.R1011
5'-most EST	uC-zmflb73017d04a2
Seq. No.	284625
Contig ID	156382_1.R1011
5'-most EST	uC-zmrob73017h07a1
Method	BLASTX
NCBI GI	g4538911
BLAST score	316
E value	4.0e-29
Match length	111
% identity	57
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.	284626
Contig ID	156392_1.R1011
5'-most EST	uC-zmflb73018a12a1
Seq. No.	284627
Contig ID	156410_1.R1011
5'-most EST	uC-zmflb73018c12a1
Seq. No.	284628
Contig ID	156413_1.R1011
5'-most EST	uC-zmflb73018d04a1

Seq. No.	284629
Contig ID	156418_1.R1011
5'-most EST	xdb700341546.h1
Seq. No.	284630
Contig ID	156423_1.R1011
5'-most EST	uC-zmflb73018e05a1
Seq. No.	284631
Contig ID	156424_1.R1011
5'-most EST	uer700580961.h1
Seq. No.	284632
Contig ID	156458_1.R1011
5'-most EST	wty700163047.h1
Seq. No.	284633
Contig ID	156464_1.R1011
5'-most EST	uC-zmflb73248b04a2
Seq. No.	284634
Contig ID	156489_1.R1011
5'-most EST	uC-zmflmo17233a02a1
Seq. No.	284635
Contig ID	156489_2.R1011
5'-most EST	uC-zmflb73019f01a1
Method	BLASTX
NCBI GI	g4103152
BLAST score	224
E value	1.0e-18
Match length	58
% identity	76
NCBI Description	(AF020716) histidyl-tRNA synthetase [Triticum aestivum]
Seq. No.	284636
Contig ID	156494_1.R1011
5'-most EST	uC-zmflb73019f09a1
Seq. No.	284637
Contig ID	156500_1.R1011
5'-most EST	uC-zmflb73019g05a1
Seq. No.	284638
Contig ID	156506_1.R1011
5'-most EST	uC-zmflb73414h10a1
Seq. No.	284639
Contig ID	156512_1.R1011
5'-most EST	uC-zmflb73355a05a1
Seq. No.	284640
Contig ID	156513_1.R1011
5'-most EST	uC-zmflb73075b08a1
Seq. No.	284641
Contig ID	156515_1.R1011

5'-most EST	uC-zmflb73019h10a1
Seq. No.	284642
Contig ID	156518_1.R1011
5'-most EST	uC-zmflmo17076c07a1
Seq. No.	284643
Contig ID	156522_1.R1011
5'-most EST	uC-zmflb73020b01a1
Method	BLASTX
NCBI GI	g3023956
BLAST score	153
E value	4.0e-10
Match length	78
% identity	20
NCBI Description	VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi_607003 (L28125) beta transducin-like protein [Podospora anserina]
Seq. No.	284644
Contig ID	156524_1.R1011
5'-most EST	uC-zmflb73155g08a1
Method	BLASTX
NCBI GI	g1172761
BLAST score	311
E value	2.0e-28
Match length	97
% identity	61
NCBI Description	ADENYLOSUCCINATE LYASE (ADENYLOSUCCINASE) (ASL) >gi_1573637 (U32747) adenylosuccinate lyase (purB) [Haemophilus influenzae Rd]
Seq. No.	284645
Contig ID	156524_2.R1011
5'-most EST	uC-zmflb73020b04a1
Method	BLASTX
NCBI GI	g2832649
BLAST score	208
E value	2.0e-16
Match length	70
% identity	54
NCBI Description	(AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]
Seq. No.	284646
Contig ID	156532_1.R1011
5'-most EST	uC-zmflb73068d08a1
Seq. No.	284647
Contig ID	156542_1.R1011
5'-most EST	uC-zmflb73020d10a1
Seq. No.	284648
Contig ID	156552_1.R1011
5'-most EST	uC-zmflmo17264e03a2
Seq. No.	284649
Contig ID	156552_2.R1011

5'-most EST	uC-zmflb73068b07a1
Seq. No.	284650
Contig ID	156555_1.R1011
5'-most EST	uC-zmflb73247h01a2
Method	BLASTX
NCBI GI	g3204108
BLAST score	228
E value	8.0e-19
Match length	63
% identity	70
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]
Seq. No.	284651
Contig ID	156557_1.R1011
5'-most EST	uC-zmflmo17192h02a1
Seq. No.	284652
Contig ID	156566_1.R1011
5'-most EST	uC-zmflb73020g03a1
Seq. No.	284653
Contig ID	156573_1.R1011
5'-most EST	uC-zmflb73168c08a1
Method	BLASTX
NCBI GI	g3036796
BLAST score	208
E value	2.0e-16
Match length	56
% identity	70
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805858_emb_CAA21478_ (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	284654
Contig ID	156574_1.R1011
5'-most EST	uC-zmflb73020h07a1
Seq. No.	284655
Contig ID	156580_1.R1011
5'-most EST	uC-zmflb73021a01a2
Method	BLASTX
NCBI GI	g3776005
BLAST score	174
E value	2.0e-12
Match length	42
% identity	90
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.	284656
Contig ID	156618_1.R1011
5'-most EST	uC-zmflmo17042e04a1
Seq. No.	284657
Contig ID	156623_1.R1011
5'-most EST	cat700022073.r1

Seq. No.	284658
Contig ID	156625_1.R1011
5'-most EST	uC-zmflb73022a11a1

Seq. No.	284659
Contig ID	156638_1.R1011
5'-most EST	uC-zmflb73022c04a1

Seq. No.	284660
Contig ID	156672_1.R1011
5'-most EST	uC-zmflb73022f09a1

Seq. No.	284661
Contig ID	156681_1.R1011
5'-most EST	uC-zmflb73022g10a1
Method	BLASTX
NCBI GI	g3913517
BLAST score	244
E value	9.0e-21
Match length	64
% identity	75
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1109672 (U33283) 3'(2'),5-diphosphonucleoside 3'(2') phosphohydrolase [Oryza sativa] >gi_1586671_prf__2204308A diphosphonucleoside phosphohydrolase [Oryza sativa]

Seq. No.	284662
Contig ID	156686_1.R1011
5'-most EST	uC-zmflmo17044b03a1

Seq. No.	284663
Contig ID	156702_1.R1011
5'-most EST	cyk700048357.f1

Seq. No.	284664
Contig ID	156717_1.R1011
5'-most EST	uC-zmflb73023c09a1

Seq. No.	284665
Contig ID	156727_1.R1011
5'-most EST	uC-zmflb73023e02a1
Method	BLASTX
NCBI GI	g3080415
BLAST score	156
E value	2.0e-10
Match length	33
% identity	82
NCBI Description	(AL022604) cysteine proteinase-like protein [Arabidopsis thaliana]

Seq. No.	284666
Contig ID	156735_1.R1011
5'-most EST	gct701179031.h1
Method	BLASTX

NCBI GI	g3286691
BLAST score	340
E value	7.0e-32
Match length	83
% identity	72
NCBI Description	(AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	284667
Contig ID	156739_1.R1011
5'-most EST	uC-zmflb73023f07a1
Method	BLASTX
NCBI GI	g2983814
BLAST score	203
E value	6.0e-16
Match length	56
% identity	66
NCBI Description	(AE000739) tryptophan synthase beta subunit [Aquifex aeolicus]

Seq. No.	284668
Contig ID	156746_1.R1011
5'-most EST	uC-zmflb73397h04a1

Seq. No.	284669
Contig ID	156759_1.R1011
5'-most EST	uC-zmflmo17244f03a1

Seq. No.	284670
Contig ID	156768_1.R1011
5'-most EST	uC-zmflb73025a09a1

Seq. No.	284671
Contig ID	156772_1.R1011
5'-most EST	uC-zmflmo17418h11a1

Seq. No.	284672
Contig ID	156772_2.R1011
5'-most EST	uC-zmflb73025b03a1

Seq. No.	284673
Contig ID	156804_1.R1011
5'-most EST	uC-zmflb73025e08a1

Seq. No.	284674
Contig ID	156806_1.R1011
5'-most EST	cat700020315.r1

Seq. No.	284675
Contig ID	156820_1.R1011
5'-most EST	uC-zmflb73025g10a1
Method	BLASTX
NCBI GI	g3236256
BLAST score	248
E value	4.0e-21
Match length	58
% identity	79
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No.	284676
Contig ID	156823_1.R1011
5'-most EST	uC-zmflb73288b03a1

Seq. No.	284677
Contig ID	156829_1.R1011
5'-most EST	uC-zmflb73025h09a1

Seq. No.	284678
Contig ID	156835_1.R1011
5'-most EST	mwy700439529.h1
Method	BLASTX
NCBI GI	g3367594
BLAST score	147
E value	4.0e-09
Match length	48
% identity	58
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	284679
Contig ID	156842_1.R1011
5'-most EST	uC-zmflmo17154h04a1
Method	BLASTX
NCBI GI	g2618702
BLAST score	175
E value	2.0e-15
Match length	106
% identity	45
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	284680
Contig ID	156843_1.R1011
5'-most EST	uC-zmflb73246g04a2

Seq. No.	284681
Contig ID	156868_1.R1011
5'-most EST	uC-zmflb73027f11a1
Method	BLASTX
NCBI GI	g4049346
BLAST score	146
E value	3.0e-09
Match length	51
% identity	55
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	284682
Contig ID	156882_1.R1011
5'-most EST	uC-zmflb73113e12a2

Seq. No.	284683
Contig ID	156928_1.R1011
5'-most EST	uC-zmflb73188f01a1

Seq. No.	284684
Contig ID	156928_2.R1011

5'-most EST	uC-zmflmo17012d05a1
Seq. No.	284685
Contig ID	156933_1.R1011
5'-most EST	uC-zmflb73028f04a1
Seq. No.	284686
Contig ID	156937_1.R1011
5'-most EST	xyt700346585.h1
Seq. No.	284687
Contig ID	156957_1.R1011
5'-most EST	uC-zmflb73029a02a1
Seq. No.	284688
Contig ID	156964_1.R1011
5'-most EST	uC-zmflmo17069e01a1
Method	BLASTX
NCBI GI	g4204303
BLAST score	177
E value	8.0e-13
Match length	125
% identity	33
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	284689
Contig ID	156969_1.R1011
5'-most EST	uC-zmflb73192f10a1
Seq. No.	284690
Contig ID	156977_1.R1011
5'-most EST	xsy700211755.h1
Method	BLASTX
NCBI GI	g3341696
BLAST score	252
E value	1.0e-21
Match length	55
% identity	78
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]
Seq. No.	284691
Contig ID	156983_1.R1011
5'-most EST	uC-zmflb73133e08a1
Seq. No.	284692
Contig ID	156985_1.R1011
5'-most EST	uC-zmflb73174b09a1
Method	BLASTX
NCBI GI	g2827715
BLAST score	214
E value	4.0e-17
Match length	98
% identity	51
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	284693
Contig ID	156989_1.R1011
5'-most EST	uC-zmflmo17024h02a1
Method	BLASTX
NCBI GI	g3738338
BLAST score	274
E value	5.0e-24
Match length	111
% identity	47
NCBI Description	(AC005170) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	284694
Contig ID	156999_2.R1011
5'-most EST	xdb700339368.h1

Seq. No.	284695
Contig ID	157009_1.R1011
5'-most EST	uC-zmflmo17194b11a1

Seq. No.	284696
Contig ID	157012_1.R1011
5'-most EST	uC-zmflb73131g05a1

Seq. No.	284697
Contig ID	157013_1.R1011
5'-most EST	ceu700425958.h1

Seq. No.	284698
Contig ID	157018_1.R1011
5'-most EST	uC-zmflb73369g08a1

Seq. No.	284699
Contig ID	157022_1.R1011
5'-most EST	uC-zmrob73049d02a1

Seq. No.	284700
Contig ID	157023_1.R1011
5'-most EST	uC-zmflb73114b07a2

Seq. No.	284701
Contig ID	157032_1.R1011
5'-most EST	uC-zmflb73030b05a1

Seq. No.	284702
Contig ID	157038_1.R1011
5'-most EST	uC-zmflb73062b04a1

Seq. No.	284703
Contig ID	157069_1.R1011
5'-most EST	uC-zmflmo17365g10a1

Seq. No.	284704
Contig ID	157073_1.R1011
5'-most EST	tfd700575229.h1

Seq. No.	284705

Contig ID	157081_1.R1011
5'-most EST	uC-zmflb73030g07a1

Seq. No.	284706
Contig ID	157087_1.R1011
5'-most EST	uC-zmflb73416b11a1
Method	BLASTX
NCBI GI	g2642443
BLAST score	224
E value	3.0e-18
Match length	152
% identity	39
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	284707
Contig ID	157089_1.R1011
5'-most EST	uC-zmflb73193g07a1

Seq. No.	284708
Contig ID	157090_1.R1011
5'-most EST	uC-zmflb73030h11a1
Method	BLASTX
NCBI GI	g2190553
BLAST score	337
E value	1.0e-31
Match length	103
% identity	60
NCBI Description	(AC001229) Strong similarity to Arabidopsis zeta-crystallin-like protein (gb_Z49268). [Arabidopsis thaliana]

Seq. No.	284709
Contig ID	157096_1.R1011
5'-most EST	cat700020855.r1

Seq. No.	284710
Contig ID	157108_1.R1011
5'-most EST	uC-zmflb73106d02a1
Method	BLASTX
NCBI GI	g4512705
BLAST score	178
E value	1.0e-12
Match length	119
% identity	46
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	284711
Contig ID	157129_1.R1011
5'-most EST	uC-zmflb73031e05a1

Seq. No.	284712
Contig ID	157145_1.R1011
5'-most EST	uC-zmflmo17033d08a1
Method	BLASTN
NCBI GI	g2113846
BLAST score	88

E value	1.0e-41
Match length	204
% identity	86
NCBI Description	Hordeum vulgare mRNA for hypothetical protein, partial, clone WL5

Seq. No.	284713
Contig ID	157153_1.R1011
5'-most EST	ntr700072295.h1

Seq. No.	284714
Contig ID	157178_1.R1011
5'-most EST	uC-zmflb73148f10a1

Seq. No.	284715
Contig ID	157180_1.R1011
5'-most EST	uC-zmflb73032d03a1
Method	BLASTX
NCBI GI	g2129825
BLAST score	177
E value	7.0e-13
Match length	43
% identity	81
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	284716
Contig ID	157194_1.R1011
5'-most EST	vux700160135.h1

Seq. No.	284717
Contig ID	157197_1.R1011
5'-most EST	uC-zmflb73170c04b2
Method	BLASTX
NCBI GI	g2194119
BLAST score	199
E value	3.0e-15
Match length	66
% identity	55
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	284718
Contig ID	157198_1.R1011
5'-most EST	uC-zmflb73032g06a1

Seq. No.	284719
Contig ID	157226_1.R1011
5'-most EST	uC-zmflmo17183d10a1
Method	BLASTX
NCBI GI	g4558556
BLAST score	321
E value	9.0e-30
Match length	108
% identity	62
NCBI Description	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 284720
Contig ID 157239_1.R1011
5'-most EST uC-zmflmo17321e01a1

Seq. No. 284721
Contig ID 157240_1.R1011
5'-most EST uC-zmflmo17239b04a1

Seq. No. 284722
Contig ID 157245_1.R1011
5'-most EST uC-zmflmo17222g01a1

Seq. No. 284723
Contig ID 157261_1.R1011
5'-most EST uC-zmflb73035b11a1

Seq. No. 284724
Contig ID 157273_1.R1011
5'-most EST uer700582064.h1

Seq. No. 284725
Contig ID 157336_1.R1011
5'-most EST uC-zmflmo17323d10a1
Method BLASTX
NCBI GI g2443857
BLAST score 194
E value 1.0e-14
Match length 50
% identity 72
NCBI Description (U79961) vacuolar sorting receptor homolog [Zea mays]

Seq. No. 284726
Contig ID 157339_1.R1011
5'-most EST uC-zmflb73039e08a2
Method BLASTX
NCBI GI g3341693
BLAST score 261
E value 1.0e-22
Match length 80
% identity 61
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 284727
Contig ID 157346_1.R1011
5'-most EST uer700581310.h1
Method BLASTX
NCBI GI g3242709
BLAST score 145
E value 4.0e-09
Match length 70
% identity 40
NCBI Description (AC003040) putative guanine nucleotide-binding protein [Arabidopsis thaliana]

Seq. No. 284728
Contig ID 157378_1.R1011
5'-most EST uC-zmflb73040g04a1

Method	BLASTX
NCBI GI	g729230
BLAST score	418
E value	7.0e-41
Match length	96
% identity	83
NCBI Description	CHROMOSOME SEGREGATION PROTEIN CUT3 >gi_1076872_pir__S51622 cut3 protein - fission yeast (Schizosaccharomyces pombe) >gi_603501_dbj_BAA06454_ (D30788) cut3 protein [Schizosaccharomyces pombe]

Seq. No.	284729
Contig ID	157384_1.R1011
5'-most EST	uC-zmflmo17023d01a1

Seq. No.	284730
Contig ID	157392_1.R1011
5'-most EST	uC-zmflb73042b05a2
Method	BLASTN
NCBI GI	g312178
BLAST score	80
E value	4.0e-37
Match length	133
% identity	50
NCBI Description	Z.mays GapC2 gene

Seq. No.	284731
Contig ID	157394_1.R1011
5'-most EST	uC-zmflb73042b08a2

Seq. No.	284732
Contig ID	157405_1.R1011
5'-most EST	uC-zmflb73042d01a2

Seq. No.	284733
Contig ID	157416_1.R1011
5'-most EST	uC-zmflmo17420g11a1
Method	BLASTX
NCBI GI	g3928091
BLAST score	257
E value	5.0e-22
Match length	75
% identity	60
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	284734
Contig ID	157431_1.R1011
5'-most EST	uC-zmflb73137c08a1
Method	BLASTN
NCBI GI	g2735839
BLAST score	69
E value	2.0e-30
Match length	200
% identity	84
NCBI Description	Sorghum bicolor ADP-glucose pyrophosphorylase subunit SH2, transcriptional regulator, NADPH-dependent reductase A1-a and NADPH-dependent reductase A1-b genes, complete cds

Seq. No.	284735
Contig ID	157446_1.R1011
5'-most EST	uC-zmflmo17018a08a1
Seq. No.	284736
Contig ID	157498_1.R1011
5'-most EST	uC-zmflb73045c04a2
Seq. No.	284737
Contig ID	157499_2.R1011
5'-most EST	uC-zmflb73200g04a1
Seq. No.	284738
Contig ID	157505_1.R1011
5'-most EST	wyr700235670.h1
Seq. No.	284739
Contig ID	157516_1.R1011
5'-most EST	uwn700281709.h1
Seq. No.	284740
Contig ID	157525_1.R1011
5'-most EST	uC-zmflb73212f11a1
Seq. No.	284741
Contig ID	157532_1.R1011
5'-most EST	uC-zmflmo17019e10a1
Seq. No.	284742
Contig ID	157537_1.R1011
5'-most EST	uC-zmflb73045g05a2
Seq. No.	284743
Contig ID	157537_2.R1011
5'-most EST	uC-zmflb73417b03a1
Method	BLASTX
NCBI GI	g1729876
BLAST score	367
E value	8.0e-35
Match length	143
% identity	54
NCBI Description	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) (KIAA0002)
Seq. No.	284744
Contig ID	157547_1.R1011
5'-most EST	uC-zmflb73045h09a2
Seq. No.	284745
Contig ID	157569_1.R1011
5'-most EST	uC-zmflb73051a02a2
Seq. No.	284746
Contig ID	157570_1.R1011
5'-most EST	uC-zmflb73051a03a2
Method	BLASTX

NCBI GI	g419760
BLAST score	256
E value	6.0e-22
Match length	60
% identity	82
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	284747
Contig ID	157580_1.R1011
5'-most EST	uC-zmflb73051b08a2

Seq. No.	284748
Contig ID	157616_1.R1011
5'-most EST	uC-zmflb73128e12a1

Seq. No.	284749
Contig ID	157635_1.R1011
5'-most EST	uC-zmflb73299g08a1

Seq. No.	284750
Contig ID	157640_1.R1011
5'-most EST	uC-zmflb73051h11a2

Seq. No.	284751
Contig ID	157643_1.R1011
5'-most EST	uer700579012.h1
Method	BLASTX
NCBI GI	g1723125
BLAST score	147
E value	4.0e-09
Match length	56
% identity	54
NCBI Description	HYPOTHETICAL 27.8 KD PROTEIN SLL0194 >gi_1001604_dbj_BAA10232_ (D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	284752
Contig ID	157658_1.R1011
5'-most EST	uC-zmflb73350g01a1

Seq. No.	284753
Contig ID	157660_1.R1011
5'-most EST	uC-zmflb73057c01a2

Seq. No.	284754
Contig ID	157668_1.R1011
5'-most EST	uC-zmflb73057c11a2

Seq. No.	284755
Contig ID	157676_1.R1011
5'-most EST	uC-zmromo17111g12a1

Seq. No.	284756
Contig ID	157687_1.R1011
5'-most EST	uC-zmflb73057e07a2

Seq. No.	284757
Contig ID	157694_1.R1011
5'-most EST	uC-zmflmo17024e05a1

Seq. No.	284758
Contig ID	157699_1.R1011
5'-most EST	uC-zmflb73226g12a1

Seq. No.	284759
Contig ID	157700_1.R1011
5'-most EST	uC-zmflb73057f12a2

Seq. No.	284760
Contig ID	157709_1.R1011
5'-most EST	uC-zmflmo17023h11a1
Method	BLASTX
NCBI GI	g3290006
BLAST score	302
E value	1.0e-27
Match length	53
% identity	98
NCBI Description	(U82201) pathogenesis related protein-5 [Zea mays]

Seq. No.	284761
Contig ID	157711_1.R1011
5'-most EST	gct701171049.h1
Method	BLASTX
NCBI GI	g3249065
BLAST score	261
E value	2.0e-22
Match length	64
% identity	77
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	284762
Contig ID	157731_1.R1011
5'-most EST	uC-zmflb73059b03a2

Seq. No.	284763
Contig ID	157747_1.R1011
5'-most EST	uC-zmflb73059c12a2

Seq. No.	284764
Contig ID	157753_1.R1011
5'-most EST	clt700041557.f1

Seq. No.	284765
Contig ID	157758_1.R1011
5'-most EST	clt700044623.f1

Seq. No.	284766
Contig ID	157788_1.R1011
5'-most EST	uC-zmflb73059h03a2
Method	BLASTX

NCBI GI	g1769898
BLAST score	411
E value	3.0e-40
Match length	141
% identity	55
NCBI Description	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq. No.	284767
Contig ID	157791_1.R1011
5'-most EST	uC-zmflb73059h06a2

Seq. No.	284768
Contig ID	157796_1.R1011
5'-most EST	uC-zmflb73061a02a2
Method	BLASTX
NCBI GI	g2505874
BLAST score	173
E value	2.0e-12
Match length	41
% identity	78
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	284769
Contig ID	157801_1.R1011
5'-most EST	uC-zmflb73061a07a2

Seq. No.	284770
Contig ID	157866_1.R1011
5'-most EST	uC-zmflb73061h08a2

Seq. No.	284771
Contig ID	157867_1.R1011
5'-most EST	uC-zmrob73055e04a1

Seq. No.	284772
Contig ID	157896_1.R1011
5'-most EST	wty700165740.h1

Seq. No.	284773
Contig ID	157901_1.R1011
5'-most EST	uC-zmflb73062e06a1

Seq. No.	284774
Contig ID	157914_1.R1011
5'-most EST	uC-zmflb73062g01a1

Seq. No.	284775
Contig ID	157918_1.R1011
5'-most EST	uC-zmflb73164a02a1
Method	BLASTX
NCBI GI	g4503037
BLAST score	166
E value	1.0e-11
Match length	56
% identity	46
NCBI Description	UNKNOWN >gi_3550343 (AF084523) cellular repressor of E1A-stimulated genes CREG [Homo sapiens]

Seq. No.	284776
Contig ID	157922_1.R1011
5'-most EST	uC-zmflb73062h10a1
Seq. No.	284777
Contig ID	157925_1.R1011
5'-most EST	uC-zmflmo17324f12a1
Seq. No.	284778
Contig ID	157971_1.R1011
5'-most EST	uC-zmflb73064a01a2
Seq. No.	284779
Contig ID	157992_1.R1011
5'-most EST	uC-zmflb73326d06a1
Seq. No.	284780
Contig ID	157998_1.R1011
5'-most EST	uC-zmflmo17056d11a1
Method	BLASTX
NCBI GI	g100916
BLAST score	440
E value	1.0e-43
Match length	83
% identity	100
NCBI Description	protein kinase (EC 2.7.1.37) cdc2 homolog B - maize (fragment)
Seq. No.	284781
Contig ID	158006_1.R1011
5'-most EST	uC-zmflmo17114h04a1
Seq. No.	284782
Contig ID	158013_1.R1011
5'-most EST	uC-zmflmo17206e01a1
Seq. No.	284783
Contig ID	158028_1.R1011
5'-most EST	uC-zmflb73064g02a2
Seq. No.	284784
Contig ID	158035_1.R1011
5'-most EST	uC-zmflb73064g12a2
Method	BLASTX
NCBI GI	g4455338
BLAST score	183
E value	2.0e-13
Match length	40
% identity	82
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]
Seq. No.	284785
Contig ID	158038_1.R1011
5'-most EST	hbs701182983.h1
Seq. No.	284786

Contig ID	158059_1.R1011
5'-most EST	wyr700240752.h1
Seq. No.	284787
Contig ID	158062_1.R1011
5'-most EST	uC-zmflmo17427f10a1
Seq. No.	284788
Contig ID	158065_1.R1011
5'-most EST	xdb700340357.h1
Seq. No.	284789
Contig ID	158066_1.R1011
5'-most EST	uC-zmromo17104c10a1
Method	BLASTX
NCBI GI	g2499115
BLAST score	175
E value	2.0e-12
Match length	82
% identity	44
NCBI Description	VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1835788 (U86662) VPS41 [Lycopersicon esculentum]
Seq. No.	284790
Contig ID	158075_1.R1011
5'-most EST	uC-zmflb73065e11a1
Seq. No.	284791
Contig ID	158088_1.R1011
5'-most EST	uC-zmflb73065h03a1
Seq. No.	284792
Contig ID	158090_1.R1011
5'-most EST	uC-zmflb73250h03a2
Seq. No.	284793
Contig ID	158093_1.R1011
5'-most EST	qmh700026437.f1
Seq. No.	284794
Contig ID	158097_1.R1011
5'-most EST	cyk700050118.f1
Seq. No.	284795
Contig ID	158109_1.R1011
5'-most EST	uC-zmflb73262f03a2
Seq. No.	284796
Contig ID	158113_1.R1011
5'-most EST	cat700018675.r1
Seq. No.	284797
Contig ID	158130_1.R1011
5'-most EST	uC-zmflb73066e09a1
Seq. No.	284798
Contig ID	158132_1.R1011

5'-most EST	uC-zmflb73066f01a1
Method	BLASTX
NCBI GI	g1552379
BLAST score	160
E value	9.0e-11
Match length	48
% identity	58
NCBI Description	(Y08155) pectin methylesterase [Silene latifolia ssp. alba]

Seq. No.	284799
Contig ID	158133_1.R1011
5'-most EST	uC-zmflb73066f02a1
Method	BLASTX
NCBI GI	g3510251
BLAST score	171
E value	4.0e-12
Match length	47
% identity	62
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	284800
Contig ID	158148_1.R1011
5'-most EST	uC-zmflb73172g04a1

Seq. No.	284801
Contig ID	158170_1.R1011
5'-most EST	uC-zmflb73067c03a1

Seq. No.	284802
Contig ID	158198_1.R1011
5'-most EST	uC-zmflb73067f01a1

Seq. No.	284803
Contig ID	158207_1.R1011
5'-most EST	uC-zmflmo17250d11a1
Method	BLASTX
NCBI GI	g2827651
BLAST score	186
E value	7.0e-14
Match length	68
% identity	24
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	284804
Contig ID	158236_1.R1011
5'-most EST	uC-zmflb73068b12a1
Method	BLASTX
NCBI GI	g3128189
BLAST score	243
E value	1.0e-20
Match length	61
% identity	67
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	284805
Contig ID	158239_1.R1011
5'-most EST	uC-zmflb73068c02a1

Method	BLASTX
NCBI GI	g2739371
BLAST score	569
E value	8.0e-59
Match length	139
% identity	78
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	284806
Contig ID	158251_1.R1011
5'-most EST	uC-zmflb73068d10a1

Seq. No.	284807
Contig ID	158252_1.R1011
5'-most EST	uC-zmflb73131e02b2

Seq. No.	284808
Contig ID	158255_1.R1011
5'-most EST	uC-zmromo17010h06a1

Seq. No.	284809
Contig ID	158265_1.R1011
5'-most EST	uwh700207248.h1
Method	BLASTX
NCBI GI	g3128173
BLAST score	419
E value	4.0e-41
Match length	120
% identity	69
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284810
Contig ID	158267_1.R1011
5'-most EST	uC-zmrob73022b09a1

Seq. No.	284811
Contig ID	158267_2.R1011
5'-most EST	pmx700088429.h1
Method	BLASTX
NCBI GI	g1652942
BLAST score	295
E value	2.0e-26
Match length	197
% identity	38
NCBI Description	(D90909) extragenic suppressor [Synechocystis sp.]

Seq. No.	284812
Contig ID	158274_1.R1011
5'-most EST	uC-zmflb73279g08a2

Seq. No.	284813
Contig ID	158275_1.R1011
5'-most EST	uC-zmflb73068g08a1

Seq. No.	284814
Contig ID	158276_1.R1011
5'-most EST	uC-zmflb73102a03a1

Seq. No.	284815
Contig ID	158278_1.R1011
5'-most EST	yne700378548.h1

Seq. No.	284816
Contig ID	158285_1.R1011
5'-most EST	uC-zmflb73068h10a1

Seq. No.	284817
Contig ID	158288_1.R1011
5'-most EST	uC-zmflb73350h09a1

Seq. No.	284818
Contig ID	158331_1.R1011
5'-most EST	uC-zmrob73002f11a1
Method	BLASTX
NCBI GI	g1946372
BLAST score	273
E value	5.0e-24
Match length	98
% identity	56
NCBI Description	(U93215) yeast hypothetical protein YDB1_SCHPO isolog [Arabidopsis thaliana]

Seq. No.	284819
Contig ID	158342_1.R1011
5'-most EST	uC-zmflmo17277e12a1
Method	BLASTX
NCBI GI	g1651862
BLAST score	155
E value	3.0e-10
Match length	56
% identity	48
NCBI Description	(D90900) lysine decarboxylase [Synechocystis sp.]

Seq. No.	284820
Contig ID	158360_1.R1011
5'-most EST	gct701168804.h1

Seq. No.	284821
Contig ID	158428_1.R1011
5'-most EST	uC-zmflmo17127c09a1
Method	BLASTX
NCBI GI	g3377509
BLAST score	437
E value	2.0e-63
Match length	133
% identity	92
NCBI Description	(AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No.	284822
Contig ID	158441_1.R1011
5'-most EST	uC-zmflb73074a11a1
Method	BLASTX
NCBI GI	g3176664
BLAST score	497

E value	3.0e-50
Match length	150
% identity	62
NCBI Description	(AC004393) Contains similarity to beta scruin gb_Z47541 from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955 come from this gene. [Arabidopsis thaliana]

Seq. No.	284823
Contig ID	158445_1.R1011
5'-most EST	vux700160753.h1

Seq. No.	284824
Contig ID	158451_1.R1011
5'-most EST	uC-zmflb73074c06a1
Method	BLASTX
NCBI GI	g3510255
BLAST score	206
E value	3.0e-16
Match length	50
% identity	82
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284825
Contig ID	158461_1.R1011
5'-most EST	uC-zmflb73074d07a1

Seq. No.	284826
Contig ID	158474_1.R1011
5'-most EST	uC-zmflb73129g06a1

Seq. No.	284827
Contig ID	158519_1.R1011
5'-most EST	uC-zmflmo17241c08a1

Seq. No.	284828
Contig ID	158529_1.R1011
5'-most EST	uC-zmflb73273g10a1

Seq. No.	284829
Contig ID	158551_1.R1011
5'-most EST	uC-zmflb73354f05a1

Seq. No.	284830
Contig ID	158551_2.R1011
5'-most EST	uC-zmromo17025e08a1

Seq. No.	284831
Contig ID	158560_1.R1011
5'-most EST	uC-zmflb73075g04a1

Seq. No.	284832
Contig ID	158561_1.R1011
5'-most EST	uC-zmflb73075g05a1

Seq. No.	284833
Contig ID	158561_2.R1011
5'-most EST	xmt700258322.h1

Method	BLASTX
NCBI GI	g3023377
BLAST score	239
E value	2.0e-20
Match length	53
% identity	85
NCBI Description	LOW-TEMPERATURE INDUCED PROTEIN BLT101 (SALT-STRESS INDUCED HYDROPHOBIC PEPTIDE ESI3) >gi_629776_pir__S40406 blt101 protein - barley >gi_439273_emb_CAA80984_ (Z25537) 54 amino acids [Hordeum vulgare] >gi_551068_gb_AAA21847.1_ (U00966) salt-stress induced hydrophobic peptide [Elytrigia elongata]

Seq. No.	284834
Contig ID	158563_1.R1011
5'-most EST	uer700580916.h1

Seq. No.	284835
Contig ID	158565_1.R1011
5'-most EST	uC-zmflb73075g11a1

Seq. No.	284836
Contig ID	158565_2.R1011
5'-most EST	hbs701183606.h1

Seq. No.	284837
Contig ID	158565_3.R1011
5'-most EST	tzu700202143.h1

Seq. No.	284838
Contig ID	158575_1.R1011
5'-most EST	hbs701185792.h1

Seq. No.	284839
Contig ID	158578_1.R1011
5'-most EST	uC-zmflb73129b12a1
Method	BLASTX
NCBI GI	g1117780
BLAST score	163
E value	3.0e-11
Match length	72
% identity	57
NCBI Description	(D49367) 4-coumarate:CoA ligase [Lithospermum erythrorhizon]

Seq. No.	284840
Contig ID	158601_1.R1011
5'-most EST	uC-zmflb73077d05a1

Seq. No.	284841
Contig ID	158603_1.R1011
5'-most EST	uC-zmflmo17428d10a1

Seq. No.	284842
Contig ID	158625_1.R1011
5'-most EST	uC-zmflb73077g04a1

Seq. No.	284843
Contig ID	158640_1.R1011
5'-most EST	uC-zmflb73078b07a1
Method	BLASTX
NCBI GI	g1707015
BLAST score	340
E value	9.0e-32
Match length	127
% identity	53
NCBI Description	(U78721) protein phosphatase 2C isolog [Arabidopsis thaliana]

Seq. No.	284844
Contig ID	158642_1.R1011
5'-most EST	uC-zmflmo17153e04a1

Seq. No.	284845
Contig ID	158654_1.R1011
5'-most EST	ceu700431690.h1
Method	BLASTX
NCBI GI	g2191187
BLAST score	179
E value	1.0e-12
Match length	104
% identity	41
NCBI Description	(AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]

Seq. No.	284846
Contig ID	158660_1.R1011
5'-most EST	xyt700342601.h1
Method	BLASTX
NCBI GI	g3641868
BLAST score	276
E value	3.0e-24
Match length	92
% identity	60
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]

Seq. No.	284847
Contig ID	158665_1.R1011
5'-most EST	uC-zmflb73078e03a1
Method	BLASTX
NCBI GI	g3461814
BLAST score	205
E value	2.0e-31
Match length	131
% identity	56
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	284848
Contig ID	158667_1.R1011
5'-most EST	uC-zmflb73078e05a1

Seq. No.	284849
Contig ID	158693_1.R1011
5'-most EST	uC-zmflmo17425e09a1

Seq. No.	284850
Contig ID	158701_1.R1011
5'-most EST	fdz701l61280.h1
Seq. No.	284851
Contig ID	158739_1.R1011
5'-most EST	uC-zmflb73080g05a1
Seq. No.	284852
Contig ID	158759_1.R1011
5'-most EST	pwr700449923.h1
Seq. No.	284853
Contig ID	158760_1.R1011
5'-most EST	uC-zmflb73273c10a1
Seq. No.	284854
Contig ID	158767_1.R1011
5'-most EST	uC-zmflmo17059d12a1
Seq. No.	284855
Contig ID	158772_1.R1011
5'-most EST	uC-zmflb73082c06a2
Seq. No.	284856
Contig ID	158777_1.R1011
5'-most EST	xdb700337730.h1
Seq. No.	284857
Contig ID	158800_1.R1011
5'-most EST	uC-zmflmo17058c08a1
Method	BLASTX
NCBI GI	g2104534
BLAST score	284
E value	2.0e-25
Match length	97
% identity	58
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]
Seq. No.	284858
Contig ID	158831_1.R1011
5'-most EST	uC-zmflb73149f09a1
Seq. No.	284859
Contig ID	158833_1.R1011
5'-most EST	uC-zmflb73326d08a1
Method	BLASTX
NCBI GI	g4522008
BLAST score	249
E value	4.0e-21
Match length	109
% identity	44
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.	284860
Contig ID	158849_1.R1011

5'-most EST	uC-zmflmo17156f04a1
Method	BLASTX
NCBI GI	g3928085
BLAST score	231
E value	5.0e-22
Match length	79
% identity	65
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	284861
Contig ID	158852_1.R1011
5'-most EST	uC-zmromo17011c02a1
Method	BLASTX
NCBI GI	g4336747
BLAST score	168
E value	8.0e-12
Match length	79
% identity	47
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No.	284862
Contig ID	158855_1.R1011
5'-most EST	uC-zmflb73246f12a2

Seq. No.	284863
Contig ID	158875_1.R1011
5'-most EST	uC-zmflb73309b09a1

Seq. No.	284864
Contig ID	158880_1.R1011
5'-most EST	tfd700572384.h1

Seq. No.	284865
Contig ID	158882_1.R1011
5'-most EST	cat700016258.r1
Method	BLASTX
NCBI GI	g3047114
BLAST score	298
E value	1.0e-26
Match length	124
% identity	48
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	284866
Contig ID	158885_1.R1011
5'-most EST	uC-zmflb73085b04a1

Seq. No.	284867
Contig ID	158890_1.R1011
5'-most EST	uC-zmrob73033g02a1

Seq. No.	284868
Contig ID	158903_1.R1011
5'-most EST	uC-zmflmo17367a12a1

Seq. No.	284869
Contig ID	158921_1.R1011

5'-most EST	uC-zmflmo17211d10a1
Seq. No.	284870
Contig ID	158921_2.R1011
5'-most EST	uC-zmflmo17223c10a1
Method	BLASTN
NCBI GI	g1519252
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Oryza sativa GF14-d protein mRNA, complete cds
Seq. No.	284871
Contig ID	158922_2.R1011
5'-most EST	uC-zmflb73085f08a1
Seq. No.	284872
Contig ID	158965_1.R1011
5'-most EST	uC-zmflb73337a09a1
Method	BLASTX
NCBI GI	g3372671
BLAST score	188
E value	4.0e-14
Match length	54
% identity	63
NCBI Description	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana]
Seq. No.	284873
Contig ID	159019_1.R1011
5'-most EST	uC-zmflb73089e07a1
Seq. No.	284874
Contig ID	159021_1.R1011
5'-most EST	cat700017112.r1
Seq. No.	284875
Contig ID	159035_1.R1011
5'-most EST	uC-zmflb73090a02a2
Seq. No.	284876
Contig ID	159050_1.R1011
5'-most EST	uC-zmflb73090b08a2
Method	BLASTN
NCBI GI	g517492
BLAST score	37
E value	2.0e-11
Match length	57
% identity	91
NCBI Description	Z.Mays Zm38 gene, intron
Seq. No.	284877
Contig ID	159069_1.R1011
5'-most EST	uC-zmflb73178a08a1
Seq. No.	284878
Contig ID	159069_2.R1011

5'-most EST	xyt700346590.h1
Seq. No.	284879
Contig ID	159071_1.R1011
5'-most EST	uC-zmflmo17117c01a1
Seq. No.	284880
Contig ID	159072_1.R1011
5'-most EST	uC-zmflb73090d11a2
Seq. No.	284881
Contig ID	159087_1.R1011
5'-most EST	uC-zmflb73090f07a2
Seq. No.	284882
Contig ID	159096_1.R1011
5'-most EST	uC-zmflb73090g06a2
Seq. No.	284883
Contig ID	159098_1.R1011
5'-most EST	uC-zmflb73189a11a1
Seq. No.	284884
Contig ID	159106_1.R1011
5'-most EST	uC-zmflb73306a08a1
Seq. No.	284885
Contig ID	159107_1.R1011
5'-most EST	uC-zmflb73305f01a1
Method	BLASTX
NCBI GI	g3763921
BLAST score	235
E value	2.0e-19
Match length	67
% identity	69
NCBI Description	(AC004450) putative pirin protein [Arabidopsis thaliana]
Seq. No.	284886
Contig ID	159128_1.R1011
5'-most EST	uC-zmflb73091c10a1
Seq. No.	284887
Contig ID	159133_1.R1011
5'-most EST	uC-zmflb73208a03a2
Seq. No.	284888
Contig ID	159137_1.R1011
5'-most EST	uC-zmflb73387d01a1
Seq. No.	284889
Contig ID	159151_1.R1011
5'-most EST	uC-zmflb73092a02a1
Seq. No.	284890
Contig ID	159156_1.R1011
5'-most EST	uC-zmflb73092b04a1
Method	BLASTX

NCBI GI	g2244965
BLAST score	202
E value	2.0e-15
Match length	80
% identity	55
NCBI Description	(Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No.	284891
Contig ID	159182_1.R1011
5'-most EST	uC-zmflb73125h02a1
Method	BLASTX
NCBI GI	g3643085
BLAST score	216
E value	2.0e-22
Match length	106
% identity	61
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	284892
Contig ID	159188_1.R1011
5'-most EST	uC-zmflb73092f09a1
Method	BLASTX
NCBI GI	g4204793
BLAST score	330
E value	1.0e-30
Match length	117
% identity	25
NCBI Description	(U52079) P-glycoprotein [Solanum tuberosum]

Seq. No.	284893
Contig ID	159202_1.R1011
5'-most EST	uC-zmflb73093a11a1
Method	BLASTX
NCBI GI	g4587575
BLAST score	300
E value	3.0e-27
Match length	78
% identity	67
NCBI Description	(AC006550) Belongs to PF_01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gb_AA585719, gb_AA728503 and gb_T22272 come from this gene. [Arabidopsis thaliana]

Seq. No.	284894
Contig ID	159243_1.R1011
5'-most EST	uC-zmflb73094h03a1
Method	BLASTN
NCBI GI	g3057119
BLAST score	34
E value	2.0e-09
Match length	98
% identity	84
NCBI Description	Zea mays starch synthase DULL1 (dull1) mRNA, complete cds

Seq. No.	284895
Contig ID	159248_1.R1011

5'-most EST	uC-zmflmo17047e12a1
Method	BLASTX
NCBI GI	g3123130
BLAST score	301
E value	4.0e-27
Match length	97
% identity	61
NCBI Description	HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN T32G6.2 IN CHROMOSOME II >gi_2618685 (AC002510) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >gi_3241948 (AC004625) putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana]

Seq. No.	284896
Contig ID	159261_1.R1011
5'-most EST	uC-zmflb73094a12a1

Seq. No.	284897
Contig ID	159286_1.R1011
5'-most EST	uC-zmflb73094d11a1

Seq. No.	284898
Contig ID	159308_1.R1011
5'-most EST	uC-zmflb73094g09a1

Seq. No.	284899
Contig ID	159318_1.R1011
5'-most EST	uC-zmflb73094h11a1

Seq. No.	284900
Contig ID	159320_1.R1011
5'-most EST	uC-zmflb73095a02a1
Method	BLASTX
NCBI GI	g3327389
BLAST score	204
E value	6.0e-16
Match length	52
% identity	79
NCBI Description	(AC004483) putative DNA replication licensing factor, mcm5 [Arabidopsis thaliana]

Seq. No.	284901
Contig ID	159322_1.R1011
5'-most EST	uC-zmflb73116g09a1

Seq. No.	284902
Contig ID	159331_1.R1011
5'-most EST	cat700020651.r1
Method	BLASTX
NCBI GI	g4531442
BLAST score	159
E value	1.0e-10
Match length	38
% identity	74
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No. 284903

Contig ID	159340_1.R1011
5'-most EST	uC-zmromo17102d10a1
Method	BLASTX
NCBI GI	g731707
BLAST score	229
E value	9.0e-19
Match length	80
% identity	51
NCBI Description	SET1 PROTEIN >gi_626647_pir__S48961 hypothetical protein YHR119w - yeast (Saccharomyces cerevisiae) >gi_529135 (U00059) Set1p [Saccharomyces cerevisiae]

Seq. No.	284904
Contig ID	159340_2.R1011
5'-most EST	uC-zmflb73150f09a1

Seq. No.	284905
Contig ID	159345_1.R1011
5'-most EST	uC-zmflb73095d02a1

Seq. No.	284906
Contig ID	159354_1.R1011
5'-most EST	uC-zmflmo17168d05a1

Seq. No.	284907
Contig ID	159360_1.R1011
5'-most EST	cat700018250.r1

Seq. No.	284908
Contig ID	159371_1.R1011
5'-most EST	uC-zmflb73280b05a1
Method	BLASTX
NCBI GI	g3935183
BLAST score	246
E value	7.0e-21
Match length	93
% identity	49
NCBI Description	(AC004557) F17L21.26 [Arabidopsis thaliana]

Seq. No.	284909
Contig ID	159377_1.R1011
5'-most EST	uC-zmflmo17371b05a1

Seq. No.	284910
Contig ID	159380_1.R1011
5'-most EST	uC-zmflb73401h03a1

Seq. No.	284911
Contig ID	159381_1.R1011
5'-most EST	uC-zmflb73096a05a1

Seq. No.	284912
Contig ID	159383_1.R1011
5'-most EST	uC-zmflmo17427c03a1

Seq. No.	284913
Contig ID	159385_1.R1011

5'-most EST	uC-zmflb73149e04a1
Seq. No.	284914
Contig ID	159390_1.R1011
5'-most EST	uC-zmflb73414d04a1
Seq. No.	284915
Contig ID	159408_1.R1011
5'-most EST	uwc700155947.h1
Seq. No.	284916
Contig ID	159431_1.R1011
5'-most EST	uC-zmflb73159b10a2
Seq. No.	284917
Contig ID	159453_1.R1011
5'-most EST	uC-zmflb73274d03a1
Seq. No.	284918
Contig ID	159461_1.R1011
5'-most EST	uC-zmflb73101a08a1
Seq. No.	284919
Contig ID	159468_1.R1011
5'-most EST	fdz701161260.h1
Seq. No.	284920
Contig ID	159536_1.R1011
5'-most EST	uC-zmflb73105a06a1
Seq. No.	284921
Contig ID	159554_1.R1011
5'-most EST	uC-zmflb73224f07a1
Seq. No.	284922
Contig ID	159558_1.R1011
5'-most EST	uC-zmflb73105c12a1
Seq. No.	284923
Contig ID	159560_1.R1011
5'-most EST	uC-zmflb73105d03a1
Seq. No.	284924
Contig ID	159565_1.R1011
5'-most EST	wty700166940.h1
Method	BLASTX
NCBI GI	g134034
BLAST score	248
E value	5.0e-21
Match length	60
% identity	77
NCBI Description	30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5) (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1) >gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor, chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270) chloroplast ribosomal protein S22 [Spinacia oleracea] >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein

[Spinacia oleracea]

Seq. No.	284925
Contig ID	159566_1.R1011
5'-most EST	xjt700093478.h1
Method	BLASTX
NCBI GI	g2130139
BLAST score	975
E value	1.0e-106
Match length	183
% identity	99
NCBI Description	hypothetical protein - maize >gi_949980_emb_CAA61258_ (X88779) orf [Zea mays]

Seq. No.	284926
Contig ID	159568_1.R1011
5'-most EST	uC-zmflmo17365b04a1

Seq. No.	284927
Contig ID	159594_1.R1011
5'-most EST	uC-zmflb73108c07a1
Method	BLASTN
NCBI GI	g192760
BLAST score	173
E value	1.0e-92
Match length	283
% identity	90
NCBI Description	Mouse lens alpha-A-crystallin mRNA, 3' end

Seq. No.	284928
Contig ID	159629_1.R1011
5'-most EST	uC-zmflb73106c09a1
Method	BLASTX
NCBI GI	g4415916
BLAST score	356
E value	8.0e-34
Match length	112
% identity	57
NCBI Description	(AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	284929
Contig ID	159641_1.R1011
5'-most EST	uC-zmflb73106d12a1

Seq. No.	284930
Contig ID	159646_1.R1011
5'-most EST	uC-zmflb73106e05a1
Method	BLASTX
NCBI GI	g2896801
BLAST score	226
E value	2.0e-18
Match length	119
% identity	41
NCBI Description	(AC004155) ERCC4_MOUSE [Mus musculus]

Seq. No.	284931

Contig ID	159658_1.R1011
5'-most EST	uC-zmflb73106f07a1
Method	BLASTX
NCBI GI	g3378650
BLAST score	410
E value	7.0e-40
Match length	124
% identity	65
NCBI Description	(X97606) abscisic acid activated [Medicago sativa]

Seq. No.	284932
Contig ID	159659_1.R1011
5'-most EST	uC-zmflmo17194c08a1

Seq. No.	284933
Contig ID	159660_1.R1011
5'-most EST	uC-zmflb73106f09a1

Seq. No.	284934
Contig ID	159662_1.R1011
5'-most EST	uC-zmflb73106f11a1

Seq. No.	284935
Contig ID	159717_1.R1011
5'-most EST	uC-zmflb73210h04a1

Seq. No.	284936
Contig ID	159718_1.R1011
5'-most EST	uC-zmflb73107d03a2

Seq. No.	284937
Contig ID	159724_1.R1011
5'-most EST	uC-zmflb73107e01a2

Seq. No.	284938
Contig ID	159726_1.R1011
5'-most EST	xdb700337594.h1

Seq. No.	284939
Contig ID	159738_1.R1011
5'-most EST	uC-zmflb73107f08a2

Seq. No.	284940
Contig ID	159746_1.R1011
5'-most EST	uC-zmflb73110e04a1
Method	BLASTX
NCBI GI	g3421413
BLAST score	306
E value	9.0e-48
Match length	111
% identity	85
NCBI Description	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No.	284941
Contig ID	159746_2.R1011

5'-most EST	uC-zmflmo17156a09a1
Seq. No.	284942
Contig ID	159747_1.R1011
5'-most EST	uC-zmflmo17424c12a1
Seq. No.	284943
Contig ID	159759_1.R1011
5'-most EST	cjh700193315.h1
Seq. No.	284944
Contig ID	159777_1.R1011
5'-most EST	uC-zmflb73108b10a1
Seq. No.	284945
Contig ID	159832_1.R1011
5'-most EST	uC-zmflmo17054g11a1
Seq. No.	284946
Contig ID	159858_1.R1011
5'-most EST	dhd700198072.h1
Method	BLASTX
NCBI GI	g2979562
BLAST score	251
E value	2.0e-21
Match length	76
% identity	64
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana] >gi_3386623 (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.	284947
Contig ID	159863_1.R1011
5'-most EST	uC-zmflb73109h11a1
Seq. No.	284948
Contig ID	159885_1.R1011
5'-most EST	uC-zmflb73110c07a1
Seq. No.	284949
Contig ID	159889_1.R1011
5'-most EST	uC-zmflmo17212g08a1
Seq. No.	284950
Contig ID	159903_1.R1011
5'-most EST	ypc700801782.h1
Seq. No.	284951
Contig ID	159916_1.R1011
5'-most EST	uC-zmflb73110f09a1
Seq. No.	284952
Contig ID	159922_1.R1011
5'-most EST	uC-zmflb73110g04a1
Seq. No.	284953
Contig ID	159924_1.R1011

5'-most EST	uC-zmflb73110g06a1
Seq. No.	284954
Contig ID	159928_1.R1011
5'-most EST	uC-zmflb73110g12a1
Method	BLASTX
NCBI GI	g2944040
BLAST score	583
E value	2.0e-60
Match length	123
% identity	89
NCBI Description	(AF048900) indeterminate spikelet 1 [Zea mays]
Seq. No.	284955
Contig ID	159942_1.R1011
5'-most EST	cat700019549.r1
Seq. No.	284956
Contig ID	159943_1.R1011
5'-most EST	jfc700968592.h1
Seq. No.	284957
Contig ID	159973_1.R1011
5'-most EST	uC-zmflb73404g10a1
Seq. No.	284958
Contig ID	159987_1.R1011
5'-most EST	uC-zmflb73379f12a1
Method	BLASTX
NCBI GI	g1929998
BLAST score	171
E value	3.0e-12
Match length	67
% identity	48
NCBI Description	(U77463) NADPH-dependent HC-toxin reductase [Hordeum vulgare]
Seq. No.	284959
Contig ID	159988_1.R1011
5'-most EST	uC-zmflmo17213f09a1
Seq. No.	284960
Contig ID	159989_1.R1011
5'-most EST	uC-zmflmo17089d07a1
Seq. No.	284961
Contig ID	160022_1.R1011
5'-most EST	uC-zmflb73240f09a2
Seq. No.	284962
Contig ID	160026_1.R1011
5'-most EST	uC-zmflb73112e02a1
Seq. No.	284963
Contig ID	160032_1.R1011
5'-most EST	uC-zmflmo17334d11a1

Seq. No.	284964
Contig ID	160033_1.R1011
5'-most EST	uC-zmflb73112e12a1
Method	BLASTX
NCBI GI	g4249385
BLAST score	507
E value	2.0e-51
Match length	117
% identity	79
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	284965
Contig ID	160055_1.R1011
5'-most EST	uC-zmflb73112h07a1

Seq. No.	284966
Contig ID	160056_1.R1011
5'-most EST	uC-zmflb73305g11a1

Seq. No.	284967
Contig ID	160072_1.R1011
5'-most EST	uC-zmflmo17130h03a1
Method	BLASTX
NCBI GI	g2344889
BLAST score	243
E value	3.0e-20
Match length	93
% identity	49
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	284968
Contig ID	160078_1.R1011
5'-most EST	cat700021387.r1

Seq. No.	284969
Contig ID	160080_1.R1011
5'-most EST	uC-zmflmo17266a07a1

Seq. No.	284970
Contig ID	160084_1.R1011
5'-most EST	uC-zmflmo17155e03a1
Method	BLASTX
NCBI GI	g3342249
BLAST score	211
E value	1.0e-16
Match length	128
% identity	47
NCBI Description	(AF047719) GA3 [Arabidopsis thaliana] >gi_3342251 (AF047720) GA3 [Arabidopsis thaliana]

Seq. No.	284971
Contig ID	160097_1.R1011
5'-most EST	uC-zmflmo17318b02a1

Seq. No.	284972
Contig ID	160098_1.R1011
5'-most EST	uC-zmflb73271e07a1

Seq. No.	284973
Contig ID	160104_1.R1011
5'-most EST	ntr700071916.h1
Method	BLASTX
NCBI GI	g729944
BLAST score	225
E value	2.0e-18
Match length	81
% identity	48
NCBI Description	POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524 major allergen mI protein - maize >gi_293902 (L14271) Zea mI [Zea mays]

Seq. No.	284974
Contig ID	160109_1.R1011
5'-most EST	uC-zmflmo17264f07a2

Seq. No.	284975
Contig ID	160145_1.R1011
5'-most EST	uC-zmflb73114c09a2

Seq. No.	284976
Contig ID	160150_1.R1011
5'-most EST	uC-zmflb73389c12a1
Method	BLASTX
NCBI GI	g2213594
BLAST score	239
E value	6.0e-20
Match length	62
% identity	63
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	284977
Contig ID	160155_1.R1011
5'-most EST	uC-zmflb73157g04a1

Seq. No.	284978
Contig ID	160173_1.R1011
5'-most EST	uC-zmflmo17180b02a1
Method	BLASTX
NCBI GI	g2961380
BLAST score	259
E value	3.0e-22
Match length	76
% identity	64
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	284979
Contig ID	160213_1.R1011
5'-most EST	uC-zmflmo17362f11a1

Seq. No.	284980
Contig ID	160216_1.R1011
5'-most EST	uC-zmflb73115e04a1

Seq. No.	284981

Contig ID 160222_1.R1011
5'-most EST uC-zmflb73115e10a1

Seq. No. 284982
Contig ID 160242_1.R1011
5'-most EST uC-zmflb73333d01a1

Seq. No. 284983
Contig ID 160251_1.R1011
5'-most EST uC-zmflb73210h11a1
Method BLASTX
NCBI GI g2129854
BLAST score 281
E value 1.0e-30
Match length 130
% identity 54
NCBI Description early nodulin 8 precursor - alfalfa >gi_304037 (L18899) early nodulin [Medicago sativa]

Seq. No. 284984
Contig ID 160252_1.R1011
5'-most EST uC-zmflmo17263d12a2

Seq. No. 284985
Contig ID 160258_1.R1011
5'-most EST uC-zmflmo17223f04a1

Seq. No. 284986
Contig ID 160259_1.R1011
5'-most EST uC-zmflb73228g04a1

Seq. No. 284987
Contig ID 160264_1.R1011
5'-most EST uC-zmflmo17135g03a1

Seq. No. 284988
Contig ID 160272_1.R1011
5'-most EST uC-zmflmo17023h06a1

Seq. No. 284989
Contig ID 160279_1.R1011
5'-most EST uC-zmflb73116d07a1

Seq. No. 284990
Contig ID 160281_1.R1011
5'-most EST uwc700154728.h1

Seq. No. 284991
Contig ID 160306_1.R1011
5'-most EST uC-zmflb73116g10a1

Seq. No. 284992
Contig ID 160307_1.R1011
5'-most EST uC-zmflb73116g11a1

Seq. No. 284993
Contig ID 160311_1.R1011

5'-most EST	uC-zmflb73116h03a1
Seq. No.	284994
Contig ID	160323_1.R1011
5'-most EST	uC-zmflb73117a09a1
Seq. No.	284995
Contig ID	160331_1.R1011
5'-most EST	uC-zmflb73117b08a1
Seq. No.	284996
Contig ID	160335_1.R1011
5'-most EST	uC-zmflb73117c03a1
Seq. No.	284997
Contig ID	160363_1.R1011
5'-most EST	uC-zmflb73117f05a1
Seq. No.	284998
Contig ID	160376_1.R1011
5'-most EST	uC-zmflb73117g10a1
Seq. No.	284999
Contig ID	160378_1.R1011
5'-most EST	uC-zmflb73117h02a1
Seq. No.	285000
Contig ID	160390_1.R1011
5'-most EST	uC-zmflb73119a04a1
Seq. No.	285001
Contig ID	160391_1.R1011
5'-most EST	wen700336687.h1
Method	BLASTX
NCBI GI	g3482908
BLAST score	162
E value	2.0e-11
Match length	78
% identity	55
NCBI Description	(AC005551) R26529_2, partial CDS [Homo sapiens]
Seq. No.	285002
Contig ID	160403_1.R1011
5'-most EST	uC-zmflb73119c03a1
Seq. No.	285003
Contig ID	160406_1.R1011
5'-most EST	uC-zmflb73119c06a1
Seq. No.	285004
Contig ID	160410_1.R1011
5'-most EST	uC-zmflb73119c10a1
Method	BLASTX
NCBI GI	g2833373
BLAST score	227
E value	1.0e-18
Match length	56

% identity	77
NCBI Description	DNA-3-METHYLADENINE GLYCOSIDASE (3-METHYLADENINE DNA GLYCOSYLASE) >gi_429157_emb_CAA53763_ (X76169) 3-methyladenine glycosylase [Arabidopsis thaliana]

Seq. No.	285005
Contig ID	160452_1.R1011
5'-most EST	tfd700575190.h1
Method	BLASTX
NCBI GI	g2809251
BLAST score	242
E value	2.0e-20
Match length	112
% identity	44
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No.	285006
Contig ID	160459_1.R1011
5'-most EST	uC-zmflb73242c04a1
Method	BLASTX
NCBI GI	g4455278
BLAST score	148
E value	2.0e-09
Match length	99
% identity	34
NCBI Description	(AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285007
Contig ID	160460_1.R1011
5'-most EST	uC-zmromo17111g10a1

Seq. No.	285008
Contig ID	160477_1.R1011
5'-most EST	uC-zmflb73243g12a1

Seq. No.	285009
Contig ID	160481_1.R1011
5'-most EST	uC-zmflb73120a09a1

Seq. No.	285010
Contig ID	160485_1.R1011
5'-most EST	uC-zmflb73120b02a1
Method	BLASTX
NCBI GI	g2262158
BLAST score	355
E value	1.0e-33
Match length	129
% identity	57
NCBI Description	(AC002329) putative mitochondrial phosphate translocator protein [Arabidopsis thaliana]

Seq. No.	285011
Contig ID	160495_1.R1011
5'-most EST	uC-zmflb73345d07a2

Seq. No.	285012
Contig ID	160501_1.R1011

5'-most EST	uC-zmflmo17240e09a1
Seq. No.	285013
Contig ID	160526_1.R1011
5'-most EST	uC-zmflb73191g08a1
Seq. No.	285014
Contig ID	160531_1.R1011
5'-most EST	uC-zmflb73214a10a1
Seq. No.	285015
Contig ID	160541_1.R1011
5'-most EST	uC-zmflb731215c03a1
Method	BLASTX
NCBI GI	g2737882
BLAST score	180
E value	4.0e-13
Match length	96
% identity	41
NCBI Description	(U46014) polyphenol oxidase [Saccharum sp.]
Seq. No.	285016
Contig ID	160546_1.R1011
5'-most EST	uC-zmflmo17363e04a1
Seq. No.	285017
Contig ID	160558_1.R1011
5'-most EST	uC-zmflb731215e08a1
Seq. No.	285018
Contig ID	160561_1.R1011
5'-most EST	uC-zmflmo17335h02a1
Seq. No.	285019
Contig ID	160563_1.R1011
5'-most EST	uC-zmflb73214f03a1
Method	BLASTX
NCBI GI	g2660677
BLAST score	382
E value	1.0e-36
Match length	129
% identity	61
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]
Seq. No.	285020
Contig ID	160567_1.R1011
5'-most EST	uC-zmflb73130e03a1
Seq. No.	285021
Contig ID	160586_1.R1011
5'-most EST	uC-zmflb731216a10a1
Method	BLASTX
NCBI GI	g2435514
BLAST score	214
E value	4.0e-17
Match length	51
% identity	78

NCBI Description	(AF024504) Similar to serine/threonine protein kinase; coded for by A. thaliana cDNA T20930; coded for by A. thaliana cDNA T43472 [Arabidopsis thaliana]

Seq. No.	285022
Contig ID	160591_1.R1011
5'-most EST	uC-zmflb731216c03a1

Seq. No.	285023
Contig ID	160618_1.R1011
5'-most EST	cat700018649.r1
Method	BLASTX
NCBI GI	g4559381
BLAST score	282
E value	6.0e-25
Match length	76
% identity	71
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285024
Contig ID	160619_1.R1011
5'-most EST	uC-zmflb73216f12b2

Seq. No.	285025
Contig ID	160656_1.R1011
5'-most EST	uC-zmflb73121a12b2
Method	BLASTX
NCBI GI	g2232017
BLAST score	249
E value	3.0e-21
Match length	51
% identity	96
NCBI Description	(U95953) viviparous-14 [Zea mays]

Seq. No.	285026
Contig ID	160657_1.R1011
5'-most EST	uC-zmflb73121b01a1

Seq. No.	285027
Contig ID	160725_1.R1011
5'-most EST	xdb700341581.h1

Seq. No.	285028
Contig ID	160726_1.R1011
5'-most EST	uC-zmflb73160h10a1

Seq. No.	285029
Contig ID	160730_1.R1011
5'-most EST	uC-zmflb73247b01b3

Seq. No.	285030
Contig ID	160744_1.R1011
5'-most EST	pmx700081990.h1
Method	BLASTX
NCBI GI	g3757523
BLAST score	457
E value	1.0e-45

Match length	117
% identity	72
NCBI Description	(AC005167) putative transportin [Arabidopsis thaliana]

Seq. No.	285031
Contig ID	160758_1.R1011
5'-most EST	uC-zmflb73246c04a2

Seq. No.	285032
Contig ID	160769_1.R1011
5'-most EST	uC-zmflb73121h08a1

Seq. No.	285033
Contig ID	160770_1.R1011
5'-most EST	uC-zmflb73121h08b2

Seq. No.	285034
Contig ID	160779_1.R1011
5'-most EST	uC-zmflb73122a02a1
Method	BLASTX
NCBI GI	g4220537
BLAST score	406
E value	2.0e-39
Match length	100
% identity	74
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	285035
Contig ID	160830_1.R1011
5'-most EST	uC-zmflb73122d01a1

Seq. No.	285036
Contig ID	160830_2.R1011
5'-most EST	uC-zmflmo17391e01a1

Seq. No.	285037
Contig ID	160842_1.R1011
5'-most EST	uC-zmflmo17158h07a1

Seq. No.	285038
Contig ID	160853_1.R1011
5'-most EST	gct701174174.h1
Method	BLASTX
NCBI GI	g2982301
BLAST score	193
E value	2.0e-14
Match length	69
% identity	49
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

Seq. No.	285039
Contig ID	160854_1.R1011
5'-most EST	ntr700072777.h1

Seq. No.	285040
Contig ID	160865_1.R1011
5'-most EST	uC-zmflb73288h02a1

Method	BLASTX
NCBI GI	g3695392
BLAST score	177
E value	8.0e-13
Match length	57
% identity	53
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	285041
Contig ID	160873_1.R1011
5'-most EST	uC-zmflb73122f04a1

Seq. No.	285042
Contig ID	160876_1.R1011
5'-most EST	gct701172303.h1

Seq. No.	285043
Contig ID	160877_1.R1011
5'-most EST	xdb700340033.h1
Method	BLASTX
NCBI GI	g4490294
BLAST score	784
E value	1.0e-83
Match length	185
% identity	79
NCBI Description	(AL035678) WD-repeat protein-like protein [Arabidopsis thaliana]

Seq. No.	285044
Contig ID	160881_1.R1011
5'-most EST	uC-zmflb73122f08a1

Seq. No.	285045
Contig ID	160895_1.R1011
5'-most EST	xsy700211478.h1

Seq. No.	285046
Contig ID	160897_1.R1011
5'-most EST	xsy700217249.h1

Seq. No.	285047
Contig ID	160909_1.R1011
5'-most EST	nbm700468303.h1
Method	BLASTX
NCBI GI	g3880026
BLAST score	148
E value	2.0e-09
Match length	49
% identity	47
NCBI Description	(Z75550) Similarity with Schizosaccharomyces hypothetical gene (TREMBL ID G847708); cDNA EST EMBL:M89418 comes from this gene [Caenorhabditis elegans]

Seq. No.	285048
Contig ID	160943_1.R1011
5'-most EST	uC-zmflmo17031e07a1

Seq. No.	285049
Contig ID	160946_1.R1011
5'-most EST	cat700019370.r1
Seq. No.	285050
Contig ID	160950_1.R1011
5'-most EST	uC-zmflmo17321c12a1
Seq. No.	285051
Contig ID	160958_1.R1011
5'-most EST	uC-zmflmo17123g05a1
Method	BLASTN
NCBI GI	g22245
BLAST score	93
E value	9.0e-45
Match length	121
% identity	94
NCBI Description	Zea mays DNA for cin4 element (showing homology to reverse transcriptase)
Seq. No.	285052
Contig ID	160966_1.R1011
5'-most EST	uC-zmflb731234b12a1
Seq. No.	285053
Contig ID	160982_1.R1011
5'-most EST	uC-zmflmo17133c04a1
Seq. No.	285054
Contig ID	160992_1.R1011
5'-most EST	wyr700240621.h1
Seq. No.	285055
Contig ID	161032_1.R1011
5'-most EST	uC-zmflb731237c09a1
Seq. No.	285056
Contig ID	161044_1.R1011
5'-most EST	cat700019514.r1
Seq. No.	285057
Contig ID	161061_1.R1011
5'-most EST	uC-zmflmo17364e06a1
Seq. No.	285058
Contig ID	161072_1.R1011
5'-most EST	nbm700467724.h1
Seq. No.	285059
Contig ID	161092_2.R1011
5'-most EST	ymt700222751.h1
Seq. No.	285060
Contig ID	161119_1.R1011
5'-most EST	uC-zmflb73124b03a1
Seq. No.	285061

Contig ID	161127_1.R1011
5'-most EST	uC-zmflb73124b12a1
Seq. No.	285062
Contig ID	161133_1.R1011
5'-most EST	uC-zmflb73124c07a1
Seq. No.	285063
Contig ID	161147_1.R1011
5'-most EST	uC-zmflb73207g12a1
Seq. No.	285064
Contig ID	161165_1.R1011
5'-most EST	ypc700801648.h1
Method	BLASTX
NCBI GI	g2244772
BLAST score	320
E value	1.0e-40
Match length	120
% identity	71
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]
Seq. No.	285065
Contig ID	161171_1.R1011
5'-most EST	uC-zmflmo17052h09a1
Seq. No.	285066
Contig ID	161172_1.R1011
5'-most EST	uC-zmflb73124g07a1
Seq. No.	285067
Contig ID	161174_1.R1011
5'-most EST	uC-zmflmo17009a08a1
Seq. No.	285068
Contig ID	161176_1.R1011
5'-most EST	uC-zmflb73124h02a1
Seq. No.	285069
Contig ID	161184_1.R1011
5'-most EST	uC-zmflmo17107d04a1
Seq. No.	285070
Contig ID	161186_1.R1011
5'-most EST	uC-zmflb73125a02a1
Seq. No.	285071
Contig ID	161191_1.R1011
5'-most EST	uC-zmflb73125a06a1
Seq. No.	285072
Contig ID	161192_1.R1011
5'-most EST	uC-zmflb73125a07a1
Seq. No.	285073
Contig ID	161196_1.R1011
5'-most EST	uC-zmflb73125a09a1

Seq. No.	285074
Contig ID	161197_1.R1011
5'-most EST	uC-zmflb73125a09b2

Seq. No.	285075
Contig ID	161206_1.R1011
5'-most EST	ymt700221989.h1

Seq. No.	285076
Contig ID	161236_1.R1011
5'-most EST	dyk700103010.h1
Method	BLASTX
NCBI GI	g3786009
BLAST score	208
E value	2.0e-16
Match length	61
% identity	70
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	285077
Contig ID	161274_1.R1011
5'-most EST	uC-zmflb73125e12b2

Seq. No.	285078
Contig ID	161279_1.R1011
5'-most EST	xdb700338635.h1

Seq. No.	285079
Contig ID	161296_1.R1011
5'-most EST	uC-zmflmo17322c06a1

Seq. No.	285080
Contig ID	161296_3.R1011
5'-most EST	uC-zmflb73372h03a1

Seq. No.	285081
Contig ID	161309_1.R1011
5'-most EST	uC-zmflb73125g11a1
Method	BLASTX
NCBI GI	g2129753
BLAST score	228
E value	1.0e-18
Match length	57
% identity	74
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	285082
Contig ID	161325_1.R1011
5'-most EST	uC-zmflmo17316d09a1
Method	BLASTX
NCBI GI	g2105137
BLAST score	149
E value	2.0e-09
Match length	49

% identity	67
NCBI Description	(U66876) ADP-glucose pyrophosphorylase large subunit [Hordeum vulgare]

Seq. No.	285083
Contig ID	161343_1.R1011
5'-most EST	uC-zmflmo17075g08a1

Seq. No.	285084
Contig ID	161344_1.R1011
5'-most EST	uC-zmflmo17056b06a1

Seq. No.	285085
Contig ID	161413_1.R1011
5'-most EST	uC-zmflb73127a07b2
Method	BLASTX
NCBI GI	g3242717
BLAST score	507
E value	2.0e-51
Match length	130
% identity	75
NCBI Description	(AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No.	285086
Contig ID	161418_1.R1011
5'-most EST	uC-zmflb73127b01b2
Method	BLASTX
NCBI GI	g4263695
BLAST score	150
E value	2.0e-09
Match length	154
% identity	29
NCBI Description	(AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No.	285087
Contig ID	161436_1.R1011
5'-most EST	pmx700088385.h1
Method	BLASTX
NCBI GI	g2408073
BLAST score	259
E value	3.0e-22
Match length	83
% identity	60
NCBI Description	(Z99167) chromodomain helicase [Schizosaccharomyces pombe]

Seq. No.	285088
Contig ID	161438_1.R1011
5'-most EST	nbm700471623.h1

Seq. No.	285089
Contig ID	161445_1.R1011
5'-most EST	nbm700469003.h1

Seq. No.	285090
Contig ID	161450_1.R1011
5'-most EST	wty700164054.h1

Seq. No.	285091
Contig ID	161496_1.R1011
5'-most EST	cyk700049596.f1
Method	BLASTX
NCBI GI	g2979555
BLAST score	150
E value	8.0e-10
Match length	100
% identity	31
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	285092
Contig ID	161498_1.R1011
5'-most EST	uC-zmflmo17403g08a1

Seq. No.	285093
Contig ID	161502_1.R1011
5'-most EST	xdb700341541.h1

Seq. No.	285094
Contig ID	161508_1.R1011
5'-most EST	uC-zmflb73128a06a1

Seq. No.	285095
Contig ID	161530_1.R1011
5'-most EST	uC-zmflb73128c12a1

Seq. No.	285096
Contig ID	161534_1.R1011
5'-most EST	uC-zmflb73128d04a1
Method	BLASTX
NCBI GI	g1001708
BLAST score	151
E value	1.0e-09
Match length	47
% identity	55
NCBI Description	(D64004) NifS [Synechocystis sp.]

Seq. No.	285097
Contig ID	161548_1.R1011
5'-most EST	uC-zmflb73128f03a1

Seq. No.	285098
Contig ID	161552_1.R1011
5'-most EST	uC-zmflb73128f08a1

Seq. No.	285099
Contig ID	161559_1.R1011
5'-most EST	uC-zmflb73128g04a1

Seq. No.	285100
Contig ID	161586_1.R1011
5'-most EST	uC-zmflmo17057g08a1

Seq. No.	285101
Contig ID	161652_1.R1011

5'-most EST	uC-zmflmo17334a07a1
Seq. No.	285102
Contig ID	161658_1.R1011
5'-most EST	uC-zmflb73175e03a2
Seq. No.	285103
Contig ID	161679_1.R1011
5'-most EST	uC-zmflb73305g12a1
Seq. No.	285104
Contig ID	161712_1.R1011
5'-most EST	nbm700473479.h1
Method	BLASTX
NCBI GI	g1171642
BLAST score	251
E value	2.0e-21
Match length	93
% identity	51
NCBI Description	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK >gi_481206_pir__S38326 protein kinase - Arabidopsis thaliana >gi_166809 (L07248) protein kinase [Arabidopsis thaliana]
Seq. No.	285105
Contig ID	161732_1.R1011
5'-most EST	uC-zmflb73130e03b2
Method	BLASTX
NCBI GI	g4206196
BLAST score	342
E value	5.0e-32
Match length	171
% identity	45
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]
Seq. No.	285106
Contig ID	161767_1.R1011
5'-most EST	uC-zmflb73360b10a1
Seq. No.	285107
Contig ID	161778_1.R1011
5'-most EST	uC-zmflb73130g11a1
Seq. No.	285108
Contig ID	161782_1.R1011
5'-most EST	uC-zmflb73130h07a1
Seq. No.	285109
Contig ID	161783_1.R1011
5'-most EST	uC-zmflb73260d10a1
Seq. No.	285110
Contig ID	161812_1.R1011
5'-most EST	uwc700154034.h1
Method	BLASTX
NCBI GI	g3047114
BLAST score	187

E value	6.0e-14
Match length	52
% identity	69
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	285111
Contig ID	161860_1.R1011
5'-most EST	fwa700099317.h1
Method	BLASTX
NCBI GI	g2760327
BLAST score	329
E value	1.0e-30
Match length	79
% identity	44
NCBI Description	(AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No.	285112
Contig ID	161883_1.R1011
5'-most EST	uC-zmflb73131f03a1

Seq. No.	285113
Contig ID	161914_1.R1011
5'-most EST	uC-zmflb73131h02a1

Seq. No.	285114
Contig ID	161917_1.R1011
5'-most EST	uC-zmflb73131h04a1
Method	BLASTX
NCBI GI	g3859570
BLAST score	231
E value	3.0e-19
Match length	58
% identity	83
NCBI Description	(AF098753) unknown [Oryza sativa]

Seq. No.	285115
Contig ID	161931_1.R1011
5'-most EST	uC-zmrob73024d04a1
Method	BLASTX
NCBI GI	g4204283
BLAST score	247
E value	4.0e-21
Match length	89
% identity	55
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	285116
Contig ID	161933_1.R1011
5'-most EST	uC-zmflb73132a10a1

Seq. No.	285117
Contig ID	161934_1.R1011
5'-most EST	uC-zmflb73132a06a1
Method	BLASTX
NCBI GI	g3133287
BLAST score	258
E value	1.0e-25

Match length	95
% identity	65
NCBI Description	(AF020203) stearoyl-ACP desaturase [Pelargonium x hortorum]

Seq. No.	285118
Contig ID	161943_1.R1011
5'-most EST	dyk700102563.h1

Seq. No.	285119
Contig ID	161944_1.R1011
5'-most EST	uC-zmflmo17245f12a1

Seq. No.	285120
Contig ID	161954_1.R1011
5'-most EST	uC-zmflb73132c11a1

Seq. No.	285121
Contig ID	161961_1.R1011
5'-most EST	uC-zmflmo17337e11a1

Seq. No.	285122
Contig ID	161962_1.R1011
5'-most EST	uC-zmflb73300e05a1

Seq. No.	285123
Contig ID	161969_1.R1011
5'-most EST	uC-zmflb73132e08a1

Seq. No.	285124
Contig ID	161979_1.R1011
5'-most EST	uC-zmflb73132f10a1

Seq. No.	285125
Contig ID	162003_1.R1011
5'-most EST	pmx700086168.h1
Method	BLASTX
NCBI GI	g629670
BLAST score	279
E value	1.0e-24
Match length	79
% identity	63
NCBI Description	hypothetical protein - tomato

Seq. No.	285126
Contig ID	162006_1.R1011
5'-most EST	uC-zmflmo17020e04a1

Seq. No.	285127
Contig ID	162006_2.R1011
5'-most EST	uC-zmflb73250c11a2

Seq. No.	285128
Contig ID	162008_1.R1011
5'-most EST	uC-zmflb73417c02a1

Seq. No.	285129
Contig ID	162029_1.R1011

5'-most EST	uC-zmflb73133h12a1
Method	BLASTX
NCBI GI	g4467095
BLAST score	181
E value	3.0e-13
Match length	39
% identity	92
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	285130
Contig ID	162041_1.R1011
5'-most EST	uC-zmflb73133h09a1

Seq. No.	285131
Contig ID	162049_1.R1011
5'-most EST	uC-zmflb73134a08a2

Seq. No.	285132
Contig ID	162065_1.R1011
5'-most EST	uC-zmflmo17263h05a2

Seq. No.	285133
Contig ID	162069_1.R1011
5'-most EST	xdb700341847.h1

Seq. No.	285134
Contig ID	162103_1.R1011
5'-most EST	uC-zmflb73163c05a1

Seq. No.	285135
Contig ID	162112_1.R1011
5'-most EST	uC-zmflb73135d04b2

Seq. No.	285136
Contig ID	162116_1.R1011
5'-most EST	uC-zmflb73163d08a1

Seq. No.	285137
Contig ID	162137_1.R1011
5'-most EST	pmx700090523.h1

Seq. No.	285138
Contig ID	162147_1.R1011
5'-most EST	uC-zmflb73135g08b2
Method	BLASTX
NCBI GI	g3327110
BLAST score	175
E value	2.0e-12
Match length	159
% identity	32
NCBI Description	(AB014548) KIAA0648 protein [Homo sapiens]

Seq. No.	285139
Contig ID	162148_1.R1011
5'-most EST	uC-zmflb73135g09b2
Method	BLASTX
NCBI GI	g4584257

BLAST score	448
E value	2.0e-44
Match length	104
% identity	79
NCBI Description	(Y18472) SINA2p [Vitis vinifera]

Seq. No.	285140
Contig ID	162159_1.R1011
5'-most EST	uC-zmflb73163h10a1

Seq. No.	285141
Contig ID	162164_1.R1011
5'-most EST	uC-zmflmo17427h06a1

Seq. No.	285142
Contig ID	162173_1.R1011
5'-most EST	uC-zmflmo17396c12a1

Seq. No.	285143
Contig ID	162182_1.R1011
5'-most EST	uC-zmflb73136c02a1

Seq. No.	285144
Contig ID	162198_1.R1011
5'-most EST	dyk700103168.h1
Method	BLASTX
NCBI GI	g4581164
BLAST score	237
E value	7.0e-20
Match length	145
% identity	41
NCBI Description	(AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No.	285145
Contig ID	162199_1.R1011
5'-most EST	uC-zmflmo17069c02a1
Method	BLASTX
NCBI GI	g4038034
BLAST score	308
E value	3.0e-28
Match length	71
% identity	80
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	285146
Contig ID	162217_1.R1011
5'-most EST	uC-zmflb73136f06a1

Seq. No.	285147
Contig ID	162219_1.R1011
5'-most EST	uC-zmflb73136f08a1

Seq. No.	285148
Contig ID	162247_1.R1011
5'-most EST	gct701174288.h1
Method	BLASTX
NCBI GI	g2832643

BLAST score	181
E value	2.0e-13
Match length	80
% identity	55
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285149
Contig ID	162269_1.R1011
5'-most EST	uC-zmflb73137c11a1

Seq. No.	285150
Contig ID	162287_1.R1011
5'-most EST	uC-zmflmo17319e03a1
Method	BLASTN
NCBI GI	g4185305
BLAST score	346
E value	0.0e+00
Match length	454
% identity	94
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	285151
Contig ID	162313_1.R1011
5'-most EST	uC-zmflmo17391e11a1

Seq. No.	285152
Contig ID	162327_1.R1011
5'-most EST	uC-zmflb73308d02a1
Method	BLASTX
NCBI GI	g2589162
BLAST score	189
E value	3.0e-14
Match length	60
% identity	67
NCBI Description	(D88451) aldehyde oxidase [Zea mays]

Seq. No.	285153
Contig ID	162352_1.R1011
5'-most EST	uC-zmflmo17425g12a1
Method	BLASTX
NCBI GI	g3877256
BLAST score	167
E value	2.0e-11
Match length	104
% identity	40
NCBI Description	(Z50177) similar to lipase [Caenorhabditis elegans]

Seq. No.	285154
Contig ID	162353_1.R1011
5'-most EST	uC-zmflb73146a05a2

Seq. No.	285155
Contig ID	162359_1.R1011
5'-most EST	uC-zmflmo17203d12a1

Seq. No.	285156
Contig ID	162364_1.R1011
5'-most EST	uC-zmflmo17223b03a1

Seq. No.	285157
Contig ID	162389_1.R1011
5'-most EST	uC-zmflb73308a03a1
Method	BLASTX
NCBI GI	g2370232
BLAST score	199
E value	2.0e-15
Match length	39
% identity	90
NCBI Description	(AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

Seq. No.	285158
Contig ID	162395_1.R1011
5'-most EST	uC-zmflb73146f01a2

Seq. No.	285159
Contig ID	162404_1.R1011
5'-most EST	uC-zmflmo17037f08a1

Seq. No.	285160
Contig ID	162429_1.R1011
5'-most EST	uC-zmflmo17215f02a1
Method	BLASTX
NCBI GI	g2194119
BLAST score	145
E value	3.0e-09
Match length	30
% identity	63
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	285161
Contig ID	162436_1.R1011
5'-most EST	uC-zmflb73148g09a1
Method	BLASTN
NCBI GI	g575425
BLAST score	72
E value	2.0e-32
Match length	126
% identity	91
NCBI Description	Z.mays mRNA for sugar-starvation induced protein

Seq. No.	285162
Contig ID	162467_1.R1011
5'-most EST	uC-zmflmo17058c09a1

Seq. No.	285163
Contig ID	162469_1.R1011
5'-most EST	uC-zmflb73148e11a1
Method	BLASTX
NCBI GI	g3559935
BLAST score	287
E value	1.0e-25

Match length	94
% identity	57
NCBI Description	(AJ005253) ClpP protease [Mus musculus] >gi_4454289_emb_CAA09966_ (AJ012249) ClpP protease [Mus musculus]

Seq. No.	285164
Contig ID	162503_1.R1011
5'-most EST	uC-zmflb73149a07a1

Seq. No.	285165
Contig ID	162523_1.R1011
5'-most EST	uC-zmflb73149c12a1
Method	BLASTX
NCBI GI	g2459435
BLAST score	142
E value	6.0e-09
Match length	38
% identity	71
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	285166
Contig ID	162538_1.R1011
5'-most EST	uC-zmflb73149e06a1

Seq. No.	285167
Contig ID	162555_1.R1011
5'-most EST	uC-zmflb73149g03a1

Seq. No.	285168
Contig ID	162578_1.R1011
5'-most EST	uC-zmflb73150a11a1

Seq. No.	285169
Contig ID	162584_1.R1011
5'-most EST	uC-zmflb73150b08a1

Seq. No.	285170
Contig ID	162588_1.R1011
5'-most EST	uC-zmflb73150c02a1

Seq. No.	285171
Contig ID	162589_1.R1011
5'-most EST	uC-zmflb73150c03a1
Method	BLASTX
NCBI GI	g1617219
BLAST score	145
E value	3.0e-09
Match length	41
% identity	68
NCBI Description	(X99301) CPD photolyase [Arabidopsis thaliana] >gi_2984707 (AF053365) type II CPD photolyase PHR1 [Arabidopsis thaliana]

Seq. No.	285172
Contig ID	162619_1.R1011

5'-most EST	uC-zmflb73150g10a1
Seq. No.	285173
Contig ID	162622_1.R1011
5'-most EST	uC-zmflb73150h03a1
Method	BLASTN
NCBI GI	g609261
BLAST score	40
E value	4.0e-13
Match length	108
% identity	84
NCBI Description	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
Seq. No.	285174
Contig ID	162634_1.R1011
5'-most EST	uC-zmflb73279a06a2
Seq. No.	285175
Contig ID	162642_1.R1011
5'-most EST	uC-zmflb73151b04a2
Method	BLASTX
NCBI GI	g2982434
BLAST score	167
E value	2.0e-11
Match length	75
% identity	45
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]
Seq. No.	285176
Contig ID	162654_1.R1011
5'-most EST	uC-zmflb73151c09a2
Method	BLASTX
NCBI GI	g1167955
BLAST score	177
E value	8.0e-13
Match length	75
% identity	51
NCBI Description	(U43497) putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein [Hordeum vulgare]
Seq. No.	285177
Contig ID	162664_1.R1011
5'-most EST	uC-zmflb73243e07a1
Method	BLASTX
NCBI GI	g3738312
BLAST score	244
E value	1.0e-20
Match length	83
% identity	63
NCBI Description	(AC005309) hypothetical protein [Arabidopsis thaliana]
Seq. No.	285178
Contig ID	162668_1.R1011
5'-most EST	uC-zmflb73301c06a1
Seq. No.	285179

Contig ID	162671_1.R1011
5'-most EST	uC-zmflb73151e03a2
Method	BLASTN
NCBI GI	g168641
BLAST score	76
E value	1.0e-34
Match length	137
% identity	89
NCBI Description	Maize Mu transposable element MRS-A

Seq. No.	285180
Contig ID	162685_1.R1011
5'-most EST	uC-zmflb73151f07a2

Seq. No.	285181
Contig ID	162691_1.R1011
5'-most EST	uC-zmflb73151g02a2

Seq. No.	285182
Contig ID	162695_1.R1011
5'-most EST	uC-zmflb73151g05a2

Seq. No.	285183
Contig ID	162712_1.R1011
5'-most EST	uC-zmflb73151h09a1

Seq. No.	285184
Contig ID	162716_1.R1011
5'-most EST	uC-zmflb73158h10a1
Method	BLASTX
NCBI GI	g2688842
BLAST score	258
E value	5.0e-22
Match length	85
% identity	55
NCBI Description	(AF004830) serine palmitoyltransferase LCB2 subunit [Cricetulus griseus]

Seq. No.	285185
Contig ID	162725_1.R1011
5'-most EST	uC-zmflmo17240f05a1

Seq. No.	285186
Contig ID	162734_1.R1011
5'-most EST	uC-zmflb73152b12a1

Seq. No.	285187
Contig ID	162746_1.R1011
5'-most EST	uC-zmflmo17319a03a1

Seq. No.	285188
Contig ID	162750_1.R1011
5'-most EST	uC-zmflb73152e08a1

Seq. No.	285189
Contig ID	162760_1.R1011
5'-most EST	uC-zmflb73152g02a1

Method	BLASTN
NCBI GI	g22477
BLAST score	74
E value	2.0e-33
Match length	82
% identity	98
NCBI Description	Z.mays ruq-st transposon

Seq. No.	285190
Contig ID	162819_1.R1011
5'-most EST	uC-zmflb73154e11a1

Seq. No.	285191
Contig ID	162828_1.R1011
5'-most EST	cat700020390.r1

Seq. No.	285192
Contig ID	162847_1.R1011
5'-most EST	uC-zmflb73154h06b2

Seq. No.	285193
Contig ID	162885_1.R1011
5'-most EST	uC-zmflb73155d04b2
Method	BLASTX
NCBI GI	g2244790
BLAST score	179
E value	7.0e-13
Match length	134
% identity	43
NCBI Description	(Z97336) kinesin homolog [Arabidopsis thaliana]

Seq. No.	285194
Contig ID	162888_1.R1011
5'-most EST	pmx700087383.h1

Seq. No.	285195
Contig ID	162898_1.R1011
5'-most EST	uC-zmflb73155e05a1

Seq. No.	285196
Contig ID	162941_1.R1011
5'-most EST	gct701167346.h1
Method	BLASTN
NCBI GI	g4185305
BLAST score	65
E value	5.0e-28
Match length	201
% identity	84
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	285197
Contig ID	162965_1.R1011
5'-most EST	xdb700338020.h1

Seq. No.	285198
Contig ID	162990_1.R1011
5'-most EST	uC-zmflb73157b09b2

Seq. No.	285199
Contig ID	163050_1.R1011
5'-most EST	uC-zmflb73157f08b2

Seq. No.	285200
Contig ID	163062_1.R1011
5'-most EST	uC-zmflb73157g06a1
Method	BLASTN
NCBI GI	g4321977
BLAST score	65
E value	4.0e-28
Match length	97
% identity	92
NCBI Description	Zea mays beta-amylase (Amy2) gene, complete cds

Seq. No.	285201
Contig ID	163068_1.R1011
5'-most EST	uC-zmflb73157g09b2

Seq. No.	285202
Contig ID	163074_1.R1011
5'-most EST	uC-zmflb73157h02a1

Seq. No.	285203
Contig ID	163076_1.R1011
5'-most EST	uC-zmflb73157h02b2

Seq. No.	285204
Contig ID	163099_2.R1011
5'-most EST	fdz701166845.h1
Method	BLASTX
NCBI GI	g4220491
BLAST score	227
E value	4.0e-23
Match length	148
% identity	41
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285205
Contig ID	163103_1.R1011
5'-most EST	uC-zmflb73158a09b2

Seq. No.	285206
Contig ID	163112_1.R1011
5'-most EST	pmx700085347.h1
Method	BLASTX
NCBI GI	g4510377
BLAST score	726
E value	5.0e-77
Match length	182
% identity	74
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	285207
Contig ID	163156_1.R1011
5'-most EST	cyk700050352.f1

Seq. No.	285208
Contig ID	163159_1.R1011
5'-most EST	uC-zmflb73158e05b2

Seq. No.	285209
Contig ID	163204_1.R1011
5'-most EST	uC-zmflb73158f12b2
Method	BLASTX
NCBI GI	g3152613
BLAST score	180
E value	3.0e-13
Match length	137
% identity	39
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285210
Contig ID	163206_1.R1011
5'-most EST	gwl700617808.h1

Seq. No.	285211
Contig ID	163218_1.R1011
5'-most EST	uC-zmflb73158g09a1
Method	BLASTN
NCBI GI	g2695924
BLAST score	83
E value	1.0e-38
Match length	171
% identity	87
NCBI Description	Hordeum vulgare mRNA for hypothetical protein, clone RG28

Seq. No.	285212
Contig ID	163245_1.R1011
5'-most EST	uC-zmflb73159a01b2

Seq. No.	285213
Contig ID	163260_1.R1011
5'-most EST	uC-zmflb73159a12a2

Seq. No.	285214
Contig ID	163268_1.R1011
5'-most EST	uC-zmflb73159b06a2

Seq. No.	285215
Contig ID	163291_1.R1011
5'-most EST	pmx700090504.h1
Method	BLASTX
NCBI GI	g3776581
BLAST score	162
E value	4.0e-11
Match length	44
% identity	66
NCBI Description	(AC005388) Similar to Beta integral membrane protein homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	285216
Contig ID	163299_1.R1011
5'-most EST	uC-zmflb73159d04a2

Seq. No.	285217
Contig ID	163325_1.R1011
5'-most EST	hbs701l85554.h1
Method	BLASTX
NCBI GI	g3983663
BLAST score	514
E value	2.0e-52
Match length	117
% identity	90
NCBI Description	(AB011270) importin-beta1 [Oryza sativa]

Seq. No.	285218
Contig ID	163329_1.R1011
5'-most EST	uC-zmflb73159f04b2
Method	BLASTX
NCBI GI	g4510377
BLAST score	423
E value	8.0e-61
Match length	252
% identity	46
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	285219
Contig ID	163379_1.R1011
5'-most EST	uC-zmflb73160e08b2

Seq. No.	285220
Contig ID	163386_1.R1011
5'-most EST	uC-zmflmo17346a08a1

Seq. No.	285221
Contig ID	163417_1.R1011
5'-most EST	uC-zmflmo17421f08a1

Seq. No.	285222
Contig ID	163429_1.R1011
5'-most EST	uC-zmflb73204e05a1
Method	BLASTX
NCBI GI	g3983663
BLAST score	609
E value	3.0e-63
Match length	142
% identity	85
NCBI Description	(AB011270) importin-beta1 [Oryza sativa]

Seq. No.	285223
Contig ID	163429_2.R1011
5'-most EST	uC-zmflb73160d03a1
Method	BLASTN
NCBI GI	g3983662
BLAST score	39
E value	2.0e-12

Match length	180
% identity	82
NCBI Description	Oryza sativa mRNA for importin-beta1, complete cds

Seq. No.	285224
Contig ID	163455_1.R1011
5'-most EST	uC-zmflb73160e09b2
Method	BLASTX
NCBI GI	g2147484
BLAST score	185
E value	2.0e-13
Match length	41
% identity	95
NCBI Description	homeotic protein - Phalaenopsis sp >gi_1173622 (U34743) homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No.	285225
Contig ID	163468_1.R1011
5'-most EST	uC-zmflb73160f05a1
Method	BLASTX
NCBI GI	g4455338
BLAST score	179
E value	5.0e-13
Match length	55
% identity	67
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	285226
Contig ID	163530_1.R1011
5'-most EST	tzu700206653.h1

Seq. No.	285227
Contig ID	163544_1.R1011
5'-most EST	uwc700155615.h1
Method	BLASTX
NCBI GI	g2316016
BLAST score	688
E value	2.0e-72
Match length	206
% identity	65
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	285228
Contig ID	163554_1.R1011
5'-most EST	uC-zmflb73161c03b2
Method	BLASTX
NCBI GI	g3128195
BLAST score	205
E value	4.0e-16
Match length	45
% identity	87
NCBI Description	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]

Seq. No.	285229

Contig ID	163558_1.R1011
5'-most EST	uC-zmflb73161c06a1
Method	BLASTX
NCBI GI	g3236240
BLAST score	230
E value	5.0e-19
Match length	67
% identity	67
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	285230
Contig ID	163565_1.R1011
5'-most EST	tzu700203766.h1

Seq. No.	285231
Contig ID	163581_1.R1011
5'-most EST	uC-zmflb73161d12a1

Seq. No.	285232
Contig ID	163608_1.R1011
5'-most EST	uC-zmflb73161f02b2

Seq. No.	285233
Contig ID	163637_1.R1011
5'-most EST	pwf700321647.h1

Seq. No.	285234
Contig ID	163653_1.R1011
5'-most EST	uC-zmflb73161h08b2

Seq. No.	285235
Contig ID	163713_1.R1011
5'-most EST	pmx700090241.h1
Method	BLASTX
NCBI GI	g3176874
BLAST score	420
E value	5.0e-45
Match length	142
% identity	72
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	285236
Contig ID	163734_1.R1011
5'-most EST	ymt700218812.h1

Seq. No.	285237
Contig ID	163795_1.R1011
5'-most EST	uC-zmflb73188d02a1

Seq. No.	285238
Contig ID	163808_1.R1011
5'-most EST	uC-zmflb73303d09a2

Seq. No.	285239
Contig ID	163809_1.R1011
5'-most EST	uC-zmflb73163e02a1

Method	BLASTX
NCBI GI	g3152596
BLAST score	168
E value	1.0e-11
Match length	73
% identity	53
NCBI Description	(AC002986) YUP8H12R.36 [Arabidopsis thaliana]

Seq. No.	285240
Contig ID	163826_1.R1011
5'-most EST	uC-zmflb73227f07a1

Seq. No.	285241
Contig ID	163847_1.R1011
5'-most EST	uC-zmflb73163g06b2

Seq. No.	285242
Contig ID	163857_1.R1011
5'-most EST	clt700045002.f1

Seq. No.	285243
Contig ID	163890_1.R1011
5'-most EST	uC-zmflb73262c02a2

Seq. No.	285244
Contig ID	163945_1.R1011
5'-most EST	uC-zmflmo17272g11a1

Seq. No.	285245
Contig ID	163954_1.R1011
5'-most EST	uC-zmflmo17046f10a1

Seq. No.	285246
Contig ID	163966_1.R1011
5'-most EST	uC-zmflb73164h11a1

Seq. No.	285247
Contig ID	164014_1.R1011
5'-most EST	uC-zmflb73165c01a1

Seq. No.	285248
Contig ID	164017_1.R1011
5'-most EST	uC-zmflb73165c02b2

Seq. No.	285249
Contig ID	164018_1.R1011
5'-most EST	uC-zmflb73165c03a1

Seq. No.	285250
Contig ID	164023_1.R1011
5'-most EST	uC-zmflb73165d01b2

Seq. No.	285251
Contig ID	164047_1.R1011
5'-most EST	vux700159430.h1
Method	BLASTX
NCBI GI	g1209756

BLAST score	262
E value	7.0e-23
Match length	129
% identity	44
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	285252
Contig ID	164090_1.R1011
5'-most EST	uC-zmflb73166a10b2

Seq. No.	285253
Contig ID	164098_1.R1011
5'-most EST	uC-zmflb73166b11a1

Seq. No.	285254
Contig ID	164107_1.R1011
5'-most EST	uC-zmflb73166b10a1

Seq. No.	285255
Contig ID	164108_1.R1011
5'-most EST	uC-zmflb73166b10b2
Method	BLASTX
NCBI GI	g1710663
BLAST score	211
E value	7.0e-17
Match length	125
% identity	43
NCBI Description	PUTATIVE DNA-DIRECTED RNA POLYMERASE III 130 KD POLYPEPTIDE (RNA POLYMERASE III SUBUNIT 2) >gi_1204209_emb_CAA93558_ (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe]

Seq. No.	285256
Contig ID	164116_1.R1011
5'-most EST	xjt700094439.h1

Seq. No.	285257
Contig ID	164152_1.R1011
5'-most EST	uC-zmflb73166e02b2

Seq. No.	285258
Contig ID	164157_1.R1011
5'-most EST	wty700164613.h1
Method	BLASTN
NCBI GI	g4185305
BLAST score	150
E value	6.0e-79
Match length	258
% identity	91
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	285259
Contig ID	164167_1.R1011
5'-most EST	uC-zmflb73166e11b2

Seq. No.	285260
Contig ID	164175_1.R1011
5'-most EST	uC-zmflb73166f03a1
Method	BLASTX
NCBI GI	g125580
BLAST score	191
E value	2.0e-14
Match length	40
% identity	93
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat

Seq. No.	285261
Contig ID	164184_1.R1011
5'-most EST	uC-zmflb73305b09a1

Seq. No.	285262
Contig ID	164185_1.R1011
5'-most EST	uC-zmflb73166f09a1

Seq. No.	285263
Contig ID	164186_1.R1011
5'-most EST	uC-zmflmo17247g08a1

Seq. No.	285264
Contig ID	164191_1.R1011
5'-most EST	uC-zmflb73378e06a2

Seq. No.	285265
Contig ID	164229_1.R1011
5'-most EST	uwc700154864.h1

Seq. No.	285266
Contig ID	164234_1.R1011
5'-most EST	xsy700211045.h1
Method	BLASTX
NCBI GI	g1546694
BLAST score	575
E value	3.0e-59
Match length	174
% identity	64
NCBI Description	(X98806) peroxidase ATP20a [Arabidopsis thaliana]

Seq. No.	285267
Contig ID	164245_1.R1011
5'-most EST	uC-zmflmo17403h10a1
Method	BLASTN
NCBI GI	g22378
BLAST score	36
E value	9.0e-11
Match length	48
% identity	94
NCBI Description	Z.mays gene for nucleic acid binding protein

Seq. No.	285268

Contig ID	164261_1.R1011
5'-most EST	uC-zmflb73167b08b2
Seq. No.	285269
Contig ID	164285_1.R1011
5'-most EST	uC-zmflb73167c11a1
Seq. No.	285270
Contig ID	164293_1.R1011
5'-most EST	uC-zmflb73167d03b2
Seq. No.	285271
Contig ID	164326_1.R1011
5'-most EST	uC-zmflb73167f03a1
Method	BLASTX
NCBI GI	g4490702
BLAST score	252
E value	2.0e-21
Match length	96
% identity	46
NCBI Description	(AL035680) hypothetical protein [Arabidopsis thaliana]
Seq. No.	285272
Contig ID	164330_1.R1011
5'-most EST	uC-zmflb73167f06a1
Seq. No.	285273
Contig ID	164346_1.R1011
5'-most EST	uC-zmflb73167g06a1
Seq. No.	285274
Contig ID	164361_1.R1011
5'-most EST	uC-zmflb73167h08a1
Seq. No.	285275
Contig ID	164362_1.R1011
5'-most EST	uC-zmflb73167h08b2
Method	BLASTX
NCBI GI	g3402697
BLAST score	447
E value	4.0e-59
Match length	166
% identity	68
NCBI Description	(AC004261) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]
Seq. No.	285276
Contig ID	164400_1.R1011
5'-most EST	uC-zmflb73397e10a1
Seq. No.	285277
Contig ID	164419_1.R1011
5'-most EST	uC-zmflb73169a10a1
Seq. No.	285278
Contig ID	164452_1.R1011
5'-most EST	uC-zmflmo17059c02a1

Seq. No.	285279
Contig ID	164459_1.R1011
5'-most EST	uC-zmflb73169c12b2

Seq. No.	285280
Contig ID	164475_1.R1011
5'-most EST	uC-zmflmo17247g10a1

Seq. No.	285281
Contig ID	164506_1.R1011
5'-most EST	cyk700048891.f1

Seq. No.	285282
Contig ID	164514_1.R1011
5'-most EST	uC-zmflb73169g01b2
Method	BLASTX
NCBI GI	g1351030
BLAST score	424
E value	7.0e-42
Match length	127
% identity	64
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_289365 (M35599) 60-kDa chaperonin-60 alpha-polypeptide precursor [Brassica napus]

Seq. No.	285283
Contig ID	164517_1.R1011
5'-most EST	uC-zmflb73169g03a1

Seq. No.	285284
Contig ID	164557_1.R1011
5'-most EST	uC-zmflb73224d07a1
Method	BLASTX
NCBI GI	g2739168
BLAST score	203
E value	6.0e-16
Match length	75
% identity	49
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	285285
Contig ID	164598_1.R1011
5'-most EST	hvj700623609.h1
Method	BLASTX
NCBI GI	g3763932
BLAST score	676
E value	3.0e-81
Match length	195
% identity	78
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	285286
Contig ID	164601_1.R1011
5'-most EST	wty700165633.h1

Seq. No.	285287
Contig ID	164602_1.R1011
5'-most EST	uC-zmflmo17014h03a1
Seq. No.	285288
Contig ID	164604_1.R1011
5'-most EST	uC-zmflb73170f01a1
Seq. No.	285289
Contig ID	164612_1.R1011
5'-most EST	uC-zmflb73170f09b2
Seq. No.	285290
Contig ID	164620_1.R1011
5'-most EST	uC-zmflmo17040d12a1
Seq. No.	285291
Contig ID	164624_1.R1011
5'-most EST	uC-zmflb73185h12a1
Seq. No.	285292
Contig ID	164625_1.R1011
5'-most EST	wyr700236045.h1
Seq. No.	285293
Contig ID	164633_1.R1011
5'-most EST	zla700379844.h1
Method	BLASTN
NCBI GI	g516549
BLAST score	51
E value	8.0e-20
Match length	73
% identity	93
NCBI Description	Zea mays B73 cyclin IIZm mRNA, partial cds
Seq. No.	285294
Contig ID	164635_1.R1011
5'-most EST	uC-zmflb73170h05a1
Seq. No.	285295
Contig ID	164638_1.R1011
5'-most EST	uC-zmflb73170h06b2
Method	BLASTX
NCBI GI	g4586061
BLAST score	366
E value	8.0e-35
Match length	176
% identity	43
NCBI Description	(AC007020) putative BOP1 protein [Arabidopsis thaliana]
Seq. No.	285296
Contig ID	164656_1.R1011
5'-most EST	uC-zmflb73172a11b2
Method	BLASTN
NCBI GI	g2832242
BLAST score	68

E value	8.0e-30
Match length	205
% identity	89
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	285297
Contig ID	164658_1.R1011
5'-most EST	uC-zmflmo17304h09a1

Seq. No.	285298
Contig ID	164697_1.R1011
5'-most EST	uC-zmflb73172d03b2

Seq. No.	285299
Contig ID	164700_1.R1011
5'-most EST	uC-zmflb73172d11b2

Seq. No.	285300
Contig ID	164701_1.R1011
5'-most EST	uC-zmflmo17352f06a1

Seq. No.	285301
Contig ID	164710_1.R1011
5'-most EST	uC-zmflmo17025c05a1

Seq. No.	285302
Contig ID	164727_1.R1011
5'-most EST	yyf700348350.h1
Method	BLASTX
NCBI GI	g3096922
BLAST score	331
E value	1.0e-30
Match length	99
% identity	70
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	285303
Contig ID	164731_1.R1011
5'-most EST	uC-zmflb73172g06b2
Method	BLASTX
NCBI GI	g2459436
BLAST score	454
E value	3.0e-45
Match length	104
% identity	82
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	285304
Contig ID	164745_1.R1011
5'-most EST	uC-zmflb73172h04a1

Seq. No.	285305
Contig ID	164746_1.R1011
5'-most EST	dyk700102932.h1

Seq. No.	285306
Contig ID	164783_1.R1011

5'-most EST	uC-zmflb73174d08a1
Seq. No.	285307
Contig ID	164788_1.R1011
5'-most EST	uC-zmflmo17039g05a1
Seq. No.	285308
Contig ID	164793_1.R1011
5'-most EST	uC-zmflb73174e09a1
Method	BLASTX
NCBI GI	g2746086
BLAST score	256
E value	5.0e-22
Match length	59
% identity	85
NCBI Description	(AF025292) putative high-affinity potassium transporter [Hordeum vulgare]
Seq. No.	285309
Contig ID	164832_1.R1011
5'-most EST	yyf700347508.h1
Seq. No.	285310
Contig ID	164871_1.R1011
5'-most EST	uC-zmflb73325a12a1
Method	BLASTX
NCBI GI	g1519680
BLAST score	150
E value	2.0e-09
Match length	62
% identity	40
NCBI Description	(U67953) contains similarity to C3HC4-class zinc finger (PS:PS00518) [Caenorhabditis elegans]
Seq. No.	285311
Contig ID	164881_1.R1011
5'-most EST	uC-zmflb73175h01a2
Seq. No.	285312
Contig ID	164918_1.R1011
5'-most EST	uC-zmflb73176d09b2
Method	BLASTX
NCBI GI	g2501572
BLAST score	177
E value	6.0e-13
Match length	112
% identity	34
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]
Seq. No.	285313
Contig ID	164922_1.R1011
5'-most EST	uC-zmflb73176e03b2
Seq. No.	285314
Contig ID	164923_1.R1011
5'-most EST	uC-zmflb73176e04b2

Method	BLASTX
NCBI GI	g4210504
BLAST score	309
E value	2.0e-28
Match length	103
% identity	61
NCBI Description	(AC002392) putative cadmium-transporting ATPase [Arabidopsis thaliana]

Seq. No.	285315
Contig ID	164924_1.R1011
5'-most EST	uC-zmflb73176e05b2

Seq. No.	285316
Contig ID	164962_1.R1011
5'-most EST	uC-zmflb73283h02a1

Seq. No.	285317
Contig ID	164979_1.R1011
5'-most EST	uC-zmflb73177f01a1

Seq. No.	285318
Contig ID	164998_1.R1011
5'-most EST	uC-zmflb73178b01a1

Seq. No.	285319
Contig ID	165003_1.R1011
5'-most EST	uC-zmflb73178b07a1

Seq. No.	285320
Contig ID	165007_1.R1011
5'-most EST	uC-zmflb73360f07a1

Seq. No.	285321
Contig ID	165016_1.R1011
5'-most EST	uC-zmflb73178c12a1

Seq. No.	285322
Contig ID	165018_1.R1011
5'-most EST	uC-zmflb73178d02a1

Seq. No.	285323
Contig ID	165023_1.R1011
5'-most EST	uC-zmflb73178d09a1
Method	BLASTX
NCBI GI	g2244965
BLAST score	144
E value	6.0e-09
Match length	65
% identity	48
NCBI Description	(Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No.	285324
Contig ID	165029_1.R1011
5'-most EST	uC-zmflb73178e05a1
Method	BLASTX
NCBI GI	g3122313

BLAST score	263
E value	9.0e-23
Match length	68
% identity	68
NCBI Description	LEC14B HOMOLOG >gi_2351587 (U82760) LEC14B homolog [Prunus armeniaca]

Seq. No.	285325
Contig ID	165055_1.R1011
5'-most EST	uC-zmflb73178h06a1

Seq. No.	285326
Contig ID	165059_1.R1011
5'-most EST	uC-zmflb73178h10a1

Seq. No.	285327
Contig ID	165070_1.R1011
5'-most EST	uC-zmflmo17314d03a1

Seq. No.	285328
Contig ID	165074_1.R1011
5'-most EST	xdb700337878.h1

Seq. No.	285329
Contig ID	165089_1.R1011
5'-most EST	uC-zmflb73179d03a2

Seq. No.	285330
Contig ID	165126_1.R1011
5'-most EST	cat700019749.r1

Seq. No.	285331
Contig ID	165135_1.R1011
5'-most EST	uC-zmflb73180a06a1

Seq. No.	285332
Contig ID	165137_1.R1011
5'-most EST	uC-zmflb73180a08a1

Seq. No.	285333
Contig ID	165138_1.R1011
5'-most EST	uC-zmflb73180a09a1

Seq. No.	285334
Contig ID	165149_1.R1011
5'-most EST	uC-zmflmo17152h06a1

Seq. No.	285335
Contig ID	165165_1.R1011
5'-most EST	uC-zmflb73180d09a1

Seq. No.	285336
Contig ID	165167_1.R1011
5'-most EST	uC-zmflmo17009e09a1

Seq. No.	285337
Contig ID	165183_1.R1011

5'-most EST	uC-zmflb73180g01a1
Method	BLASTX
NCBI GI	g4586245
BLAST score	175
E value	9.0e-13
Match length	62
% identity	56
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	285338
Contig ID	165252_1.R1011
5'-most EST	uC-zmflb73213e02a1

Seq. No.	285339
Contig ID	165264_2.R1011
5'-most EST	pmx700085782.h1
Method	BLASTX
NCBI GI	g2980641
BLAST score	305
E value	9.0e-28
Match length	150
% identity	47
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	285340
Contig ID	165278_1.R1011
5'-most EST	uC-zmflb73182c08b1

Seq. No.	285341
Contig ID	165280_1.R1011
5'-most EST	uC-zmflb73182c11a1
Method	BLASTX
NCBI GI	g4567251
BLAST score	217
E value	2.0e-17
Match length	52
% identity	67
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	285342
Contig ID	165280_2.R1011
5'-most EST	bdu700382727.h1

Seq. No.	285343
Contig ID	165306_1.R1011
5'-most EST	uC-zmflb73182e08b1

Seq. No.	285344
Contig ID	165325_1.R1011
5'-most EST	uC-zmflb73182f12a1

Seq. No.	285345
Contig ID	165346_1.R1011
5'-most EST	uC-zmflb73298e04a1

Seq. No.	285346
Contig ID	165376_1.R1011

5'-most EST	uC-zmf1b73369c10a1
Method	BLASTN
NCBI GI	g416144
BLAST score	368
E value	0.0e+00
Match length	372
% identity	100
NCBI Description	Zea mays beta-4 tubulin (tub4) mRNA, complete cds

Seq. No.	285347
Contig ID	165430_1.R1011
5'-most EST	uC-zmflmo17177b06a1

Seq. No.	285348
Contig ID	165432_1.R1011
5'-most EST	uC-zmflb73184c06a1

Seq. No.	285349
Contig ID	165462_1.R1011
5'-most EST	uC-zmflb73184f10a1

Seq. No.	285350
Contig ID	165484_1.R1011
5'-most EST	uC-zmflmo17052c05a1

Seq. No.	285351
Contig ID	165498_1.R1011
5'-most EST	uC-zmflmo17399e03a1

Seq. No.	285352
Contig ID	165512_1.R1011
5'-most EST	uC-zmflb73185d02a1

Seq. No.	285353
Contig ID	165528_1.R1011
5'-most EST	vux700161843.h1

Seq. No.	285354
Contig ID	165541_1.R1011
5'-most EST	uC-zmflb73185g01a1

Seq. No.	285355
Contig ID	165599_1.R1011
5'-most EST	uC-zmflb73186h03a1

Seq. No.	285356
Contig ID	165603_1.R1011
5'-most EST	uC-zmflmo17292d07a1

Seq. No.	285357
Contig ID	165607_1.R1011
5'-most EST	uC-zmflb73187a10a1

Seq. No.	285358
Contig ID	165610_1.R1011
5'-most EST	rvt700550752.h1

Seq. No.	285359
Contig ID	165610_2.R1011
5'-most EST	uC-zmflb73187b03a1

Seq. No.	285360
Contig ID	165628_1.R1011
5'-most EST	uC-zmflb73187d07a1

Seq. No.	285361
Contig ID	165636_1.R1011
5'-most EST	uC-zmflb73187e07a1
Method	BLASTX
NCBI GI	g2651302
BLAST score	182
E value	1.0e-13
Match length	56
% identity	62
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285362
Contig ID	165638_1.R1011
5'-most EST	uC-zmflb73187e12a1

Seq. No.	285363
Contig ID	165652_1.R1011
5'-most EST	uC-zmflb73298f02a1

Seq. No.	285364
Contig ID	165682_1.R1011
5'-most EST	uC-zmflb73188c09a1
Method	BLASTX
NCBI GI	g3894190
BLAST score	155
E value	3.0e-10
Match length	55
% identity	49
NCBI Description	(AC005662) putative RNA polymerase [Arabidopsis thaliana]

Seq. No.	285365
Contig ID	165689_1.R1011
5'-most EST	uC-zmflb73299c09a1

Seq. No.	285366
Contig ID	165700_1.R1011
5'-most EST	uC-zmflb73188e06a1

Seq. No.	285367
Contig ID	165722_1.R1011
5'-most EST	uC-zmflb73188g11a1

Seq. No.	285368
Contig ID	165746_1.R1011
5'-most EST	uC-zmflb73189c09a1

Seq. No.	285369
Contig ID	165758_1.R1011
5'-most EST	uC-zmflb73189e06a1

Seq. No.	285370
Contig ID	165764_1.R1011
5'-most EST	uC-zmflb73189f06a1
Method	BLASTX
NCBI GI	g4432867
BLAST score	150
E value	1.0e-09
Match length	70
% identity	39
NCBI Description	(AC006300) putative dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	285371
Contig ID	165771_1.R1011
5'-most EST	uC-zmflb73189g03a1
Method	BLASTX
NCBI GI	g3193324
BLAST score	197
E value	5.0e-15
Match length	56
% identity	66
NCBI Description	(AF069299) contains similarity to WD domains, G-beta repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84) [Arabidopsis thaliana]

Seq. No.	285372
Contig ID	165810_1.R1011
5'-most EST	uC-zmflb73190e03a1

Seq. No.	285373
Contig ID	165837_1.R1011
5'-most EST	uC-zmflb73309d01a1

Seq. No.	285374
Contig ID	165867_1.R1011
5'-most EST	uC-zmflmo17064d10a1

Seq. No.	285375
Contig ID	165867_2.R1011
5'-most EST	uC-zmflmo17064d09a1

Seq. No.	285376
Contig ID	165888_1.R1011
5'-most EST	uC-zmflmo17371g03a1

Seq. No.	285377
Contig ID	165894_1.R1011
5'-most EST	uC-zmflb73191h07a1

Seq. No.	285378
Contig ID	165906_1.R1011
5'-most EST	uC-zmflmo17140a05a1

Seq. No.	285379
Contig ID	165925_1.R1011
5'-most EST	uC-zmflb73192c04a1

Seq. No.	285380
Contig ID	165930_1.R1011
5'-most EST	uC-zmflb73192c09a1
Seq. No.	285381
Contig ID	165945_1.R1011
5'-most EST	uC-zmflb73333b08a1
Seq. No.	285382
Contig ID	165948_1.R1011
5'-most EST	uC-zmflb73192e07a1
Seq. No.	285383
Contig ID	165977_1.R1011
5'-most EST	uC-zmflb73193a02a1
Seq. No.	285384
Contig ID	165997_1.R1011
5'-most EST	uC-zmflb73193c03a1
Seq. No.	285385
Contig ID	166007_1.R1011
5'-most EST	ymt700222435.h1
Seq. No.	285386
Contig ID	166010_1.R1011
5'-most EST	uC-zmflb73193d06a1
Seq. No.	285387
Contig ID	166025_1.R1011
5'-most EST	uC-zmflmo17291d05a1
Seq. No.	285388
Contig ID	166063_1.R1011
5'-most EST	uC-zmflb73196b05a2
Seq. No.	285389
Contig ID	166070_1.R1011
5'-most EST	uC-zmrob73051c04a1
Seq. No.	285390
Contig ID	166086_1.R1011
5'-most EST	uC-zmflb73243h11a1
Seq. No.	285391
Contig ID	166095_1.R1011
5'-most EST	uC-zmromo17031h10a1
Method	BLASTX
NCBI GI	g984756
BLAST score	259
E value	3.0e-22
Match length	90
% identity	59
NCBI Description	(Z54153) chilling-inducible protein [Oryza sativa]
Seq. No.	285392

Contig ID	166101_1.R1011
5'-most EST	uC-zmflb73196f05a2
Seq. No.	285393
Contig ID	166112_1.R1011
5'-most EST	uC-zmflb73196h02a2
Seq. No.	285394
Contig ID	166124_1.R1011
5'-most EST	uC-zmflmo17222f06a1
Seq. No.	285395
Contig ID	166141_1.R1011
5'-most EST	uC-zmflb73197d08a1
Seq. No.	285396
Contig ID	166143_1.R1011
5'-most EST	uC-zmflb73197e03a1
Method	BLASTX
NCBI GI	g4587987
BLAST score	147
E value	4.0e-09
Match length	55
% identity	47
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]
Seq. No.	285397
Contig ID	166147_1.R1011
5'-most EST	uC-zmromo17100h11a1
Method	BLASTX
NCBI GI	g4490304
BLAST score	220
E value	1.0e-17
Match length	51
% identity	75
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]
Seq. No.	285398
Contig ID	166159_1.R1011
5'-most EST	uC-zmflb73325c08a1
Seq. No.	285399
Contig ID	166161_1.R1011
5'-most EST	uC-zmflb73197h07a1
Seq. No.	285400
Contig ID	166232_1.R1011
5'-most EST	uC-zmflb73203b02a1
Method	BLASTX
NCBI GI	g2244749
BLAST score	724
E value	8.0e-77
Match length	172
% identity	79
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	285401
Contig ID	166258_1.R1011
5'-most EST	uC-zmflb73203e06a1

Seq. No.	285402
Contig ID	166280_1.R1011
5'-most EST	uC-zmflb73203h01a1
Method	BLASTX
NCBI GI	g3763934
BLAST score	326
E value	5.0e-30
Match length	125
% identity	51
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285403
Contig ID	166305_1.R1011
5'-most EST	uC-zmflb73204c02a1
Method	BLASTX
NCBI GI	g1722839
BLAST score	166
E value	2.0e-11
Match length	72
% identity	43
NCBI Description	WEE1-LIKE PROTEIN KINASE >gi_1041819 (U17223) Wee1 kinase [Drosophila melanogaster]

Seq. No.	285404
Contig ID	166309_1.R1011
5'-most EST	uC-zmflb73204c06a1

Seq. No.	285405
Contig ID	166320_1.R1011
5'-most EST	uC-zmflb73238d10a1

Seq. No.	285406
Contig ID	166328_1.R1011
5'-most EST	uC-zmflb73204e03a1
Method	BLASTX
NCBI GI	g3298441
BLAST score	410
E value	4.0e-40
Match length	127
% identity	59
NCBI Description	(AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]

Seq. No.	285407
Contig ID	166332_1.R1011
5'-most EST	gct701176635.h1

Seq. No.	285408
Contig ID	166333_1.R1011
5'-most EST	uC-zmflb73204e11a1

Seq. No.	285409
Contig ID	166341_1.R1011

5'-most EST	uC-zmflb73204f11a1
Seq. No.	285410
Contig ID	166350_1.R1011
5'-most EST	uC-zmflb73204h02a1
Seq. No.	285411
Contig ID	166370_1.R1011
5'-most EST	uC-zmflb73205b03b2
Seq. No.	285412
Contig ID	166396_1.R1011
5'-most EST	uC-zmflb73205f05b2
Seq. No.	285413
Contig ID	166411_1.R1011
5'-most EST	uC-zmflb73205h04b2
Seq. No.	285414
Contig ID	166427_1.R1011
5'-most EST	uC-zmflb73206b02a2
Method	BLASTX
NCBI GI	g2947063
BLAST score	150
E value	1.0e-09
Match length	113
% identity	39
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]
Seq. No.	285415
Contig ID	166431_1.R1011
5'-most EST	uC-zmflb73206b06a2
Seq. No.	285416
Contig ID	166484_1.R1011
5'-most EST	uC-zmflb73207f11a1
Method	BLASTX
NCBI GI	g3860763
BLAST score	189
E value	5.0e-22
Match length	101
% identity	58
NCBI Description	(AJ235270) ADRENODOXIN PRECURSOR (adx1) [Rickettsia prowazekii]
Seq. No.	285417
Contig ID	166502_1.R1011
5'-most EST	tfd700573369.h1
Seq. No.	285418
Contig ID	166517_1.R1011
5'-most EST	uC-zmflb73208b06a1
Method	BLASTN
NCBI GI	g22183
BLAST score	219
E value	1.0e-120

Match length	235
% identity	98
NCBI Description	Maize mRNA for beta 2 tubulin

Seq. No.	285419
Contig ID	166530_1.R1011
5'-most EST	uC-zmflb73208c08a2

Seq. No.	285420
Contig ID	166560_1.R1011
5'-most EST	uC-zmflb73208e01a1

Seq. No.	285421
Contig ID	166561_1.R1011
5'-most EST	uC-zmflb73208e02a1

Seq. No.	285422
Contig ID	166589_1.R1011
5'-most EST	uC-zmflb73208g08a1
Method	BLASTX
NCBI GI	g1362162
BLAST score	724
E value	8.0e-77
Match length	175
% identity	72
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	285423
Contig ID	166591_1.R1011
5'-most EST	uC-zmflb73208g09a2

Seq. No.	285424
Contig ID	166593_1.R1011
5'-most EST	uC-zmflb73208g11a2
Method	BLASTX
NCBI GI	g1170621
BLAST score	210
E value	1.0e-16
Match length	51
% identity	75
NCBI Description	KINESIN-LIKE PROTEIN C >gi_1084342_pir__S48020 kinesin-related protein katC - Arabidopsis thaliana >gi_1438844_dbj_BAA04674_ (D21138) heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana]

Seq. No.	285425
Contig ID	166594_1.R1011
5'-most EST	uC-zmromo17102c09a1

Seq. No.	285426
Contig ID	166606_1.R1011
5'-most EST	uC-zmflb73250d11a2

Seq. No.	285427
Contig ID	166608_1.R1011
5'-most EST	uC-zmflb73210b04a1

Method	BLASTX
NCBI GI	g4586021
BLAST score	791
E value	1.0e-84
Match length	170
% identity	88
NCBI Description	(AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No.	285428
Contig ID	166625_1.R1011
5'-most EST	wyr700240018.h1
Method	BLASTX
NCBI GI	g3386604
BLAST score	196
E value	6.0e-15
Match length	71
% identity	58
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	285429
Contig ID	166672_1.R1011
5'-most EST	uC-zmflb73210h12a1

Seq. No.	285430
Contig ID	166677_1.R1011
5'-most EST	uC-zmflmo17215h05a1

Seq. No.	285431
Contig ID	166682_1.R1011
5'-most EST	uC-zmflb73211b01a2

Seq. No.	285432
Contig ID	166690_1.R1011
5'-most EST	uC-zmflb73211b12a2

Seq. No.	285433
Contig ID	166698_1.R1011
5'-most EST	uC-zmflb73211c11a2
Method	BLASTX
NCBI GI	g2739379
BLAST score	168
E value	8.0e-12
Match length	48
% identity	65
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285434
Contig ID	166703_1.R1011
5'-most EST	uC-zmflb73211d08a2

Seq. No.	285435
Contig ID	166729_1.R1011
5'-most EST	uC-zmflb73211g05a2

Seq. No.	285436
Contig ID	166740_1.R1011

5'-most EST	uwn700281794.h1
Seq. No.	285437
Contig ID	166748_1.R1011
5'-most EST	uC-zmflb73212a09a1
Seq. No.	285438
Contig ID	166769_1.R1011
5'-most EST	uC-zmflb73212d04a1
Seq. No.	285439
Contig ID	166770_1.R1011
5'-most EST	uC-zmflb73212d06a1
Seq. No.	285440
Contig ID	166774_1.R1011
5'-most EST	uC-zmflb73212d12a1
Method	BLASTX
NCBI GI	g4585999
BLAST score	198
E value	2.0e-15
Match length	71
% identity	55
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	285441
Contig ID	166784_1.R1011
5'-most EST	uC-zmflb73212f05a1
Seq. No.	285442
Contig ID	166791_1.R1011
5'-most EST	uC-zmflb73212g11a1
Method	BLASTN
NCBI GI	g1617473
BLAST score	411
E value	0.0e+00
Match length	451
% identity	98
NCBI Description	Z.mays mRNA for Rb1 protein
Seq. No.	285443
Contig ID	166817_1.R1011
5'-most EST	uC-zmflb73213b04b1
Method	BLASTX
NCBI GI	g3668092
BLAST score	474
E value	1.0e-47
Match length	117
% identity	79
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	285444
Contig ID	166826_1.R1011
5'-most EST	uC-zmflb73213b10a1
Method	BLASTX
NCBI GI	g2623783
BLAST score	586

E value	1.0e-60
Match length	131
% identity	83
NCBI Description	(AF030166) glucanase [Oryza sativa]

Seq. No.	285445
Contig ID	166831_1.R1011
5'-most EST	xmt700264904.h1

Seq. No.	285446
Contig ID	166838_1.R1011
5'-most EST	uC-zmflb73299h05a1

Seq. No.	285447
Contig ID	166843_1.R1011
5'-most EST	uC-zmflb73213c11a1

Seq. No.	285448
Contig ID	166870_1.R1011
5'-most EST	nbm700466810.h1
Method	BLASTX
NCBI GI	g2129553
BLAST score	353
E value	4.0e-34
Match length	73
% identity	90
NCBI Description	calcium-dependent protein kinase 6 - Arabidopsis thaliana

Seq. No.	285449
Contig ID	166888_1.R1011
5'-most EST	gct701167593.h1

Seq. No.	285450
Contig ID	166899_1.R1011
5'-most EST	uC-zmflb73215d05a2

Seq. No.	285451
Contig ID	166916_1.R1011
5'-most EST	uC-zmflb73213g08a1

Seq. No.	285452
Contig ID	166930_1.R1011
5'-most EST	uC-zmflb73213h05b1

Seq. No.	285453
Contig ID	166932_1.R1011
5'-most EST	uC-zmflb73213h09a1
Method	BLASTX
NCBI GI	g4585925
BLAST score	227
E value	1.0e-18
Match length	71
% identity	65
NCBI Description	(AC007211) unknown protein [Arabidopsis thaliana]

Seq. No.	285454
Contig ID	166994_1.R1011

5'-most EST	uC-zmflb73215b12a2
Method	BLASTX
NCBI GI	g3341697
BLAST score	176
E value	1.0e-12
Match length	73
% identity	49
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285455
Contig ID	166998_1.R1011
5'-most EST	uC-zmflmo17157e01a1

Seq. No.	285456
Contig ID	167036_1.R1011
5'-most EST	uC-zmflb73308h09a1

Seq. No.	285457
Contig ID	167040_1.R1011
5'-most EST	uC-zmflb73215g10a2
Method	BLASTX
NCBI GI	g4371293
BLAST score	150
E value	1.0e-09
Match length	78
% identity	49
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	285458
Contig ID	167071_1.R1011
5'-most EST	nbm700477989.h1

Seq. No.	285459
Contig ID	167090_1.R1011
5'-most EST	uC-zmflb73216d11b2
Method	BLASTX
NCBI GI	g4102600
BLAST score	939
E value	1.0e-102
Match length	193
% identity	90
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	285460
Contig ID	167106_1.R1011
5'-most EST	uC-zmflb73230d04b2
Method	BLASTX
NCBI GI	g1871192
BLAST score	273
E value	5.0e-24
Match length	160
% identity	42
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	285461
Contig ID	167137_1.R1011

5'-most EST	uC-zmflb73217a10b2
Seq. No.	285462
Contig ID	167145_1.R1011
5'-most EST	uC-zmflb73217b08b2
Seq. No.	285463
Contig ID	167218_1.R1011
5'-most EST	dyk700102787.h1
Seq. No.	285464
Contig ID	167225_1.R1011
5'-most EST	uC-zmflb73218b11b2
Method	BLASTX
NCBI GI	g4239692
BLAST score	735
E value	4.0e-78
Match length	170
% identity	74
NCBI Description	(AJ132745) hypothetical protein [Arabidopsis thaliana]
Seq. No.	285465
Contig ID	167320_1.R1011
5'-most EST	ymt700218845.h1
Method	BLASTX
NCBI GI	g4406780
BLAST score	211
E value	1.0e-16
Match length	41
% identity	85
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]
Seq. No.	285466
Contig ID	167348_1.R1011
5'-most EST	uC-zmflb73220c07b2
Method	BLASTX
NCBI GI	g1561575
BLAST score	156
E value	2.0e-10
Match length	50
% identity	62
NCBI Description	(Y08273) cyclophilin [Digitalis lanata]
Seq. No.	285467
Contig ID	167357_1.R1011
5'-most EST	uC-zmflb73220d10b2
Method	BLASTX
NCBI GI	g4323296
BLAST score	370
E value	2.0e-35
Match length	136
% identity	58
NCBI Description	(AF099095) pulvinus inward-rectifying channel for potassium SPICK1 [Samanea saman]
Seq. No.	285468

Contig ID	167370_1.R1011
5'-most EST	uC-zmflb73220f05b2
Method	BLASTX
NCBI GI	g4335762
BLAST score	236
E value	2.0e-19
Match length	151
% identity	36
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	285469
Contig ID	167391_1.R1011
5'-most EST	dhd700l98033.h1

Seq. No.	285470
Contig ID	167404_1.R1011
5'-most EST	uC-zmflb73221b09a2
Method	BLASTX
NCBI GI	g3426048
BLAST score	265
E value	4.0e-23
Match length	66
% identity	79
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	285471
Contig ID	167414_1.R1011
5'-most EST	uC-zmflb73221d04a2
Method	BLASTX
NCBI GI	g2655098
BLAST score	169
E value	9.0e-13
Match length	81
% identity	54
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	285472
Contig ID	167496_1.R1011
5'-most EST	uC-zmflmo17263b04a2

Seq. No.	285473
Contig ID	167523_1.R1011
5'-most EST	fdz701l58755.h1
Method	BLASTX
NCBI GI	g3080396
BLAST score	382
E value	1.0e-36
Match length	99
% identity	70
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	285474
Contig ID	167549_1.R1011
5'-most EST	gct701l68815.h1
Method	BLASTX
NCBI GI	g1001939

BLAST score	436
E value	3.0e-43
Match length	176
% identity	48
NCBI Description	(U13152) guanine nucleotide-binding protein beta 5 [Mesocricetus auratus]

Seq. No.	285475
Contig ID	167551_1.R1011
5'-most EST	uC-zmflb73223d11b2
Method	BLASTX
NCBI GI	g3047114
BLAST score	457
E value	3.0e-45
Match length	112
% identity	69
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	285476
Contig ID	167562_1.R1011
5'-most EST	uC-zmflb73223e11b2

Seq. No.	285477
Contig ID	167607_1.R1011
5'-most EST	uC-zmflmo17172g07a1

Seq. No.	285478
Contig ID	167609_1.R1011
5'-most EST	uC-zmflb73224b05b1
Method	BLASTX
NCBI GI	g2500624
BLAST score	1440
E value	1.0e-160
Match length	290
% identity	98
NCBI Description	DNA-DIRECTED RNA POLYMERASE DELTA CHAIN >gi_1652442_dbj_BAA17364_ (D90905) RNA polymerase beta prime subunit [Synechocystis sp.]

Seq. No.	285479
Contig ID	167610_1.R1011
5'-most EST	uC-zmflb73224b07a1

Seq. No.	285480
Contig ID	167614_1.R1011
5'-most EST	uC-zmflb73224c01b1
Method	BLASTX
NCBI GI	g1001574
BLAST score	626
E value	5.0e-65
Match length	126
% identity	94
NCBI Description	(D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	285481
Contig ID	167620_1.R1011
5'-most EST	uC-zmflb73224c07b1

Method	BLASTN
NCBI GI	g1652844
BLAST score	642
E value	0.0e+00
Match length	674
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418

Seq. No.	285482
Contig ID	167624_1.R1011
5'-most EST	uC-zmflb73245g01a1

Seq. No.	285483
Contig ID	167633_1.R1011
5'-most EST	uC-zmflb73224e10b1
Method	BLASTN
NCBI GI	g1001200
BLAST score	514
E value	0.0e+00
Match length	526
% identity	99
NCBI Description	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766

Seq. No.	285484
Contig ID	167640_1.R1011
5'-most EST	uC-zmflmo17228g12a1

Seq. No.	285485
Contig ID	167667_1.R1011
5'-most EST	kem700610993.h1
Method	BLASTN
NCBI GI	g342633
BLAST score	161
E value	3.0e-85
Match length	190
% identity	95
NCBI Description	Maize mitochondrial ATP-alpha gene encoding F1-ATPase alpha subunit, complete cds

Seq. No.	285486
Contig ID	167690_1.R1011
5'-most EST	uC-zmflb73225f09a1

Seq. No.	285487
Contig ID	167712_1.R1011
5'-most EST	uC-zmflb73305d10a1

Seq. No.	285488
Contig ID	167722_1.R1011
5'-most EST	uC-zmflb73226c10a1
Method	BLASTX
NCBI GI	g4510348
BLAST score	319
E value	2.0e-29
Match length	116

% identity 52
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 285489
Contig ID 167749_1.R1011
5'-most EST uC-zmflb73227a02a1

Seq. No. 285490
Contig ID 167758_1.R1011
5'-most EST uC-zmflb73227b01a1

Seq. No. 285491
Contig ID 167758_2.R1011
5'-most EST hvj700619506.h1

Seq. No. 285492
Contig ID 167802_1.R1011
5'-most EST uC-zmflb73227f10a1

Seq. No. 285493
Contig ID 167815_1.R1011
5'-most EST uC-zmflb73227h05a1
Method BLASTX
NCBI GI g4522009
BLAST score 691
E value 1.0e-72
Match length 273
% identity 47
NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 285494
Contig ID 167817_1.R1011
5'-most EST uC-zmflb73227h08a1

Seq. No. 285495
Contig ID 167842_1.R1011
5'-most EST uC-zmflb73228c04a1

Seq. No. 285496
Contig ID 167846_1.R1011
5'-most EST wyr700242305.h1

Seq. No. 285497
Contig ID 167848_1.R1011
5'-most EST uC-zmflb73228c12a1
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 285498
Contig ID 167856_1.R1011
5'-most EST nbm700472380.h1
Method BLASTX

NCBI GI g4432848
BLAST score 266
E value 5.0e-23
Match length 74
% identity 72
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 285499
Contig ID 167867_1.R1011
5'-most EST uC-zmflmo17060f02a1

Seq. No. 285500
Contig ID 167881_1.R1011
5'-most EST uC-zmromo17017c07a1

Seq. No. 285501
Contig ID 167892_1.R1011
5'-most EST xyt700346081.h1
Method BLASTX
NCBI GI g3786000
BLAST score 327
E value 4.0e-30
Match length 180
% identity 46
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 285502
Contig ID 167962_1.R1011
5'-most EST uC-zmflb73230d07b2

Seq. No. 285503
Contig ID 167962_2.R1011
5'-most EST xmt700258580.h1

Seq. No. 285504
Contig ID 167975_1.R1011
5'-most EST uC-zmflb73230e11b2

Seq. No. 285505
Contig ID 167978_1.R1011
5'-most EST uC-zmflb73230f02b2
Method BLASTX
NCBI GI g4508068
BLAST score 148
E value 2.0e-09
Match length 43
% identity 70
NCBI Description (AC005882) 3063 [Arabidopsis thaliana]

Seq. No. 285506
Contig ID 168015_1.R1011
5'-most EST uC-zmflmo17371d02a1

Seq. No. 285507
Contig ID 168025_1.R1011
5'-most EST uC-zmflmo17408a04a1

Seq. No.	285508
Contig ID	168042_1.R1011
5'-most EST	uC-zmflb73234a03b2

Seq. No.	285509
Contig ID	168049_1.R1011
5'-most EST	uC-zmflb73244a08b2
Method	BLASTX
NCBI GI	g2129635
BLAST score	308
E value	4.0e-28
Match length	146
% identity	46
NCBI Description	light repressible receptor protein kinase - Arabidopsis thaliana >gi_1321686_emb_CAA66376_ (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No.	285510
Contig ID	168067_1.R1011
5'-most EST	nbm700476129.h1
Method	BLASTN
NCBI GI	g2735839
BLAST score	281
E value	1.0e-157
Match length	452
% identity	91
NCBI Description	Sorghum bicolor ADP-glucose pyrophosphorylase subunit SH2, transcriptional regulator, NADPH-dependent reductase A1-a and NADPH-dependent reductase A1-b genes, complete cds

Seq. No.	285511
Contig ID	168137_1.R1011
5'-most EST	uC-zmflmo17058d11a1

Seq. No.	285512
Contig ID	168172_1.R1011
5'-most EST	uC-zmflb73235f07b2

Seq. No.	285513
Contig ID	168189_1.R1011
5'-most EST	xdb700338212.h1

Seq. No.	285514
Contig ID	168208_1.R1011
5'-most EST	uC-zmflb73236b07a1
Method	BLASTX
NCBI GI	g3201627
BLAST score	173
E value	2.0e-12
Match length	48
% identity	56
NCBI Description	(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	285515
Contig ID	168208_2.R1011
5'-most EST	uC-zmflmo17171h12a1
Method	BLASTX

NCBI GI g3201627
BLAST score 247
E value 5.0e-21
Match length 64
% identity 64
NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 285516
Contig ID 168214_1.R1011
5'-most EST uC-zmflmo17359c10a1

Seq. No. 285517
Contig ID 168219_1.R1011
5'-most EST uC-zmflb73236c09a1

Seq. No. 285518
Contig ID 168224_1.R1011
5'-most EST uC-zmflmo17213f01a1

Seq. No. 285519
Contig ID 168236_1.R1011
5'-most EST uC-zmflb73236e07a1

Seq. No. 285520
Contig ID 168320_1.R1011
5'-most EST ntr700074763.h1

Seq. No. 285521
Contig ID 168331_1.R1011
5'-most EST uC-zmflb73238a01a1

Seq. No. 285522
Contig ID 168334_1.R1011
5'-most EST uC-zmflb73238a03b2

Seq. No. 285523
Contig ID 168343_1.R1011
5'-most EST uC-zmflb73238a09b2

Seq. No. 285524
Contig ID 168347_1.R1011
5'-most EST uC-zmflb73238b01a1

Seq. No. 285525
Contig ID 168364_1.R1011
5'-most EST uC-zmflb73238c01a1

Seq. No. 285526
Contig ID 168379_1.R1011
5'-most EST zvd700460569.h1
Method BLASTX
NCBI GI g3776023
BLAST score 233
E value 3.0e-19
Match length 74
% identity 62
NCBI Description (AJ010473) RNA helicase [Arabidopsis thaliana]

Seq. No.	285527
Contig ID	168393_1.R1011
5'-most EST	uC-zmflmo17160c09a1
Method	BLASTX
NCBI GI	g1209703
BLAST score	279
E value	8.0e-25
Match length	75
% identity	60
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	285528
Contig ID	168430_1.R1011
5'-most EST	uC-zmflb73238f08a1

Seq. No.	285529
Contig ID	168445_1.R1011
5'-most EST	uC-zmflb73238g04a1
Method	BLASTX
NCBI GI	g4567308
BLAST score	184
E value	2.0e-13
Match length	58
% identity	52
NCBI Description	(AC005956) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	285530
Contig ID	168447_1.R1011
5'-most EST	uC-zmflb73238g05a1

Seq. No.	285531
Contig ID	168461_1.R1011
5'-most EST	uC-zmflb73238h04a1
Method	BLASTX
NCBI GI	g2435522
BLAST score	232
E value	4.0e-19
Match length	86
% identity	51
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No.	285532
Contig ID	168472_1.R1011
5'-most EST	uC-zmflb73402b09a2

Seq. No.	285533
Contig ID	168508_1.R1011
5'-most EST	uC-zmflb73239b12b2

Seq. No.	285534
Contig ID	168516_2.R1011
5'-most EST	uC-zmromo17031c05a1

Seq. No.	285535

Contig ID 168598_1.R1011
5'-most EST uC-zmflb73239h07b2

Seq. No. 285536
Contig ID 168601_1.R1011
5'-most EST ymt700222155.h1

Seq. No. 285537
Contig ID 168651_1.R1011
5'-most EST uC-zmflb73297e01a1
Method BLASTN
NCBI GI g4468795
BLAST score 91
E value 1.0e-43
Match length 211
% identity 93
NCBI Description Zea mays mRNA for glutathione transferase GST6

Seq. No. 285538
Contig ID 168665_1.R1011
5'-most EST uC-zmflb73303c01a2

Seq. No. 285539
Contig ID 168666_1.R1011
5'-most EST cyk700050281.f1

Seq. No. 285540
Contig ID 168674_1.R1011
5'-most EST uC-zmflb73280c07a1

Seq. No. 285541
Contig ID 168675_1.R1011
5'-most EST uC-zmflmo17202b07a1

Seq. No. 285542
Contig ID 168678_1.R1011
5'-most EST uC-zmflb73240h04a2

Seq. No. 285543
Contig ID 168680_1.R1011
5'-most EST uC-zmflmo17351d10a1

Seq. No. 285544
Contig ID 168716_1.R1011
5'-most EST wyr700244080.h1
Method BLASTX
NCBI GI g2739168
BLAST score 378
E value 3.0e-36
Match length 126
% identity 55
NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No. 285545
Contig ID 168720_1.R1011
5'-most EST uC-zmflb73241e03b2

Seq. No. 285546
Contig ID 168739_1.R1011
5'-most EST uC-zmflb73349f06a2
Method BLASTX
NCBI GI g3068713
BLAST score 146
E value 7.0e-13
Match length 90
% identity 56
NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 285547
Contig ID 168769_1.R1011
5'-most EST uC-zmflb73242a07a1

Seq. No. 285548
Contig ID 168803_1.R1011
5'-most EST uC-zmflb73242b11b1

Seq. No. 285549
Contig ID 168818_1.R1011
5'-most EST uC-zmflb73242c08a1

Seq. No. 285550
Contig ID 168823_1.R1011
5'-most EST qmh700030656.f1

Seq. No. 285551
Contig ID 168824_1.R1011
5'-most EST tzu700206667.h1

Seq. No. 285552
Contig ID 168829_1.R1011
5'-most EST qmh700028885.f1

Seq. No. 285553
Contig ID 168867_1.R1011
5'-most EST uC-zmflb73242e08b1

Seq. No. 285554
Contig ID 168886_1.R1011
5'-most EST uC-zmflb73242f03b2
Method BLASTX
NCBI GI g2760830
BLAST score 264
E value 4.0e-23
Match length 74
% identity 66
NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 285555
Contig ID 168911_1.R1011
5'-most EST uC-zmflb73242g02b2
Method BLASTX
NCBI GI g1888357

BLAST score	623
E value	5.0e-65
Match length	161
% identity	73
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	285556
Contig ID	168916_1.R1011
5'-most EST	uC-zmflmo17183d09a1

Seq. No.	285557
Contig ID	168917_1.R1011
5'-most EST	uC-zmflb73242g04b1

Seq. No.	285558
Contig ID	168942_2.R1011
5'-most EST	uC-zmflb73242h02b2
Method	BLASTX
NCBI GI	g3193330
BLAST score	162
E value	5.0e-21
Match length	100
% identity	58
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	285559
Contig ID	168942_3.R1011
5'-most EST	uC-zmflb73242h07a1

Seq. No.	285560
Contig ID	168957_1.R1011
5'-most EST	uC-zmflb73242h08b1

Seq. No.	285561
Contig ID	168977_1.R1011
5'-most EST	uC-zmflb73243b05a1

Seq. No.	285562
Contig ID	169000_1.R1011
5'-most EST	tfd700573764.h1

Seq. No.	285563
Contig ID	169016_1.R1011
5'-most EST	uC-zmflb73243f04a1

Seq. No.	285564
Contig ID	169043_1.R1011
5'-most EST	uC-zmflmo17367b11a1

Seq. No.	285565
Contig ID	169055_1.R1011
5'-most EST	ypc700806313.h1
Method	BLASTX
NCBI GI	g3257262